

Feb 20 09:21:41 2003

GenCore version 5.1.3
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OM protein - protein search, using sw model
February 15, 2003, 16:56:00 ; Search time 24.5 Seconds
(without alignments)
1765.734 Million cell updates/sec

Run on:

US-09-636-259b-3

Title: 2381
Sequence: 1 MGSLOPDGAGNANWNGTEAPG.....HDFRRAFKILCRGDRKRIV 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Minimum DB seq length: 2000000000
Maximum DB seq length: 0
Maximum Match 0%
Post-processing: Minimum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2227	93.5	450	2 A38316	alpha-2A-adrenergic
2	2222	93.3	450	2 A34169	alpha-2-adrenergic
3	2199	92.4	450	2 I49481	alpha-2-adrenergic
4	2132	89.5	450	2 B40392	alpha-2-adrenergic
5	2111	88.7	450	2 JH0190	alpha-2-adrenergic
6	1175	49.3	458	2 A40392	alpha-2-adrenergic
7	1169	49.1	458	2 I49480	alpha-2A-adrenergic
8	1169	49.1	458	2 A37869	alpha-2C-adrenergic
9	1165.5	49.0	452	2 I50829	alpha-2B-adrenergic
10	1130.5	47.3	450	2 A37223	alpha-2C-adrenergic
11	1125.5	46.6	455	2 I35821	alpha-2B-adrenergic
12	1119.5	46.1	453	2 A35642	alpha-2B-adrenergic
13	1110.5	45.3	453	2 S58868	serotonin receptor
14	1098.5	44.1	453	2 S58868	serotonin receptor
15	693.5	28.1	379	2 JCS042	G protein-coupled
16	681.5	28.6	379	2 JCS042	tyramine receptor
17	651	27.3	476	2 S12004	octopamine receptor
18	648	27.2	601	2 JH0170	dopamine receptor
19	648	27.2	601	2 JH0170	dopamine receptor
20	629	26.4	444	1 DYH022	dopamine receptor
21	626.5	25.3	444	1 DYH022	dopamine receptor
22	616	25.9	444	1 S08146	dopamine receptor
23	616	25.9	444	1 S08146	dopamine receptor
24	612	25.7	511	2 C56849	G protein-coupled
25	611	25.7	511	2 C56849	G protein-coupled
26	596.5	25.1	442	2 DYX1D2	dopamine receptor
27	596.5	25.1	442	2 DYX1D2	hypothetical prote
28	594	24.9	422	2 I38209	serotonin receptor

us-09-636-259b-3.rpt

30	586.5	24.6	377	2 S68423	serotonin receptor
31	585.5	24.6	377	2 A53279	serotonin receptor
32	585	24.6	421	2 I49375	serotonin receptor
33	578.5	24.3	514	2 D56849	dopamine receptor
34	577.5	24.3	390	2 JH0268	serotonin receptor
35	577	24.2	422	2 JH0315	alpha-1B-adrenergic
36	573.5	24.1	517	2 A45121	serotonin receptor
37	564	23.7	374	2 I77467	serotonin receptor
38	563	23.6	564	2 S68422	serotonin receptor
39	561.5	23.6	389	2 DYH044	dopamine receptor
40	561	23.5	387	2 A40491	alpha-1-adrenergic
41	560	23.5	515	2 S58126	serotonin receptor
42	559.5	23.4	390	2 A42688	serotonin receptor
43	558	23.4	501	2 I18863	hypothetical prote
44	557.5	23.4	515	2 JCS125	alpha-1B-adrenergic
45	556.5	23.4	515	2 JCS125	alpha-1B-adrenergic

ALIGNMENTS

RESULT 1	A38316	alpha-2-adrenergic receptor - pig
C:Species	Sus scrofa domestica (domestic pig) 1993	#text_change 13-Aug-1999
C:Date	22-Jan-1993	#sequence_revision 22-Jan-1993
C:Accession	A38316	
R:Guyer, C.A.; Horstman, D.A.; Wilson, A.L.; Clark, J.D.; Craige Jr., E.J.; Limbird, J. Biol. Chem. 265, 17307-17317, 1990		
A:Title	Cloning, sequencing, and expression of the gene encoding the porcine alpha-2	
A:Reference number	A38316; M01D:9109167; PMID:2170371	
A:Accession	A38316	
A:Molecule type	DNA	
A:Residues	1-450 <GB>	
A:Cross-reference	vertebrate rhodopsin	
A:Superfamily	vertebrate rhodopsin	
C:Keywords	G protein-coupled receptor; glycoprotein; transmembrane protein	
Query Match	93.5% Score 2227; DB 2; Length 450;	
Best Local Similarity	94.0% 3; Mismatches 24; Indels 0; Gaps 0;	
Matches	423; Conservative	
1	MGSLOPDGAGNANWNGTEAPGAGARATPSLOYTLVLCAGLMLTFTVGNVLIIVFT	60
1	MGSLOPDGAGNANWNGTEAPGAGARATPSLOYTLVLCAGLMLTFTVGNVLIIVFT	60
61	SRALKAPONLFLVSLASADIVATLVIPSLANEMGWYFGKMCETIYALDVLCTSS	120
61	SRALKAPONLFLVSLASADIVATLVIPSLANEMGWYFGKMCETIYALDVLCTSS	120
121	IYHICATSLDRWYSITQALEYNLKRTPRRIKAITTWYISAVISFPLISIEKKGSGG	180
121	IYHICATSLDRWYSITQALEYNLKRTPRRIKAITTWYISAVISFPLISIEKKGSGG	180
121	IYHICATSLDRWYSITQALEYNLKRTPRRIKAITTWYISAVISFPLISIEKKGSGG	240
181	POPAPREINDOKWYVYSSICISFPAPCLIMLVYVYIYQIAKRTTVPSPRRGPDAA	240
181	POPAPREINDOKWYVYSSICISFPAPCLIMLVYVYIYQIAKRTTVPSPRRGPDAA	300
181	POPAPREINDOKWYVYSSICISFPAPCLIMLVYVYIYQIAKRTTVPSPRRGPDAA	300
241	APPGTEPRPNIGPERSAGPGGAEPPLPTONGAPGPAAGPRTDMLDESSSSD	300
241	APPGTEPRPNIGPERSAGPGGAEPPLPTONGAPGPAAGPRTDMLDESSSSD	360
241	APPGTEPRPNIGPERSAGPGGAEPPLPTONGAPGPAAGPRTDMLDESSSSD	360
301	HAERPGRPRERPGKRGKARASOVKPGSILPRGCGATGTGTPAAGGREGVGAAS	360
301	HAERPGRPRERPGKRGKARASOVKPGSILPRGCGATGTGTPAAGGREGVGAAS	420
301	HAERPGRPRERPGKRGKARASOVKPGSILPRGCGATGTGTPAAGGREGVGAAS	420
361	RMRGRONRKRRTYVLAIVGVVCPFFFTYTLTVAGCSVPRTLKFFFWFCNNS	420
361	RMRGRONRKRRTYVLAIVGVVCPFFFTYTLTVAGCSVPRTLKFFFWFCNNS	480
421	LNPIYITTFNHDFRRAFKILCRGDRKRIV	450
421	LNPIYITTFNHDFRRAFKILCRGDRKRIV	450

RESULT 2

A34169

alpha-2A-adrenergic receptor - human
N:Alternate names: alpha-2C10-adrenergic receptor
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence

R:Accession: A34169; revision 22-Jan-1993 #text_change 29-Oct-1999
J: Biol. Chem. 264, 11754-11761, 1989
A:Title: Cloning, sequence analysis, and permanent expression of a human alpha2-adrenergic
cycloase attenuator and activation

A:Accession number: A34169; MUID:89308571; PMID:256836
A:Residues: 1-450 <FRA>
A:Molecule type: DNA

A:Cross-references: GB:M23533; NID:9178195; PID:AAA51665.1; PID:9178196
R:Koblika, B.R.; Matsui, H.; Koblika, T.S.; Yang-Feng, T.L.; Francke, U.; Caron, M.G.;
Science 238, 650-656, 1987
A:Title: Cloning, sequencing, and expression of the gene coding for the human platelet
A:Reference number: A40132; MUID:88042789; PMID:2823383
A:Accession: A40132
A:Molecule type: DNA

A:Residues: 1-103, 'T', 105-156, 'C', 158-367, 'L', 369-450 <ROB>
A:Cross-references: GB:M18415; NID:9178191; PID:AAA51664.1; PID:9178192
R:Chhajlani, V.; Rangell, N.; Uhlen, S.; Wikberg, J.E.S.
FEBS Lett. 280, 241-244, 1991
A:Title: Identification of an additional gene belonging to the alpha(2) adrenergic recep

A:Accession number: S14308; MUID:91192139; PMID:1849483
A:Molecule type: DNA
A:Residues: 77-123, 'P', 125-209 <CHN>
A:Gene: GDB:ADRA2A; ADRAR: ADRA2; ADRA2R
A:Cross-references: GDB:120538; OMIM:104210
A:Map position: 10q25-10q25
A:Introns: #status absent
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match
Best Local Similarity 93.3%; Score 2222; DB 2; Length 450;
Matches 425; Conservative 1; Mismatches 24; Indels 0; Gaps 0;

QY	1	MSGLQPDAGNSMNGTEAPGAGARATPYSLOVTLTLVCLAGLMLTLTVGNVLIIVAF	60
DB	1	MSGLQPDAGNSMNGTEAPGAGARATPYSLOVTLTLVCLAGLMLTLTVGNVLIIVAF	60
QY	61	SRALKAPQNLFLVSLASADIIATLVIPFSLANVGVWYFEGKMCETIYALDVLCTSS	120
DB	61	SRALKAPQNLFLVSLASADIIATLVIPFSLANVGVWYFEGKMCETIYALDVLCTSS	120
QY	121	IVHLCATISDRYWSITQAIENLKRPRRIKAIITVWISAVISFPLISTEKKGGGG	180
DB	121	IVHLCATISDRYWSITQAIENLKRPRRIKAIITVWISAVISFPLISTEKKGGGG	180
QY	181	POPAPRCEINDOKWYIYSSIGSFAPCLIMLIVYRIYQIAKRRTRPPSRGPDAA	240
DB	181	POPAPRCEINDOKWYIYSSIGSFAPCLIMLIVYRIYQIAKRRTRPPSRGPDAA	240
QY	241	APPGETERRRNGIGPERSAGPGAEAPLPTQINGAPGEPAPAGRDTDLDESSSSD	300
DB	241	APPGETERRRNGIGPERSAGPGAEAPLPTQINGAPGEPAPAGRDTDLDESSSSD	300
QY	301	HAERPGRPRRERGRGKARASQVKGDSLPBRGPGATIGTPAAGPEERVAAS	360
DB	301	HAERPGRPRRERGRGKARASQVKGDSLPBRGPGATIGTPAAGPEERVAAS	360
QY	361	RMRGRKRRRTFVLAVVIGVYVCMPEFFETVTLTAVGCVPTLKEFFFMGVCNNS	420
DB	361	RMRGRKRRRTFVLAVVIGVYVCMPEFFETVTLTAVGCVPTLKEFFFMGVCNNS	420

RESULT 3

I49481

alpha-2 adrenergic receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence
C:Accession: I49481
Mol. Pharmacol. 42, 16-27, 1992
A:Title: Cloning of two mouse genes encoding alpha-2 adrenergic receptor subtypes and
in antagonist binding.

A:Reference number: I49481; MUID:92342131; PMID:1353249
A:Accession: I49481
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-450 <RES>

A:Cross-references: GB:M99377; NID:9191882; PID:AAA37213.1; PID:9191883
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor

Query Match
Best Local Similarity 92.2%; Score 2199; DB 2; Length 450;
Matches 415; Conservative 8; Mismatches 27; Indels 0; Gaps 0;

QY	1	MSGLQPDAGNSMNGTEAPGAGARATPYSLOVTLTLVCLAGLMLTLTVGNVLIIVAF	60
DB	1	MSGLQPDAGNSMNGTEAPGAGARATPYSLOVTLTLVCLAGLMLTLTVGNVLIIVAF	60
QY	61	SRALKAPQNLFLVSLASADIIATLVIPFSLANVGVWYFEGKMCETIYALDVLCTSS	120
DB	61	SRALKAPQNLFLVSLASADIIATLVIPFSLANVGVWYFEGKMCETIYALDVLCTSS	120
QY	121	IVHLCATISDRYWSITQAIENLKRPRRIKAIITVWISAVISFPLISTEKKGGGG	180
DB	121	IVHLCATISDRYWSITQAIENLKRPRRIKAIITVWISAVISFPLISTEKKGGGG	180
QY	181	POPAPRCEINDOKWYIYSSIGSFAPCLIMLIVYRIYQIAKRRTRPPSRGPDAA	240
DB	181	POPAPRCEINDOKWYIYSSIGSFAPCLIMLIVYRIYQIAKRRTRPPSRGPDAA	240
QY	241	APPGETERRRNGIGPERSAGPGAEAPLPTQINGAPGEPAPAGRDTDLDESSSSD	300
DB	241	APPGETERRRNGIGPERSAGPGAEAPLPTQINGAPGEPAPAGRDTDLDESSSSD	300
QY	301	HAERPGRPRRERGRGKARASQVKGDSLPBRGPGATIGTPAAGPEERVAAS	360
DB	301	HAERPGRPRRERGRGKARASQVKGDSLPBRGPGATIGTPAAGPEERVAAS	360
QY	361	RMRGRKRRRTFVLAVVIGVYVCMPEFFETVTLTAVGCVPTLKEFFFMGVCNNS	420
DB	361	RMRGRKRRRTFVLAVVIGVYVCMPEFFETVTLTAVGCVPTLKEFFFMGVCNNS	420

RESULT 4

B40392

alpha-2-adrenergic receptor (clone RG10) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Dec-1991 #sequence
C:Accession: B40392
R:Blair, S.M.; Downing, S.; Duzic, E.; Homcy, C.J.
J. Biol. Chem. 266, 10470-10478, 1991
A:Title: Isolation of rat genomic clones encoding subtypes of the alpha-2-adrenergic
A:Reference number: A40392; MUID:91244823; PMID 1643530

Query Match
Best Local Similarity 92.4%; Score 2199; DB 2; Length 450;
Matches 415; Conservative 8; Mismatches 27; Indels 0; Gaps 0;

A:Accession: BA0392
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-450 <LAN>
 A:Cross-references: GB:M62372; NID:g206615; PIDN:AAA42034.1; PID:g206616
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 89.5%; Score 2132; DB 2; Length 450;
 Best Local Similarity 89.3%; Pred. No. 6e-130;
 Matches 404; Conservative 10; Mismatches 36; Indels 0; Gaps 0;

```

OY 1 MGSLOPDAGNSMNGTEAPGGGATPYSLQVTLTLVCLAGLMLTLVFGNVLIATFT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGSLOPDAGNSMNGTEAPGGGATPYSLQVTLTLVCLAGLMLTLVFGNVLIATFT 60

OY 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANFVGWYFGKAMCEIYALDVLCTSS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANFVGWYFGKAMCEIYALDVLCTSS 120

OY 121 IYHLCALISDRWYSTQAEYMLKTRPRRIKAIITVWISAVISFPPLISIEKKGGGG 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 IYHLCALISDRWYSTQAEYMLKTRPRRIKAIITVWISAVISFPPLISIEKKGGGG 180

OY 181 POBAEPCEINDQKWYVISSCIGSFAPCLIMILVYVRIYQIAKRRTVPSPRGPDVA 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 POBAEPCEINDQKWYVISSCIGSFAPCLIMILVYVRIYQIAKRRTVPSPRGPDVA 240

OY 241 APPGCTERRNGIGPERSAPGGAEPPLPTOLNAPGAPAPAGPRDLDLESSSSD 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 APPGCTERRNGIGPERSAPGGAEPPLPTOLNAPGAPAPAGPRDLDLESSSSD 300

OY 301 HAERPPGRRRNGIGPERSAPGGAEPPLPTOLNAPGAPAPAGPRDLDLESSSSD 360
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 HAERPPGRRRNGIGPERSAPGGAEPPLPTOLNAPGAPAPAGPRDLDLESSSSD 360

OY 361 RWRGRONREKRFETFLAVVIGVYVCMFPFFTYTLTAAGCSVPRTLFKFFMFGYCNS 420
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 RWRGRONREKRFETFLAVVIGVYVCMFPFFTYTLTAAGCSVPRTLFKFFMFGYCNS 420

OY 421 LNPVITYTFNHDFRRAFKILCRGDKRRIV 450
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 LNPVITYTFNHDFRRAFKILCRGDKRRIV 450

```

RESULT 5

JH0190
 A:Accession: JH0190
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-450 <CHN>
 A:Experimental source: brain
 C:Comment: Alpha-2-adrenergic receptor is a predominant catecholamine receptor. It mediates the effects of norepinephrine and epinephrine on the heart.
 C:Superfamily: G protein-coupled receptor; transmembrane protein
 C:Keywords: G protein-coupled receptor; transmembrane protein
 F:34-59/Domain: hydrophobic <HDI>
 F:71-96/Domain: hydrophobic <HDI>
 F:106-131/Domain: hydrophobic <HDI>
 F:150-175/Domain: hydrophobic <HDI>
 F:193-218/Domain: hydrophobic <HDI>
 F:375-400/Domain: hydrophobic <HDI>
 F:405-430/Domain: hydrophobic <HDI>

Query Match 88.7%; Score 2111; DB 2; Length 450;
 Best Local Similarity 89.3%; Pred. No. 1.3e-128;
 Matches 402; Conservative 9; Mismatches 39; Indels 0; Gaps 0;

```

OY 1 MGSLOPDAGNSMNGTEAPGGGATPYSLQVTLTLVCLAGLMLTLVFGNVLIATFT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGSLOPDAGNSMNGTEAPGGGATPYSLQVTLTLVCLAGLMLTLVFGNVLIATFT 60

OY 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANFVGWYFGKAMCEIYALDVLCTSS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANFVGWYFGKAMCEIYALDVLCTSS 120

OY 121 IYHLCALISDRWYSTQAEYMLKTRPRRIKAIITVWISAVISFPPLISIEKKGGGG 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 IYHLCALISDRWYSTQAEYMLKTRPRRIKAIITVWISAVISFPPLISIEKKGGGG 180

OY 181 POBAEPCEINDQKWYVISSCIGSFAPCLIMILVYVRIYQIAKRRTVPSPRGPDVA 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 POBAEPCEINDQKWYVISSCIGSFAPCLIMILVYVRIYQIAKRRTVPSPRGPDVA 240

OY 241 APPGCTERRNGIGPERSAPGGAEPPLPTOLNAPGAPAPAGPRDLDLESSSSD 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 APPGCTERRNGIGPERSAPGGAEPPLPTOLNAPGAPAPAGPRDLDLESSSSD 300

OY 301 HAERPPGRRRNGIGPERSAPGGAEPPLPTOLNAPGAPAPAGPRDLDLESSSSD 360
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 HAERPPGRRRNGIGPERSAPGGAEPPLPTOLNAPGAPAPAGPRDLDLESSSSD 360

OY 361 RWRGRONREKRFETFLAVVIGVYVCMFPFFTYTLTAAGCSVPRTLFKFFMFGYCNS 420
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 RWRGRONREKRFETFLAVVIGVYVCMFPFFTYTLTAAGCSVPRTLFKFFMFGYCNS 420

OY 421 LNPVITYTFNHDFRRAFKILCRGDKRRIV 450
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 LNPVITYTFNHDFRRAFKILCRGDKRRIV 450

```

RESULT 6

alpha-2-adrenergic receptor (clone Rg10) - rat
 A:Accession: A40392
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-458 <LAN>
 A:Cross-references: GB:M62371; NID:g206612; PIDN:AAA42033.1; PID:g206613
 C:Superfamily: G protein-coupled receptor; transmembrane protein
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 49.3%; Score 1175; DB 2; Length 458;
 Best Local Similarity 54.1%; Pred. No. 1.9e-68;
 Matches 252; Conservative 48; Mismatches 104; Indels 62; Gaps 12;

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OY 14 NGTEA-----PGGARAT-----PYSLOVTLTLVCLAGLMLTLVFGNVLIATFT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 14 NGTEA-----PGGARAT-----PYSLOVTLTLVCLAGLMLTLVFGNVLIATFT 60

OY 19 NGSADGEMSGSGGANASTDWCPPGQYSAGAVAGLAAYVGFIVFVGVNVLVIAVLT 78
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 19 NGSADGEMSGSGGANASTDWCPPGQYSAGAVAGLAAYVGFIVFVGVNVLVIAVLT 78

OY 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANFVGWYFGKAMCEIYALDVLCTSS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANFVGWYFGKAMCEIYALDVLCTSS 120

OY 121 IYHLCALISDRWYSTQAEYMLKTRPRRIKAIITVWISAVISFPPLISIEKKGGGG 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 IYHLCALISDRWYSTQAEYMLKTRPRRIKAIITVWISAVISFPPLISIEKKGGGG 180

OY 181 POBAEPCEINDQKWYVISSCIGSFAPCLIMILVYVRIYQIAKRRTVPSPRGPDVA 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 POBAEPCEINDQKWYVISSCIGSFAPCLIMILVYVRIYQIAKRRTVPSPRGPDVA 240

OY 241 APPGCTERRNGIGPERSAPGGAEPPLPTOLNAPGAPAPAGPRDLDLESSSSD 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 APPGCTERRNGIGPERSAPGGAEPPLPTOLNAPGAPAPAGPRDLDLESSSSD 300

```

```

Db 252 RDGASPTTENGIG--KAAGENGHCAPP-RREV-----EP-----DESSAAE 290
OY 301 HAERPPGRRRPRRGKRGKARASQVKGDSLPRRGGATGIGTPAAGPEERVGAAKAS 360
Db 291 RRRRGAVERKGRRRREGAGDGTGSADGPGGLAAEGGARTASRSP--GPGGRLSRASRS 348
OY 361 -----RMRGR-----QNRKRTFTFLAVVIGVFVVCWPFPPFFTYTLTAV---GC 401
Db 349 VEFPLSRRRRARSSVCRRKVAQAAREKRTFTFLAVVAGVFVLCWPFPPFFSYSLGICREAC 408
OY 402 SVPTLRFKFFFWFGYCNSSLNPVITYTTFNDRRAFKKILCRGDRK 447
Db 409 QLPFLRFKFFFWIGYCNSSLNPVITYTTFNDRFRSFKHILFRRRR 454

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RESULT 7

```

149480
alpha-2 adrenergic receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C:Accession: I49480
R:Link, R.: Dautt, D.; Barsh, G.S.; Chruscinski, A.; Kobilka, B.
Mol. Pharmacol. 42, 16-27, 1992
A:Title: Cloning of two mouse genes encoding alpha-2 adrenergic receptor subtypes and its
in antagonist binding.
A:Reference number: I49480; MUID:92342131; PMID:1353249
A:Accession: I49480
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-458 <RES>
A:Cross-references: GB:M99376; NID:g191880; PIDN:AAA37212.1; PID:g191881
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor

```

```

Query Match 49.3%; Score 1175; DB 2; Length 458;
Best Local Similarity 54.1%; Pred. No. 1,9e-68;
Matches 252; Conservative 48; Mismatches 104; Indels 62; Gaps 12;

```

```

OY 14 NGTEA----PGGARAT-----PYSIQVTLTVCLAGLMLTFVGNVLIYAVT 60
Db 19 NGSDAGEMSGGGANASGTDWVPPGQYSAGAVAGLAAVGFLVFTVGNVLIYAVLT 78
OY 61 SRLLKAPQNLFLVSLASADILVATLVIPSLANEVWGVIYFGKACETIYALDVLCTSS 120
Db 79 SRLLKAPQNLFLVSLASADILVATLVIPSLANEVWGVIYFGKACETIYALDVLCTSS 138
OY 121 IVHLCAISLDRTWSITQAEIENMLKTRPRRIKAIITVWISAVISFPLISIEKKGGGG 180
Db 139 IVHLCAISLDRTWSITQAEIENMLKTRPRRIKAIITVWISAVISFPLISIEKKGGGG 197
OY 181 POAERCEINQOKWYVISGSGFFAPCLMILVYRIYQIARRTRVPSRRGPDVA 240
Db 198 ---AYPOGLNDETWIILSSCGSFAPCLMGLVYRIYVAKLRRTTSEKRG---A 251
OY 241 AAPGGETRRPNGLPERSAGGAEAEPPLTQNLGAPGEPAAPRDTALDLESSSSD 300
Db 252 GPDGASPTTENGIG--KAAGENGHCAPP-RREV-----EP-----DESSAAE 290
OY 301 HAERPPGRRRPRRGKRGKARASQVKGDSLPRRGGATGIGTPAAGPEERVGAAKAS 360
Db 291 RRRRGAVERKGRRRREGAGDGTGSADGPGGLAAEGGARTASRSP--GPGGRLSRASRS 348
OY 361 -----RMRGR-----QNRKRTFTFLAVVIGVFVVCWPFPPFFTYTLTAV---GC 401
Db 349 VEFPLSRRRRARSSVCRRKVAQAAREKRTFTFLAVVAGVFVLCWPFPPFFSYSLGICREAC 408
OY 402 SVPTLRFKFFFWFGYCNSSLNPVITYTTFNDRRAFKKILCRGDRK 447
Db 409 QLPFLRFKFFFWIGYCNSSLNPVITYTTFNDRFRSFKHILFRRRR 454

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RESULT 8

```

A48392
alpha 2C4 adrenoceptor subtype - mouse
N:Alternate names: alpha 2C4 Isoceptor
C:Species: Mus musculus (house mouse)
C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C:Accession: A48392
R:Chang, Y.H.; Chang, N.C.; Chen, W.M.; Chang, A.C.
Biochem. Mol. Biol. Int. 29, 467-474, 1993
A:Title: Molecular characterization of a murine homologue of alpha 2C4 adrenoceptor s
A:Reference number: A48392; MUID:93250567; PMID:8387367
A:Accession: A48392
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-458 <CHAS>
A:Cross-references: GB:M97516; NID:g191728; PIDN:AAA37183.1; PID:g191729
A:Experimental source: DBA/2, liver
A>Note: sequence extracted from NCBI backbone (NCBIN:131475, NCBIPI:131476)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

```

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Query Match 49.1%; Score 1169; DB 2; Length 458;
Best Local Similarity 54.0%; Pred. No. 4.6e-68;
Matches 252; Conservative 48; Mismatches 103; Indels 64; Gaps 13;

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```

OY 14 NGTEA----PGGARAT-----PYSIQVTLTVCLAGLMLTFVGNVLIYAVT 60
Db 19 NGSDAGEMSGGGANASGTDWVPPGQYSAGAVAGLAAVGFLVFTVGNVLIYAVLT 78
OY 61 SRLLKAPQNLFLVSLASADILVATLVIPSLANEVWGVIYFGKACETIYALDVLCTSS 120
Db 79 SRLLKAPQNLFLVSLASADILVATLVIPSLANEVWGVIYFGKACETIYALDVLCTSS 138
OY 121 IVHLCAISLDRTWSITQAEIENMLKTRPRRIKAIITVWISAVISFPLISIEKKGGGG 180
Db 139 IVHLCAISLDRTWSITQAEIENMLKTRPRRIKAIITVWISAVISFPLISIEKKGGGG 193
OY 181 POAERCEINQOKWYVISGSGFFAPCLMILVYRIYQIARRTRVPSRRGPDVA 239
Db 194 PDVAALPOGGLNDETWIILSSCGSFAPCLMGLVYRIYVAKLRRTTSEKRG--- 250
OY 240 AAPGGETRRPNGLPERSAGGAEAEPPLTQNLGAPGEPAAPRDTALDLESSSS 299
Db 251 AGPDGASPTTENGIG--KAAGENGHCAPP-RREV-----EP-----DESSAA 289
OY 300 DHAERPPGRRRPRRGKRGKARASQVKGDSLPRRGGATGIGTPAAGPEERVGAAKA 359
Db 290 ERRRRAAVRKGRRRREGAGDGTGSADGPGGLAAEGGARTASRSP--GPGGRLSRASRS 347
OY 360 S-----RMRGR-----QNRKRTFTFLAVVIGVFVVCWPFPPFFTYTLTAV---G 400
Db 348 VEFPLSRRRRARSSVCRRKVAQAAREKRTFTFLAVVAGVFVLCWPFPPFFSYSLGICREA 407
OY 401 GSVPRTLRFKFFFWFGYCNSSLNPVITYTTFNDRRAFKKILCRGDRK 447
Db 408 QLPFLRFKFFFWIGYCNSSLNPVITYTTFNDRFRSFKHILFRRRR 454

```

RESULT 9

```

A37869
alpha-2B-adrenergic receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
C:Accession: A37869; S13023
R:Floriodelis, C.S.; Handy, D.E.; Bresnahan, M.R.; Zannis, V.I.; Gaviras, H.
Proc. Natl. Acad. Sci. U.S.A. 88, 1019-1023, 1991
A:Title: Cloning and expression of a rat brain alpha-2B-adrenergic receptor.
A:Reference number: A37869; MUID:91126047; PMID:1704126
A:Accession: A37869
A:Molecule type: mRNA
A:Residues: 1-458 <FLO>
A:Cross-references: GB:M58316; NID:g202585; PIDN:AAA0634.1; PID:g202586
A>Note: the authors translated the codon ACC for residue 69 as Asn and GCG for residu
R:Voigt, M.M.; McCune, S.K.; Kanterman, R.Y.; Felder, C.C.

```

```

RESULT 8

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FEBS Lett. 278, 45-50, 1991

A:Title: The rat alpha(2)-C4 adrenergic receptor gene encodes a novel pharmacological sub

A:Reference number: S13023; MUID:91130596; PMID:1704314

A:Accession: S13023

A:Molecule type: DNA

A:Residues: 1-39, 'G', '41-68, 'N', '70-154, 'E', '156-244, 'S', '246-458 <VOI>

A:Cross-references: GB:X57659; NID:g288044; PIDN:CAA40861.1; PID:g288045

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match

Best Local Similarity 49.1%; Score 1169; DB 2; Length 458;

Matches 251; Conservative 48; Mismatches 109; Indels 62; Gaps 12;

14 NGTEA----PGGAGAT-----PYSLOVTLVLCAGLMLTLVFGNVLIIVFT 60

19 NSGDAEEMSGGGANASGDMAPPGQYSAGAVAGLAAGVGLIVTGVGLVIAVLT 78

61 SRALKAPQNLFLVSLASADILVATLVIPSLANEMVGVYFGKACETIYALDVLCFTSS 120

79 SRALKAPQNLFLVSLASADILVATLVIPSLANEMVGVYFGQVWCGLYALDVLCFTSS 138

121 IVHLCALSIDRYWSTQAEVNLKRTPRRIKAIITVWISAVISFPPLISIEKKGGGG 180

139 IVHLCALSIDRYWSTQAEVNLKRTPRRKATIVAVWLISAVISFPPLVSFRPDGA- 197

181 POPAEPCETINDOKWYVSSCTGSPFAPCLIMLYVRIYQIARTRVPSRRGPDAVA 240

198 ---AYPOGGLNDEWYIISCSIGSFAPCLIMGLVARIYAKITRLTLTEKRG--A 251

241 APGGTERPNGLGPERSGAGAEAPLPTOLNGAPGEPAPAGPDTDALDEESSSSD 300

252 GPDGASPTTENGAG--KAAGENHCAP-RTEY-----EP-----DESSAE 290

301 HAERPPRRPERRGPRGKARASQVKGPDSLPRRGATGIGTPAAGPEERVAKAAS 360

291 RRRRRALRGRRRGAEGDTSADGPGGLAAEQARTASRSP--CGGLSRASSSS 348

361 -----RMGR-----QNRERFFFLVAVVGVVCMFPFFFTYTLAV---GC 401

349 VEEFLSRRRRARSSVCRKVAQAERKRFVFLVAVMGVFLCMFPFFFTSLGICREAC 408

402 SVPRTLKFFFFMGYCNSSLNPIYITIFNHFRRARFKILCRDGR 447

409 QLEPPLKFFFFMGYCNSSLNPIYITVFNDFRRSRFKHILFRRRR 454

RESULT 10

A31237

alpha-2C-adrenergic receptor - human

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 13-Aug-1999

C:Accession: A31237; S14309; S14310

R:Regan, J.W.; Koblika, T.S.; Yang-Feng, T.L.; Caron, M.G.; Lefkowitz, R.J.; Koblika, B.

Proc. Natl. Acad. Sci. U.S.A. 85, 6301-6305, 1988

A:Title: Cloning and expression of a human kidney cDNA for an alpha-2-adrenergic recepto

A:Reference number: A31237; MUID:88320430; PMID:2842764

A:Accession: A31237

A:Molecule type: mRNA

A:Residues: 1-461 <REG>

A:Cross-references: GB:J03853; NID:q178193; PIDN:AAA55513.1; PID:q178194

R:Chahaml, V.; Rangel, N.; Uhlen, S.; Wikberg, J.E.S.

FEBS Lett. 280, 241-244, 1991

A:Title: Identification of an additional gene belonging to the alpha(2) adrenergic recep

A:Reference number: S14308; MUID:91192139; PMID:1849485

A:Accession: S14309

A:Molecule type: DNA

A:Status: preliminary

A:Residues: 95-223 <CHH>

A:Accession: S14310

A:Molecule type: DNA

A:Residues: 95-223 <CH2>

C:Genetics:

A:Gene: GDB:ADRA2C; ADRA2L2; ADRA2RL2

A:Cross-references: GDB:120540; OMIM:104250

A:Map position: 4p16.3-4p15

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match

Best Local Similarity 49.0%; Score 1165.5; DB 2; Length 461;

Matches 252; Conservative 39; Mismatches 100; Indels 95; Gaps 11;

10 NASWNGTEAPGGAGAT-----PYSLOVTLVLCAGLMLTLVFGNVLIIVFT 60

19 NASGAGEGSGGVANASGASWGPQYSGAGAVAGLAAGVGLIVTGVGLVIAVLT 78

61 SRALKAPQNLFLVSLASADILVATLVIPSLANEMVGVYFGKACETIYALDVLCFTSS 120

79 SRALKAPQNLFLVSLASADILVATLVIPSLANEMVGVYFGQVWCGLYALDVLCFTSS 138

121 IVHLCALSIDRYWSTQAEVNLKRTPRRIKAIITVWISAVISFPPLISIEKKGGGG 180

139 IVHLCALSIDRYWSTQAEVNLKRTPRRKATIVAVWLISAVISFPPLVSFRPDGA- 197

181 POPAEPCETINDOKWYVSSCTGSPFAPCLIMLYVRIYQIARTRVPSRRGPDAVA 240

198 ---AYPOGGLNDEWYIISCSIGSFAPCLIMGLVARIYAKITRLTLTEKRG--V 251

241 APGGTERPNGLGPERSGAGAEAPLPTOLNGAPGEPAPAGPDTDALDEESSSSD 300

252 GPDGASPTTENGAG--AAAGEART-----GTAPRRP-----TNSRTR 287

301 HAERP-----PGRRPERRGPRGKARASQVKGPDSLPRRGATGIGTPAAGPEERVA 356

288 AAGRPRGAGPGLR--RCGRRRAGAE-----GAGGADQAGGAPAAOSGA 331

357 AKASWRG-----RONEKRTFFLAIVAGV 384

332 IYASRPPGGLSRASSRVEFLSRRRRARSSVCRKVAQAERKRFVFLAVVVGPFV 391

385 VCMFPFFFTYTLAV---GCSVPRTLKFFFFMGYCNSSLNPIYITIFNHFRRARFKIL 441

392 ICMFPFFFTYTLAV---GCSVPRTLKFFFFMGYCNSSLNPIYITVFNDFRRSRFKHIL 451

442 CRGDRK 447

452 FRRRRR 457

RESULT 11

I50829

alpha 2-adrenoceptor - cuckoo wrasse

C:Species: Labrus ossifagus (cuckoo wrasse)

C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 13-Aug-1999

C:Accession: I50829

R:Swenson, S.P.; Bailey, T.J.; Pepperl, D.J.; Grundstrom, N.; Ala-Votila, S.; Schein

Br. J. Pharmacol. 110, 54-60, 1993

A:Title: Cloning and expression of a fish a2-adrenoceptor.

A:Reference number: I50829; MUID:94035926; PMID:7693288

A:Accession: I50829

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-432 <SVS>

A:Cross-references: EMBL:U07743; NID:g467287; PIDN:AAA17386.1; PID:g467288

C:Superfamily: vertebrate rhodopsin

Query Match

Best Local Similarity 47.5%; Score 1130.5; DB 2; Length 432;

Matches 242; Conservative 48; Mismatches 115; Indels 41; Gaps 11;

10 NASWNGTEAPGGAGATPYSLQVTLVLCAGLMLTLVFGNVLIIVFTSRALKAPON 69

18 NASWS---ADSG-----YSLAAIASIALVSEFLIFVGNILVIAVLTFRALKAPON 68

70 LFLVSLASADILVATLVIPSLANEMVGVYFGKACETIYALDVLCFTSSIVHLCALSL 129

Db	69	LFVLSLADILVATLVAPWSFLANELMGWIFGKVGITLADLVFTCSYIHLAIST	128
QY	130	DRYSITQAIYENKRTPTRRRIKALITIVWYISAVISEPPLTISEKKGGGQPOAPCEB	189
Db	129	DRYSVTQAVEYENKRTPTRRKCIITIVWYISAFISSPPLSLD---SNNTYISSQPOCM	184
QY	190	INDOKWYISSCISFPAPCLIMLVVYRIQIAKRTTRVPPSRGPDVAAPAPGTEERR	249
Db	185	INDITWYLLSSMSFPAPCLIMLVYIRIYQVAKTR---SMSGKE---PRPDVOTQ	238
QY	250	PNGIGPEKSADPGGAE-----AEPPLPOLGAPGEPPAPBPOTDALLDEESSSDHAER	304
Db	239	ENGLMKANSPPCHGRBENGHCOPPTPSQGRVITIQ-----QTDADHDESSSESGKH	291
QY	305	PPGRRPBRGCRGKGKAPASOVKPDGSLPRRGATGIGTPAAGPEEERYGAAKASRMWG	364
Db	292	KPORODSORARR-GLKKSSISIKOSARISVSNKSVDLFASRRKRRRSIAEKVS----	346
QY	365	RONEKRTETFLAVIVAVFVWCPPEPFETTLAV---GGSVRYTLKPFMWGYONSSL	421
Db	347	-QAEKRTETFLAVVAVGAVFVWCPPEPFESTSLHAVCDYCKIPDTLTK-FEWIGYONSSL	404
QY	422	NPVITYTFNHDERRAFKKILCRDGRK	447
Db	405	NPAITYTFNDRFRAFQRIKCSMKK	430

126 PRKICILIFWMLIAVISLPPIL-----YKGDQREPRGRLPQCELNQEA MYLIASSIGSF 18

QY 408 FKFEEWFGYCNSLNPVIYTFIENHDERAFKILCR 443
|:||||| |||||:|:| |||||:|:|

Thu Feb 20 09:21:41 2003

us-09-636-259b-3.rpr

Page 8

Db 411 FQFFWIGYCNSSLNPVITYVFNODRRARRRILCR 446

Search completed: February 15, 2003, 18:08:03
Job time : 26.5 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 15, 2003, 14:14:47 ; Search time 13.5 Seconds
(without alignments)
1382.544 Million cell updates/sec

Title: US-09-636-259B-3

Perfect score: 2381
Sequence: 1 MGSLQPDAGNMSWNGTEAPG.....HDFRRARKILCRGDRKRIY 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SWISSProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2381	100.0	450	1 A2AA_HUMAN	P08813 homo sapien
2	2227	93.5	450	1 A2AA_PIG	P18871 sus scrofa
3	2199	92.4	450	1 A2AA_MOUSE	Q01338 mus musculu
4	2188	91.9	450	1 A2AA_CAVPO	Q60474 cavia porce
5	2166	91.0	450	1 A2AA_RAT	P22909 rattus norv
6	2120	89.0	452	1 A2AA_BOVIN	Q28838 bos taurus
7	1188	49.9	452	1 A2AC_HUMAN	P18825 homo sapien
8	1177.5	49.5	455	1 A2AC_CAVPO	Q60476 cavia porce
9	1175	49.3	458	1 A2AC_MOUSE	Q01337 mus musculu
10	1175	49.3	458	1 A2AC_RAT	P22086 rattus norv
11	1171.5	49.2	448	1 A2AB_CAVPO	Q60475 cavia porce
12	1147	48.2	469	1 A2AC_DIDMA	P35405 didelphis m
13	1130.5	47.5	432	1 A2AB_LABOS	Q91081 labrus ossi
14	1125.5	47.3	450	1 A2AB_HUMAN	P18089 homo sapien
15	1119.5	47.0	455	1 A2AB_MOUSE	P30545 mus musculu
16	1098.5	46.1	453	1 A2AB_RAT	P19328 rattus norv
17	1015.5	42.7	436	1 A2AR_CARAU	P32251 carassius a
18	946	39.7	382	1 A2AB_DIDMA	Q77715 didelphis m
19	936	39.3	384	1 A2AB_ELEMA	Q19014 elephas max
20	933	39.2	386	1 A2AB_AMBHO	Q18835 amblyscus
21	931	39.1	390	1 A2AB_DUGDU	Q77713 dugong dugo
22	930	39.1	388	1 A2AB_ORYAF	Q19032 orycteropus
23	927.5	39.0	389	1 A2AB_PROHA	Q19054 procavia ca
24	926	38.9	394	1 A2AB_RABIT	Q77830 oryctolagus
25	923	38.8	389	1 A2AB_HORSE	Q77721 equus cabal
26	922	38.7	392	1 A2AB_BOVIN	Q77700 bos taurus
27	918.5	38.6	387	1 A2AB_MACPR	Q19025 macrascalid
28	917.5	38.5	391	1 A2AB_ERIEU	Q19012 erinaceus e
29	898	37.7	384	1 A2AB_ECHTE	Q77723 echinops te
30	896.5	37.7	397	1 A2AB_TALEU	Q19091 talpa europ
31	693.5	29.1	484	1 A2AB_LOCOMI	Q25321 locusta mig
32	693.5	29.1	484	1 OAR2_LOCOMI	Q25322 locusta mig
33	681.5	28.6	379	1 GRE2_BALAM	Q93127 balanus amp

34	651	27.3	476	1 GRE1_BALAM	Q93126 balanus amp
35	648	27.2	601	1 OAR_DROME	P22270 drosophila
36	640.5	26.9	477	1 OAR_HELVI	Q25188 heliothis v
37	632.5	26.6	479	1 OAR_BOMMO	Q17222 bombyx mori
38	631.5	26.5	443	1 D2DR_CERAE	P32702 ceropithhec
39	629	26.4	444	1 D2DR_BOVIN	P20288 bos taurus
40	626.5	26.3	443	1 D2DR_HUMAN	P14416 homo sapien
41	619	26.0	463	1 D2DR_FUGRU	P53453 fugu rubrip
42	616	25.9	444	1 D2DR_MOUSE	P13953 mus musculu
43	611	25.7	377	1 SHID_CANPA	P11614 canis famil
44	606.5	25.5	442	1 D2D1_XENLA	P24628 xenopus lae
45	605	25.4	376	1 SHID_CAVPO	Q60484 cavia porce

ALIGNMENTS

RESULT 1
A2AA_HUMAN STANDARD: PRT: 450 AA.
ID A2AA_HUMAN
AC P08913;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR subtype C10).
CN ADRA2A OR ADRA2R OR ADRAR.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP MEDLINE-89308571; PubMed-2568356;
RX Fraser C.M., Arakawa S., McCombie W.R., Venter J.C.;
RA "Cloning, sequence analysis, and permanent expression of a human alpha 2-adrenergic receptor in Chinese hamster ovary cells. Evidence for independent pathways of receptor coupling to adenylylate cyclase attenuation and activation.";
RT J. Biol. Chem. 264:11754-11761(1989).
RL [2]
RN [3]
RP REVISIONS TO 333-365.
RX MEDLINE-9109167; PubMed-2170371;
RA Guyer C.A., Horstman D.A., Wilson A.L., Clark J.D., Kravog E.J. Jr.,
RA "Cloning, sequencing, and expression of the gene encoding the porcine alpha 2-adrenergic receptor. Allosteric modulation by Na⁺, H⁺, and amiloride analogs.";
RT J. Biol. Chem. 265:17307-17317(1990).
RL [4]
RN [5]
RP MUTAGENESIS OF PHE-412.
RX MEDLINE-91332079; PubMed-1678390;
RA Suryanarayana S., Daut D.A., von Zastrow M., Koblika B.K.;
RA "A point mutation in the seventh hydrophobic domain of the alpha 2 adrenergic receptor increases its affinity for a family of beta receptor antagonists.";
RT J. Biol. Chem. 266:15488-15492(1991).
RN [5]
RP MUTAGENESIS OF ASPARTIC ACID AND SERINE RESIDUES.
RX MEDLINE-91342598; PubMed-1678850;
RA Wang C.-D., Buck M.A., Fraser C.M.;
RA "Site-directed mutagenesis of alpha 2a-adrenergic receptors: Identification of amino acids involved in ligand binding and receptor activation by agonists.";

RL Mol. Pharmacol. 40:168-179(1991).
 CC - FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-
 CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G-
 CC PROTEINS. THE RANK ORDER OF POTENCY FOR AGONISTS OF THIS RECEPTOR
 CC IS OXYMETAZOLINE > CLONIDINE > EPINEPHRINE > NORPINEPHRINE >
 CC PHENYLEPHRINE > DOPAMINE > P-SYNEPHRINE > P-TYRAMINE > SEROTONIN =
 CC P-OCTOPAMINE. FOR ANTAGONISTS, THE RANK ORDER IS YOHIMBINE >
 CC PHENTOLAMINE = MANSERINE > CHLOROPROMAZINE = SPIPERONE = PRAZOSIN
 CC > PROPRANOLOL > ALPRENOLOL = PINDOLOL.
 CC - SUBCELLULAR LOCATION: Integral membrane protein.
 CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M23533; AAA51665.1; -;
 DR EMBL; M18415; AAA51664.1; -;
 DR PIR; A34169; A34169;
 DR PIR; A40132; A40132;
 DR HSSP; P29274; 1MMH.
 DR Genew; HGNC:281; ADRA2A.
 DR MIM; 104210; -;
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1;
 DR PRINTS; PR00237; GPCRHOPOPS.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 33
 FT TRANSSEM 34 59
 FT DOMAIN 60 70
 FT TRANSSEM 71 96
 FT DOMAIN 97 106
 FT TRANSSEM 107 129
 FT DOMAIN 130 149
 FT TRANSSEM 150 173
 FT DOMAIN 174 192
 FT TRANSSEM 193 217
 FT DOMAIN 218 374
 FT TRANSSEM 375 399
 FT DOMAIN 400 406
 FT TRANSSEM 407 430
 FT DOMAIN 431 450
 FT CARBOHYD 10 10
 FT CARBOHYD 14 14
 FT DISULFID 106 188
 FT LIPID 442 442
 FT SITE 113 113
 FT SITE 200 200
 FT SITE 204 204
 FT MUTAGEN 79 79
 FT MUTAGEN 113 113
 FT MUTAGEN 130 130
 FT MUTAGEN 200 200
 FT MUTAGEN 204 204
 FT MUTAGEN 412 412

FT ANTAGONIST YOHIMBINE, 3000X INCREASE FOR
 FT BETA-ANTAGONIST ALPRENOLOL.
 FT CONFLICT 104 104
 FT CONFLICT 157 157
 FT CONFLICT 333 365
 FT CONFLICT 368 368
 FT CONFLICT 450 AA; 48956 MM; A703CF262P04E8AC CRC64;
 FT SEQUENCE 450 AA; 48956 MM; A703CF262P04E8AC CRC64;
 SQ
 Query Match 100.0%; Score 2381; DB 1; Length 450;
 Best Local Similarity 100.0%; Pred. No. 6,3e-103; Indels 0; Gaps 0;
 Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSLQDPDGNASVNGTEAPGAGARATPYSLOYTLTVCLAGLMLTVGNVLIIVFT 60
 DB 1 MSLQDPDGNASVNGTEAPGAGARATPYSLOYTLTVCLAGLMLTVGNVLIIVFT 60
 QY 61 SRALKAPQNLFLVSLASADILVATLVPISLANEYGVYFGKAWCEIYALDVLFTSS 120
 DB 61 SRALKAPQNLFLVSLASADILVATLVPISLANEYGVYFGKAWCEIYALDVLFTSS 120
 QY 121 IYHLCASIDRWYSITQATEYNLKRPRRIKAIITVWISAVISPPPISTKGGGG 180
 DB 121 IYHLCASIDRWYSITQATEYNLKRPRRIKAIITVWISAVISPPPISTKGGGG 180
 QY 181 POBAERCEINDOKWYVVISCSIGSEFAPCLMILVYVRIYQIAKRRTRVPSRGPDAVA 240
 DB 181 POBAERCEINDOKWYVVISCSIGSEFAPCLMILVYVRIYQIAKRRTRVPSRGPDAVA 240
 QY 241 APPGGERPNNGIPGERSGPGAEAPLPQNLNAPGAPAGRPDADLESSSSD 300
 DB 241 APPGGERPNNGIPGERSGPGAEAPLPQNLNAPGAPAGRPDADLESSSSD 300
 QY 301 HAERPPGPRRPGRPGKAKARASOVKPDSDLPBRGPGATGIGTPAAGPGEERYGAARAS 360
 DB 301 HAERPPGPRRPGRPGKAKARASOVKPDSDLPBRGPGATGIGTPAAGPGEERYGAARAS 360
 QY 361 RMRGQNRKRTTFLVAVYGVYVWCPPEFTYTLTVAGSVPTLTKFFPFGYCNS 420
 DB 361 RMRGQNRKRTTFLVAVYGVYVWCPPEFTYTLTVAGSVPTLTKFFPFGYCNS 420
 QY 421 LNPVITYTTFHDFRRAFKKILCRGDKRRIY 450
 DB 421 LNPVITYTTFHDFRRAFKKILCRGDKRRIY 450
 RESULT 2
 A2AA_PIG STANDARD; PRT; 450 AA.
 AC P18871;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR).
 GN ADRA2A OR AZAR.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OC NCBI_TaxID=9623;
 RN [1]
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 212-232.
 RC TISSUE=Liver;
 RX MEDLINE=91009167; PubMed=2170371;
 RA Guyer C.A., Horstman D.A., Wilson A.L., Clark J.D., Kragoe E.J. Jr.,
 RA Limbird L.E.,
 RT "Cloning, sequencing, and expression of the gene encoding the porcine
 RT alpha 2-adrenergic receptor. Allosteric modulation by Nat+, H+, and
 RT amiloride analogs.";
 RL J. Biol. Chem. 265:17307-17317(1990).
 RN [2]
 RP MUTAGENESIS OF CYS-442.
 RX MEDLINE=93216775; PubMed=8385131;

RA Kennedy M.E., Limbird L.E.
 RT "Mutations of the alpha 2a-adrenergic receptor that eliminate
 RT detectable palmitoylation do not perturb receptor-G-protein
 RT coupling.";
 RL J. Biol. Chem. 268:8003-8011(1993).
 CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 CC PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC MODULATION BY NA+, H+, AND AMILORIDE ANALOGS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: J05652; AAA30984.1; -
 CC PIR: A38316; A38316.
 CC HSSP: P29274; 1MMH.
 CC InterPro: IPR000276; GPCR_Rhodopsn.
 CC Pfam: PF00001; 7tm.1; 1.
 CC PRINTS: PR00237; GPCR_RHODOPSIN.
 CC PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.
 CC PROSITE: PS0262; G_PROTEIN_REC_P1_2; 1.
 CC G-protein coupled receptor; Transmembrane; glycoprotein;
 CC Multi-gene family; Phosphorylation; Lipoprotein; Palmitate.
 CC FT DOMAIN 1 33
 CC TRANSSEM 34 59
 CC TRANSSEM 60 70
 CC TRANSSEM 71 96
 CC TRANSSEM 97 106
 CC TRANSSEM 107 129
 CC TRANSSEM 130 149
 CC TRANSSEM 150 173
 CC TRANSSEM 174 192
 CC TRANSSEM 193 217
 CC TRANSSEM 218 374
 CC TRANSSEM 375 399
 CC TRANSSEM 400 409
 CC TRANSSEM 410 430
 CC TRANSSEM 431 450
 CC DOMAIN 10 10
 CC CARBOHYD 14 14
 CC CARBOHYD 106 188
 CC LIPID 442 442
 CC SITE 113 113
 CC SITE 200 200
 CC SITE 204 204
 CC MUTAGEN 442 442
 CC SEQUENCE 450 AA; 48975 MW; 799D5847372074E CRC64;
 Query Match 93.58; Score 2227; DB 1; Length 450;
 Best Local Similarity 94.08; Pred. No. 7e-96;
 Matches 423; Conservative 3; Mismatches 24; Indels 0; Gaps 0;

DB 121 IVHLCALSDRWYSITQAIENYLNKTRPRKAIITVWVAVISFPLISIEKKAGCGG 180
 QY 181 POPAPRCEINDQKRYVSSCGSFAPCLIMIIYVYIYQIARRRTPVPSRRGPDAVA 240
 DB 181 OOPAPRCEINDQKRYVSSCGSFAPCLIMIIYVYIYQIARRRTPVPSRRGPDAVA 240
 QY 241 APPGTERPNGLGERSAPGAEAPLPTQLNAPGEPAPAGRDYDALDESSSSD 300
 DB 241 ALPGAERPNGLGERSAPGAEAPLPTQLNAPGEPAPAGRDYDALDESSSSSE 300
 QY 301 HAERPPGRRPGRGKARASQVKGDSLPRRGPGATGICPPAGGEEGVAKAAS 360
 DB 301 HAERPPGRRPGRGKARASQVKGDSLPRRGPGATGICPPAGGEEGVAKAAS 360
 QY 361 BRGRGONREKRTFVLAVIGVYVWCPFPFTYLTVAVGSVPTLTKFFFGYCNSS 420
 DB 361 BRGRGONREKRTFVLAVIGVYVWCPFPFTYLTVAVGSVPTLTKFFFGYCNSS 420
 QY 421 LNPVYITTFNHDFRRAFKKILCRGDRKRV 450
 DB 421 LNPVYITTFNHDFRRAFKKILCRGDRKRV 450
 RESULT 3
 A2AA_MOUSE STANDARD; PRT; 450 AA.
 ID A2AA_MOUSE
 AC 00138;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ALPHA-2a adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR).
 GN ADRA2A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92342131; PubMed-1353249;
 RA Link R.E., Daunt D.A., Barsh G., Chruslinski A.J., Koblika B.K.;
 RT "Cloning of two mouse genes encoding alpha 2-adrenergic receptor
 RT subtypes and identification of a single amino acid in the mouse alpha
 RT 2-C10 homolog responsible for an interspecies variation in
 RT antagonist binding.";
 RL Mol. Pharmacol. 42:16-27(1992).
 CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 CC PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M99377; AAA37213.1; -
 CC HSSP: P29274; 1MMH.
 CC MGI: 87934; Adra2a.
 CC InterPro: IPR000276; GPCR_Rhodopsn.
 CC Pfam: PF00001; 7tm.1; 1.
 CC PRINTS: PR00237; GPCR_RHODOPSIN.
 CC PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.
 CC PROSITE: PS0262; G_PROTEIN_REC_P1_2; 1.
 CC G-protein coupled receptor; Transmembrane; glycoprotein;
 CC Multi-gene family; Phosphorylation; Lipoprotein; Palmitate.
 CC FT DOMAIN 1 33
 CC TRANSSEM 34 59
 CC TRANSSEM 60 70
 CC TRANSSEM 71 96
 CC TRANSSEM 97 106
 CC TRANSSEM 107 129
 CC TRANSSEM 130 149
 CC TRANSSEM 150 173
 CC TRANSSEM 174 192
 CC TRANSSEM 193 217
 CC TRANSSEM 218 374
 CC TRANSSEM 375 399
 CC TRANSSEM 400 409
 CC TRANSSEM 410 430
 CC TRANSSEM 431 450
 CC DOMAIN 10 10
 CC CARBOHYD 14 14
 CC CARBOHYD 106 188
 CC LIPID 442 442
 CC SITE 113 113
 CC SITE 200 200
 CC SITE 204 204
 CC MUTAGEN 442 442
 CC SEQUENCE 450 AA; 48975 MW; 799D5847372074E CRC64;

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FT DOMAIN 97 106 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 107 129 3 (POTENTIAL).
FT DOMAIN 130 149 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 150 173 4 (POTENTIAL).
FT DOMAIN 174 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 217 5 (POTENTIAL).
FT DOMAIN 218 374 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 375 399 6 (POTENTIAL).
FT DOMAIN 400 409 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 410 430 7 (POTENTIAL).
FT DOMAIN 431 450 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 188 BY SIMILARITY.
FT LIPID 442 442 PALMITATE (BY SIMILARITY).
FT SITE 113 113 IMPLICATED IN LIGAND BINDING (BY SIMILARITY).
FT SITE 200 200 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
FT SITE 204 204 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
FT SITE 204 204 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
SO SEQUENCE 450 AA; 48865 MW; F07E225393AFA93B CRC64;
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Query Match 92.4%; Score 2199; DB 1; Length 450;
Best Local Similarity 92.2%; Pred. No. 1.3e-94;
Matches 415; Conservative 8; Mismatches 27; Indels 0; Gaps 0;
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QY 1 MGSLOPDGASNMNGTEAPGGARATPSLOYTLTVCLAGLMLTFEGVAVIYIAFT 60
DB 1 MGSLOPDGASNMNGTEAPGGARATPSLOYTLTVCLAGLMLTFEGVAVIYIAFT 60
QY 61 SRALKAPONLEFLVSLASADILVATLVIPFSLANEMGWYFGKAMCEIYIALDVLFC 120
DB 61 SRALKAPONLEFLVSLASADILVATLVIPFSLANEMGWYFGKAMCEIYIALDVLFC 120
QY 121 IVHCAISLDYRWSTQAIENLKRTPRIKAIITVWVISAIVSPPLISIEKKGGGG 180
DB 121 IVHCAISLDYRWSTQAIENLKRTPRIKAIITVWVISAIVSPPLISIEKKGGGG 180
QY 181 POPAPECEINDOKWYVSSICISGFAPCLIMLVYRIYIOIARRFRVPSRRGP 240
DB 181 POPAPECEINDOKWYVSSICISGFAPCLIMLVYRIYIOIARRFRVPSRRGP 240
QY 241 APPGTERPRLNGLPERSAGFGAEAPLPTOLNGAPGEPAPRDTALDLEESSSS 300
DB 241 APPGTERPRLNGLPERSAGFGAEAPLPTOLNGAPGEPAPRDTALDLEESSSS 300
QY 301 HAERPGRPRRPRGPRGKARASOVKPSLPRRGAGCIGTPRAGPEERVGAKAS 360
DB 301 HAERPGRPRRPRGPRGKARASOVKPSLPRRGAGCIGTPRAGPEERVGAKAS 360
QY 361 RMRGRONREKRTFVLAVVIGVFWCFPEFTTTLTAVGCSVPRTLKFFEFMGYCN 420
DB 361 RMRGRONREKRTFVLAVVIGVFWCFPEFTTTLTAVGCSVPRTLKFFEFMGYCN 420
QY 421 LNPVITITFNHDFRARRKIKICRDKRIY 450
DB 421 LNPVITITFNHDFRARRKIKICRDKRIY 450
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RESULT 4
A2A2A_CAVPO STANDARD: PRT: 450 AA.
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AC 060474;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR).
GN ADR2A2.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
```

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FN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Hartley N.A.
RX MEDLINE=96152573; PubMed=8573196;
RA Svensson S.P., Bailey T.J., Porter A.C., Richman J.G., Regan J.W.;
RT "heterologous expression of the cloned guinea pig alpha 2A, alpha 2B,
RT and alpha 2C adrenoceptor subtypes. Radioligand binding and
RT functional coupling to a CAMP-responsive reporter gene.";
RL Biochem. Pharmacol. 51:291-300(1996).
CC - FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC EMBL: U25722; AAA67074.1; -.
CC HSSP: P29274; 1MMH.
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PR00001; 7tm_1; 1.
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DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECPEP_F1.1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECPEP_F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 59 1 (POTENTIAL).
FT DOMAIN 60 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 96 2 (POTENTIAL).
FT DOMAIN 107 106 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 107 129 3 (POTENTIAL).
FT DOMAIN 130 149 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 150 173 4 (POTENTIAL).
FT DOMAIN 174 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 217 5 (POTENTIAL).
FT DOMAIN 218 374 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 375 399 6 (POTENTIAL).
FT DOMAIN 400 409 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 410 430 7 (POTENTIAL).
FT DOMAIN 431 450 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 187 BY SIMILARITY.
FT LIPID 442 442 PALMITATE (BY SIMILARITY).
FT SITE 113 113 IMPLICATED IN LIGAND BINDING (BY SIMILARITY).
FT SITE 199 199 IMPLICATED IN AGONIST BINDING AND RECEPTOR ACTIVATION (BY SIMILARITY).
FT SITE 203 203 IMPLICATED IN AGONIST BINDING AND RECEPTOR ACTIVATION (BY SIMILARITY).
SO SEQUENCE 450 AA; 48910 MW; E6BBE9A7FEF8DD1 CMC64;
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Query Match 91.9%; Score 2188; DB 1; Length 450;
Best Local Similarity 92.5%; Pred. No. 4.3e-94;
Matches 417; Conservative 8; Mismatches 24; Indels 2; Gaps 2;
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QY 1 MGSLOPDGASNMNGTEAPGGARATPSLOYTLTVCLAGLMLTFEGVAVIYIAFT 60
DB 1 MGSLOPDGASNMNGTEAPGGARATPSLOYTLTVCLAGLMLTFEGVAVIYIAFT 60
QY 61 SRALKAPONLEFLVSLASADILVATLVIPFSLANEMGWYFGKAMCEIYIALDVLFC 120
DB 61 SRALKAPONLEFLVSLASADILVATLVIPFSLANEMGWYFGKAMCEIYIALDVLFC 120
QY 121 IVHCAISLDYRWSTQAIENLKRTPRIKAIITVWVISAIVSPPLISIEKKGGGG 180
DB 121 IVHCAISLDYRWSTQAIENLKRTPRIKAIITVWVISAIVSPPLISIEKKGGGG 180
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Db 121 IYHLCALISLDRVSTIOAEYINLKRTPRRIKAIITVWVYISAVISPPILISFE-KAGGG 179
OY 181 POPAEPRCEINDQKWYVYSSICISFFAPCLIMLVYVRIYQIAKRRTRVPSNRGPD-V 239
180 QOPAEPRCEINDQKWYVYSSICISFFAPCLIMLVYVRIYQIAKRRTRVPSNRGPD-V 239
OY 240 AAPGCTERRPNGLGPERSGAGAEAPLPTQNGAPGEPAPGRDADLDLESSSS 299
240 AAPGCTERRPNGLGPERSGAGAEAPLPTQNGAPGEPAPGRDADLDLESSSS 299
Db 240 AAPGCTERRPNGLGPERSGAGAEAPLPTQNGAPGEPAPGRDADLDLESSSS 299
OY 300 DHAERPPGRRPGRGKGRASQVKGDSLPRRPGATGIGTPAGPGEERVGAAKA 359
300 EHAERPPGRRPGRGKGRASQVKGDSLPRRPGATGIGTPAGPGEERVGAAKA 359
Db 300 EHAERPPGRRPGRGKGRASQVKGDSLPRRPGATGIGTPAGPGEERVGAAKA 359
OY 360 SRMRGRONREKRTFVLAVVIGVYVVCWPFEEFTYTLTAVGCVPTLTKFFPFGYCN 419
360 SRMRGRONREKRTFVLAVVIGVYVVCWPFEEFTYTLTAVGCVPTLTKFFPFGYCN 419
Db 360 SRMRGRONREKRTFVLAVVIGVYVVCWPFEEFTYTLTAVGCVPTLTKFFPFGYCN 419
OY 420 SLNPVITITFNHDFRRFAFKIILCRGDRKRIV 450
420 SLNPVITITFNHDFRRFAFKIILCRGDRKRIV 450
Db 420 SLNPVITITFNHDFRRFAFKIILCRGDRKRIV 450

RESULT 5
A2AA_RAT STANDARD: PRT: 450 AA.
ID A2AA_RAT
AC P22909;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR)
DE (CA2-47) (Alpha-2D adrenergic receptor).
CN ADR2A2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=91244823; PubMed=1645350;
RA Lanier S.M., Downing S., Duzic E., Homcy C.J.;
RT Isolation of rat genomic clones encoding subtypes of the alpha 2-
RT adrenergic receptor. Identification of a unique receptor subtype.";
RL J Biol. Chem. 266:10470-10478(1991).
RN 12
RP SEQUENCE FROM N.A.
RX MEDLINE=91125329; PubMed=2177834;
RA Chabberg S.C., Duda T., Rhine J.A., Sharma R.K.;
RT Molecular cloning, sequencing and expression of an alpha 2-adrenergic
RT receptor complementary DNA from rat brain.";
RL Mol. Cell. Biochem. 97:161-172(1990).
RN 13
RP SEQUENCE FROM N.A.
RX MEDLINE=95349560; PubMed=7623790;
RA Wyslowski K., Duda T., Sharma R.K.;
RT Structural, genetic and pharmacological identity of the rat alpha
RT 2-adrenergic receptor subtype ca2-47 and its molecular
RT characterization in rat adrenal, adrenocortical carcinoma and bovine
RT retina.";
RL Mol. Cell. Biochem. 144:181-190(1995).
RN 14
RP FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
RN 15 INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
RN 16 PROTEINS.
RN 17 SUBCELLULAR LOCATION: Integral membrane protein.
RN 18 -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
RN 19 -----
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CC -----
DR EMBL: M62372; AAA42034.1; -.
DR EMBL: U79031; AAC24959.1; -.
DR PIR: B40392; B40392.
DR PIR: JH0190; JH0190.
DR HSSP: P29274; 1MMH.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G-PROTEIN_RECP_F1.1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECP_F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 33
FT TRANSMEM 34 59
FT DOMAIN 60 70
FT TRANSMEM 71 96
FT TRANSMEM 97 106
FT TRANSMEM 107 129
FT TRANSMEM 130 149
FT TRANSMEM 150 173
FT DOMAIN 174 192
FT TRANSMEM 193 217
FT DOMAIN 218 374
FT TRANSMEM 375 399
FT DOMAIN 400 409
FT TRANSMEM 410 430
FT DOMAIN 431 450
FT CAROHSD 10 10
FT CAROHSD 14 14
FT DISULFID 106 188
FT LIPID 442 442
FT SITE 113 113
FT SITE 200 200
FT SITE 204 204
FT SITE 204 204
FT CONFLICT 147 147
FT CONFLICT 154 158
FT CONFLICT 252 253
FT CONFLICT 264 264
FT CONFLICT 304 305
FT CONFLICT 333 333
FT CONFLICT 445 445
FT CONFLICT 445 445
SQ SEQUENCE 450 AA; 48939 MW; AFA078DCAAD612AC CRC64;
Query Match 91.0%; Score 2166; DB 1; Length 450;
Best Local Similarity 90.9%; Pred. No. 4, 3e-93;
Matches 409; Conservative 9; Mismatches 32; Indels 0; Gaps 0;
OY 1 MGSLOPDAGNSWNGTEAPGAGARATPYSLOYTLTVCLAGLMLTVEGNLVIIAFT 60
1 MGSLOPDAGNSWNGTEAPGAGARATPYSLOYTLTVCLAGLMLTVEGNLVIIAFT 60
Db 1 MGSLOPDAGNSWNGTEAPGAGARATPYSLOYTLTVCLAGLMLTVEGNLVIIAFT 60
OY 61 SRLKAPQNLFLVSLASADILVATLVIPSLANVGVYFGKAWCEIYALDVLFTSS 120
61 SRLKAPQNLFLVSLASADILVATLVIPSLANVGVYFGKAWCEIYALDVLFTSS 120
Db 61 SRLKAPQNLFLVSLASADILVATLVIPSLANVGVYFGKAWCEIYALDVLFTSS 120
OY 121 IYHLCALISLDRVSTIOAEYINLKRTPRRIKAIITVWVYISAVISPPILISFEKGGGG 180
121 IYHLCALISLDRVSTIOAEYINLKRTPRRIKAIITVWVYISAVISPPILISFEKGGGG 180
Db 121 IYHLCALISLDRVSTIOAEYINLKRTPRRIKAIITVWVYISAVISPPILISFEKGGGG 180
OY 181 POPAEPRCEINDQKWYVYSSICISFFAPCLIMLVYVRIYQIAKRRTRVPSNRGPD-V 240
181 POPAEPRCEINDQKWYVYSSICISFFAPCLIMLVYVRIYQIAKRRTRVPSNRGPD-V 240
Db 181 POPAEPRCEINDQKWYVYSSICISFFAPCLIMLVYVRIYQIAKRRTRVPSNRGPD-V 240
OY 241 AAPGCTERRPNGLGPERSGAGAEAPLPTQNGAPGEPAPGRDADLDLESSSSD 300
241 AAPGCTERRPNGLGPERSGAGAEAPLPTQNGAPGEPAPGRDADLDLESSSSD 300
Db 241 AAPGCTERRPNGLGPERSGAGAEAPLPTQNGAPGEPAPGRDADLDLESSSSD 300
OY 301 HAERPPGRRPGRGKGRASQVKGDSLPRRPGATGIGTPAGPGEERVGAAKAS 360
301 HAERPPGRRPGRGKGRASQVKGDSLPRRPGATGIGTPAGPGEERVGAAKAS 360

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Db 301 HAERPGCGKPERGRGAKGKTASQVKNPGDSLPRRGAGAGSGSGGGERAGAKAS 360
QY 361 RMRGRONREKRTFFVLAVVIGVFVVCWPFPTFTYTLTAVGCSVPTLTKFFKFFWFGYCNSS 420
Db 361 RMRGRONREKRTFFVLAVVIGVFVVCWPFPTFTYTLTAVGCPVPYOLFNFFFWFGYCNSS 420
QY 421 INPVTYITFNHDFRRAFKKILCRGDRKRIV 450
Db 421 INPVTYITFNHDFRRAFKKILCRGDRKRIV 450

RESULT 6
A2AA_BOVIN STANDARD; PRT; 452 AA.
ID A2AA_BOVIN STANDARD; PRT; 452 AA.
AC Q28838;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR)
DE (Alpha-2D adrenergic receptor).
GN ADRA2A.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9811113; PubMed=9450652;
RA Venkataraman V., Duda T., Sharma R.K.;
RT "The bovine alpha 2D-adrenergic receptor gene: structure, expression
RT in retina, and pharmacological characterization of the encoded
RT receptor.";
RL Mol. Cell. Biochem. 177:113-123(1997).
RN [2]
RP SEQUENCE OF 171-210 FROM N.A.
RX MEDLINE=94018366; PubMed=8412494;
RA Blaxall H.S., Heck D.A., Bylund D.B.;
RT "Molecular determinants of the alpha-2D adrenergic receptor subtype.";
RL Life Sci. 53:9-9(1993).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: RETINA, BRAIN AND OLFACTORY LOBE.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U79030; AAC24958.1; -
DR EMBL: S66295; AAB28450.1; -
DR HSSP: P29274; 1MMH.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PRO0237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 59 1 (POTENTIAL).
FT DOMAIN 60 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 96 2 (POTENTIAL).
FT DOMAIN 97 106 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 107 129 3 (POTENTIAL).
FT DOMAIN 130 149 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 150 173 4 (POTENTIAL).

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FT DOMAIN 174 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 217 5 (POTENTIAL).
FT DOMAIN 218 376 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 377 401 6 (POTENTIAL).
FT DOMAIN 402 411 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 412 432 7 (POTENTIAL).
FT DOMAIN 433 452 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 188 BY SIMILARITY.
FT LIPID 444 444 PALMITATE (BY SIMILARITY).
SQ SEQUENCE 452 AA; 49252 MW; F10C1DD286C06F9 CRC64;

Query Match 89.0%; Score 2120; DB 1; Length 452;
Best Local Similarity 90.9%; Pred. No. 5; Se-91;
Matches 412; Conservative 4; Mismatches 33; Indels 4; Gaps 4;

QY 1 MGSLQPDAGNASWNGTEAPGCGARAPPYSLOVTLITVCLAGLMLTIVGNTVITAVPT 60
Db 1 MGSLQPDAGNASWNGTEAPGCGARAPPYSLOVTLITVCLAGLMLTIVGNTVITAVPT 60
QY 61 SRLKAPQNLFLVSLASADILVATLTPPSLANEVNGWYFGKANCEIYALDVLFCYSS 120
Db 61 SRLKAPQNLFLVSLASADILVATLTPPSLANEVNGWYFGKANCEIYALDVLFCYSS 120
QY 121 IYHLCATSLDRYVSTQALEYNLKRTPRIKAITIYVWISAVISPPPLISTEKKGGGG 180
Db 121 IYHLCATSLDRYVSTQALEYNLKRTPRIKAITIYVWISAVISPPPLISTEKKGGGG 180
QY 181 POPAEPRCEINDQKMYVVISGCSFPAQLIMLVYRITQAKRRTRVPSRRGPDAVA 240
Db 181 QPAAEPRCEINDQKMYVVISGCSFPAQLIMLVYRITQAKRRTRVPSRRGPDAVA 240
QY 241 AP-PCGTERRPGLGPER-SAGPGAEAPLPTQLNGAPGEPAAPGPRDTALDEESS 298
Db 241 AELPGAERRPGLGPERGVGPAVEESLQVONGAPGEPAAG-AGAALDDEESS 299
QY 299 SDHAERPPRRPERGPRGKARASQVPRGDSLPRRGATGIGTPAAGPEEVR-CAA 357
Db 299 SDHAERPPRRPERGPRGKARASQVPRGDSLPRRGATGIGTPAAGPEEVR-CAA 357
QY 300 SEHAERPPSRSENGPRGKARASQVPRGDSLPRRGATGIGTPAAGPEEVRSGGA 359
Db 300 SEHAERPPSRSENGPRGKARASQVPRGDSLPRRGATGIGTPAAGPEEVRSGGA 359
QY 358 KASRWGRONREKRTFFVLAVVIGVFVVCWPFPTFTYTLTAVGCSVPTLTKFFWFGYC 417
Db 360 KASRWGRONREKRTFFVLAVVIGVFVVCWPFPTFTYTLTAVGCPVPTLTKFFWFGYC 419
QY 418 NSLNVPYITFNHDFRRAFKKILCRGDRKRIV 450
Db 420 NSLNVPYITFNHDFRRAFKKILCRGDRKRIV 450

RESULT 7
A2AC_HUMAN STANDARD; PRT; 462 AA.
ID A2AC_HUMAN STANDARD; PRT; 462 AA.
AC P18825; P35369; Q9H849;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-2C-adrenergic receptor (Alpha-2C adrenoceptor) (Subtype C4).
GN ADRA2C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Kidney;
RX MEDLINE=88320430; PubMed=2842764;
RA Regan J.W., Koblikka T.S., Yang-Feng T.L., Caron M.G., Lefkowitz R.J.,
RA Koblikka B.K.;
RT "Cloning and expression of a human kidney cDNA for an alpha
RT 2-adrenergic receptor subtype.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:6305(1988).
RN [2]

```

RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Brain;
 RX MEDLINE=98041882; PubMed=9371698;
 RA Sheak S., Davedjian J.C., Cayla C., Sender Y., Paris H.;
 RT "Molecular cloning, sequencing and functional study of the promoter
 RT region of the human alpha2C-adrenergic receptor gene.";
 RL Biochem. J. 328:431-438(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Yano K., Takeda M., Sugimoto E., Sagai H.;
 RT "Molecular cloning and expression of a novel human alpha2C-adrenergic
 RT receptor, alpha2CII, gene.";
 RL Submitted (Oct-1992) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT 322-GUY--PRO-325 DEL.
 RX MEDLINE=20390061; PubMed=10801795;
 RA Small K.M., Forbes S.L., Rahman F.F., Bridges K.M., Liggett S.B.;
 RT "A four amino acid deletion polymorphism in the third intracellular
 RT loop of the human alpha 2C-adrenergic receptor confers impaired
 RT coupling to multiple effectors.";
 RL J. Biol. Chem. 275:23059-23064(2000).
 CC -1- FUNCTION: ALPHA-2-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 CC PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- POLYMORPHISM: The Del322-325 variant has a significant loss of
 CC function. It is approximately 10 times more frequent in African-
 CC Americans compared with Caucasians (allele frequencies 0.381
 CC versus 0.040).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: J03853; AA35513.1; -;
 DR EMBL: U72648; AAC78723.1; -;
 DR EMBL: D13538; BA02737.1; -;
 DR EMBL: AF280399; AAC28076.1; -;
 DR EMBL: AF280400; AAC28077.1; -;
 DR PIR: A31237; A31237.
 DR HSSP: P29274; 1MMH.
 DR Genew; HGNC:283; ADRA2C.
 DR MIM: 104250; -;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECPT_FL_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECPT_FL_2; 1.
 KM G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Multigene family; Phosphorylation; Polymorphism; Alternative splicing.
 FT DOMAIN 1 51
 FT TRANSMEM 52 76
 FT TRANSMEM 77 88
 FT TRANSMEM 89 114
 FT DOMAIN 115 124
 FT TRANSMEM 125 147
 FT DOMAIN 148 168
 FT TRANSMEM 169 191
 FT DOMAIN 192 207
 FT TRANSMEM 208 231
 FT DOMAIN 232 379
 FT TRANSMEM 380 407
 FT DOMAIN 408 420
 FT TRANSMEM 421 441
 FT DOMAIN 442 462
 FT DOMAIN 294 308
 ARG-RICH (BASIC).

FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 124 202 BY SIMILARITY.
 FT VARSPIC 270 300 AGENCHCAPRAVEDESSAARRRRRGA -> EARTGT
 FT VARIANT 322 325 ARRPPTWSTRAQRGGAGGP (IN ISOFORM 2).
 FT VARIANT 322 325 MISSING.
 FT CONFLICT 239 239 /FWID=VAR_012747.
 FT CONFLICT 329 329 L -> R (IN REF. 1 AND 2).
 FT CONFLICT 401 401 E -> Q (IN REF. 1 AND 2).
 FT CONFLICT 446 446 S -> I (IN REF. 1 AND 2).
 FT CONFLICT 446 446 R -> P (IN REF. 1 AND 2).
 SQ SEQUENCE 462 AA; 49522 MW; E1EF9CA21E7F6BDA CRC64;
 Query Match 49.9%; Score 1188; DB 1; Length 462;
 Best Local Similarity 52.9%; Pred. No. 2.4e-48;
 Matches 255; Conservative 40; Mismatches 101; Indels 86; Gaps 10;
 QY 10 NASWNGTEAPGCGARAT-----PYSLOVTLTVCLAGLMLTLVFGNVIIAVPT 60
 DB 19 NASGAGERRSGGVANASGASWGPREGYSAGAVAGLAAGVGLIVFVGNVLVLAFLT 78
 QY 61 SRALKAPQNLFLVSLASADILVATLVLPFSLANWGVYTFGRACETIYALDVLCTSS 120
 DB 79 SRALARAPQNLFLVSLASADILVATLVMPFSLANELMAYWFGQWCGVYDALDVLCTSS 138
 QY 121 IVHCAISLDVWSTIQAIENLKRPRRIKATITVWVISAIVSPPLISIEKKGGCG 180
 DB 139 IVHCAISLDVWSTVTOAVEYNLKRPRRYKATIVAWLSVAISFPPLVSLRDPGA- 197
 QY 181 PQAPRCEINDOKWYVYSSCGSFAPCLIMLVYRIQIKRTRVPSRCPDVA 240
 DB 198 ---AYPCGLNDEWTVLLSSCGISFFAPCLIMGLVYRIYVAKLRTRTSEKRAP--V 251
 QY 241 APPGCTERRRPGCLPEPSAGPGAEAPLPTQLNGAGEPAPAPRDTALDEBSSSD 300
 DB 252 GPDDASPTTEGIGLAAAGENGCA-----PPPA-----DVEPDESSA 290
 QY 301 HAERPPRPRERPRGRKARASOVKPGDSLPRRGATGATGTPAGPGEERYGAAS 360
 DB 291 AAE-----RRRRKALRGRRRAGAGCG-----AGGAGGCG---AGPAAESGALTAS 336
 QY 361 RWRG-----RQNEKRFTVLAIVGVVVCWF 388
 DB 337 RSPGCGRLSRASSRSVEFLRRRRARRSSVCRKVAQAAREKFTFVLAVMGVFLVCMF 396
 QY 389 PFEFTYTLTAV---GCVPRTLRFKFFWPGYCNSSLNPVYITFNHDFRAFKILCRGD 445
 DB 397 PFEFTSYLVGICREACVPGPLFKEFFWIGYCNSSLNPVYITVFNDFRSFKHILFRR 456
 QY 446 RK 447
 DB 457 RR 458
 RESULT 8
 A2AC_CAVPO STANDARD; PRT; 455 AA.
 ID A2AC_CAVPO 060476;
 AC 060476;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Alpha-2C adrenergic receptor (Alpha-2C adrenoceptor).
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
 OC NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Hartley;
 RX MEDLINE=96152573; PubMed=8573196;
 RA Swenson S.P., Bailey T.J., Porter A.C., Richman J.G., Regan J.W.;
 RT "heterologous expression of the cloned guinea pig alpha 2b, alpha 2b,
 RT and alpha 2C adrenoceptor subtypes. Radioligand binding and

[illegible]

QY	346	AAGPEE-----	RGAKAKASRWGRORRERFFVLAVGVGVGVPPEFFFTYTLAV	399
QY	341	ASSRSVEFFLRRRRARRSSVCRKKAQAKRKFVFLVAVGVVLCVCFPEFFESYSLXGI	400	
QY	400	--GCSVPTLFFKFFFMFGYCNSSLNPVITYITFHNDFERRAKTILCRGRK	447	
Db	401	CREACQLTPLPFKFFFWIGYCNSSLNPVITYITFNDFFRSKHILFRRRR	451	
RESULT 9				
AC	A2AC_MOUSE	STANDARD;	PRT; 458 AA.	
AC	001337:			
DT	01-APR-1993	(Rel. 25, Created)		
DT	01-APR-1993	(Rel. 25, Last sequence update)		
DT	01-NOV-1997	(Rel. 35, Last annotation update)		
DE	Alpha-2C adrenergic receptor (Alpha-2C adrenoceptor) (Subtype C4).			
GN	ADRA2C.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92342131; PubMed=1353349;			
RA	Link R.E., Daut D.A., Barsh G., Chruscinski A.J., Kobilka B.K.;			
RT	"Cloning of two mouse genes encoding alpha 2-adrenergic receptor			
RT	subtypes and identification of a single amino acid in the mouse alpha			
RT	2-C10 homolog responsible for an interspecies variation in			
RT	antagonist binding.";			
RL	Mol. Pharmacol. 42:16-27(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=DBA/2;			
RX	MEDLINE=93250567; PubMed=8387367;			
RA	Chang Y.-H., Chang A.C., Chen W.-M., Chang N.-C.A.;			
RT	"Molecular characterization of a murine homologue of alpha 2C4			
RT	adrenoceptor subtype gene.";			
RL	Biochem. Mol. Biol. Int. 29:467-474(1993).			
CC	-1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-			
CC	INDUCED INHIBITION OF ADENYLYLATE CYCLASE THROUGH THE ACTION OF G			
CC	PROTEINS.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch).			
CC	-----			
DR	EMBL; M99376; AAA37212.1; -;			
DR	EMBL; M97516; AAA37183.1; -;			
DR	HSSP; P29274; IMM.			
DR	MCD; MGI:87936; Adra2c.			
DR	InterPro: IPR000276; GPCR_Rhodpsn.			
DR	Pfam: PF00001; 7tm.1; 1.			
DR	PRINTS; PR00237; GPCRHHODPSN.			
DR	PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.			
DR	PROSITE; PS50262; G-PROTEIN_RECEP_FL_2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;			
KW	Multigene family; Phosphorylation.			
FT	DOMAIN	1	51	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	52	76	1 (POTENTIAL).
FT	DOMAIN	77	88	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	89	114	2 (POTENTIAL).
FT	DOMAIN	115	124	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	125	147	3 (POTENTIAL).
FT	DOMAIN	148	168	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	169	191	4 (POTENTIAL).
FT	DOMAIN	192	207	EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 208 231 5 (POTENTIAL).
FT DOMAIN 232 379 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 380 403 6 (POTENTIAL).
FT DOMAIN 404 416 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 417 437 7 (POTENTIAL).
FT DOMAIN 438 458 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 291 305 ARG-RICH (BASIC).
FT CARBOHD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFD 124 202 BY SIMILARITY.
FT CONFLICT 196 196 G -> V (IN REF. 2).
FT CONFLICT 296 296 G -> A (IN REF. 2).
FT CONFLICT 298 298 L -> V (IN REF. 2).
SO SEQUENCE 458 AA; 49906 MW; C0A8BDF0302B1F8 CXC64;

Query Match 49.3%; Score 1175; DB 1; Length 458;
Best Local Similarity 54.1%; Pred. No. 9.5e-48;
Matches 252; Conservative 48; Mismatches 104; Indels 62; Gaps 12;

OY 14 NCTEA----PGGGARAT-----PYSLOYTLTLVCLAGLMLLTVEGNVLIAVFT 60
DB 19 NQSDAGEMSGGGANSGTDWVPPPGQYSAGAVAGLAAYVGLIVTVGNVLVIAVLT 78
OY 61 SRALKAPQMLFLVSLASADILVATLVIPESLANEYWGYPFGKACEIYALDVECTSS 120
DB 79 SRALRAPQMLFLVSLASADILVATLVIPESLANELMAYVFGQVWGVYALDVECTSS 138
OY 121 IYHLCAISLDRWSTQAEVYMLKTRPRIKAITTVWVISAVISPPPLISTEKGGGGG 180
DB 139 IYHLCAISLDRWSTQAEVYMLKTRPRIKAITTVWVISAVISPPPLISTEKGGGGG- 197
OY 181 PQAEPRCENIDOKWVIVISGIFPAPCLIMLVRYOAKTRTRVPSRGPDAVA 240
DB 198 ---AYQCGINDETWYIISGIFPAPCLIMLVRYOAKTRTRVPSRGPDAVA 251
OY 241 APPGCTERRPNGIGPERSAPGAEAPLPTQINGAPCEBAPADPRDADLDLESSSD 300
DB 252 GPDGASPTTENGIG--KAENGCHCAP-RTEV-----EP-----DESSAAE 290
OY 301 HAERPPRRPPEKPGPKKAKARASQVKPDSLPKRGPGATGICTPAAGGERVGAARAS 360
DB 291 RRRRRGALRGGRRGARAGDGTGSADGPPGALAEAGARTASRSP--GGGRLSRASRS 348
OY 361 -----RMGR-----ONREKRFYFLAVVIGVYVCMPPFFFTYTLAV---GC 401
DB 349 VERFLSRRARRASSVCRKVAQAREKRTFFVLAVMGVYVLCWPFPEYSIXGICREAC 408
OY 402 SVPRTLFKFFFWGYCNSSLNPVIYITIFNHDFRAAFKTLRGDRK 447
DB 409 QLPEPLFKFFFWGYCNSSLNPVIYITVFNQDRSRFHLFRRRR 454

RESULT 10
A2AC_RAT STANDARD; PRT; 458 AA.
AC A2AC_RAT P22086;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Alpha-2C adrenergic receptor (Alpha-2C adrenoceptor) (Subtype C4).
GN ADRA2C.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 11)
RP SEQUENCE FROM N.A.
RX MEDLINE=91130596; PubMed=1704126;
RA Flordellis C.S., Handy D.E., Bresnahan M.R., Zannis V.I., Gavras H.;
RT "Cloning and expression of a rat brain alpha 2b-adrenergic receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:1019-1023(1991).
RN 12)
RP SEQUENCE FROM N.A.

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RX MEDLINE=91130596; PubMed=1704126;
RA Voigt M.M., McCune S.K., Kanterman R.Y., Felder C.C.;
RT "The rat alpha 2-C4 adrenergic receptor gene encodes a novel
RT pharmacological subtype.";
RL FEBS Lett. 278:45-50(1991).
RN 13)
RP SEQUENCE FROM N.A.
RX MEDLINE=91244823; PubMed=1645350;
RA Lanier S.M., Downing S., Duzic E., Homcy C.J.;
RT "Isolation of rat genomic clones encoding subtypes of the alpha 2-
RT adrenergic receptor. Identification of a unique receptor subtype.";
RL J. Biol. Chem. 266:10470-10478(1991).
RN 14)
RP SEQUENCE FROM N.A.
RA Satoh M., Imai A., Shimomura H.;
RT "Cloning of rat alpha-2-B-adrenergic receptor gene and expression in
RT rat submandibular gland.";
RL Shigaku 80:317-326(1992).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; M58316; AAA0634.1; -
DR EMBL; X57659; CAA40861.1; -
DR EMBL; M62371; AAA42033.1; -
DR EMBL; D00819; BAA00700.1; -
DR PIR; A37869; A37869.
DR PIR; S13023; S13023.
DR PIR; A40392; A40392.
DR HSSP; P29274; 1MMH.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G-PROTEIN-RECEP_F1.1; 1.
DR PROSITE; PS50262; G-PROTEIN-RECEP_F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation.
FT DOMAIN 1 51 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 52 76 1 (POTENTIAL).
FT DOMAIN 77 88 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 89 114 2 (POTENTIAL).
FT DOMAIN 115 124 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 125 147 3 (POTENTIAL).
FT DOMAIN 148 168 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 169 191 4 (POTENTIAL).
FT DOMAIN 192 207 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 208 231 5 (POTENTIAL).
FT DOMAIN 232 379 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 380 403 6 (POTENTIAL).
FT DOMAIN 404 416 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 417 437 7 (POTENTIAL).
FT DOMAIN 438 458 CYTOPLASMIC (POTENTIAL).
FT CARBOHD 291 305 ARG-RICH (BASIC).
FT CARBOHD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 124 202 BY SIMILARITY.
FT CONFLICT 24 24 G -> R (IN REF. 4).
FT CONFLICT 40 40 G -> A (IN REF. 1).
FT CONFLICT 69 69 N -> T (IN REF. 1).
FT CONFLICT 155 155 O -> E (IN REF. 2).
FT CONFLICT 245 245 S -> T (IN REF. 1).
FT CONFLICT 252 252 G -> R (IN REF. 3).
FT CONFLICT 275 275 A -> R (IN REF. 4).

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FT CONFLICT 298 298 L -> V (IN REF. 3).
 SQ SEQUENCE 458 AA; 49864 MM; 6846C2AF63B3BF CRC64;
 Query Match 49.3%; Score 1175; DB 1; Length 458;
 Best Local Similarity 54.1%; Pred. No. 9.5e-46;
 Matches 252; Conservative 48; Mismatches 104; Indels 62; Gaps 12;

14 NCTEA-----PGGGRAT-----PYSLOVTLTVCLAGLMLLVFGNVLIAVFT 60
 19 NSDAGEMSGGAGANASGDWGPDPGQAGAVAGLAVALVFLVTVGVAVIAVLT 78
 61 SAKAPONLFLVSLASADILVATVTPPSLANEVMGWYKACETIYALDVLCTSS 120
 79 SRALAPONLFLVSLASADILVATVTPPSLANEVMGWYKACETIYALDVLCTSS 138
 121 IYHLAISLDKRYSTQVAVENLKRTPRIKAITTVAVISAPVSEPLTIEKGGGG 180
 139 IYHLAISLDKRYSTQVAVENLKRTPRIKAITTVAVISAPVSEPLTIEKGGGG 197
 181 POPAPCEINDOKWYVISCIGSEFAPCLIMILVYVYIYAKRRTVPSPRRGPDAVA 240
 198 ---AVPOGLNDEMTYIISCSGSEFAPCLIMGLVYVYVATKRTTSEKRG---A 251
 241 APPGCTERRPMLGPERSAGPAGAEPLPQOLNGAPGAPAGPRTDLDLESSSSD 300
 252 GPDGASPTTENGLG---KAAGENGHCAPP-RTEV-----EP-----DESSAAE 290
 301 HAERPPGRPRPGRGGRGKARASQVKGPDLSLRGPGATGIGTPAAGPGEERGAAKAS 360
 291 RRRRGALRRGGRREGEGDTGSADGPGGLAEQGARVTSRBP--GPGRLSRASSRS 348
 361 -----RMGR-----QNRKRTFVLAVYIGVAVVCMPEFFETVLTAV---GC 401
 349 VEFELSRRRRARRSSCRKRVANQARKRTFVLAVYIGVAVVCMPEFFETVLTAV---GC 408
 402 SVPRLEFFEFWFGYCNSSLNAPVYITTFNHPRAFKIICRGDRK 447
 409 QLPLELFFEFWFGYCNSSLNAPVYITTFNHPRAFKIICRGDRK 454

RESULT 11
 A2AB_CAVPO STANDARD; PRT; 448 AA.
 AC A2AB_CAVPO 060475;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor).
 CN ADRAB2B.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Hartley;
 RX MEDLINE=96152573; PubMed=8573196;
 RA Svensson S.P., Bailey T.J., Porter A.C., Richman J.G., Regan J.W.;
 RT "Heterologous expression of the cloned guinea pig alpha 2A, alpha 2B,
 RT and alpha 2C adrenoceptor subtypes. Radioligand binding and
 RT functional coupling to a CAMP-responsive reporter gene.";
 RL Biochem. Pharmacol. 51:291-300(1996).
 CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 CC PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U25723; AAA67075.1; -
 DR HSPB; P29274; 1MMH.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN_RECP_FL_1; 1.
 DR PROSITE: PS02652; G-PROTEIN_RECP_FL_2; 1.
 KW G-protein coupled receptor; transmembrane; Multigene family;
 KW Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 12
 FT TRANSMEM 13 38
 FT DOMAIN 39 49
 FT TRANSMEM 50 75
 FT DOMAIN 76 85
 FT TRANSMEM 86 108
 FT DOMAIN 109 130
 FT TRANSMEM 131 153
 FT DOMAIN 154 168
 FT TRANSMEM 169 192
 FT DOMAIN 193 370
 FT TRANSMEM 371 394
 FT DOMAIN 395 403
 FT TRANSMEM 404 427
 FT DOMAIN 428 448
 FT DISULFID 85 163
 FT LIPID 440 440
 FT DOMAIN 294 309
 FT SITE 92 92
 FT SITE 175 175
 FT SITE 175 175
 FT SITE 179 179
 SQ SEQUENCE 448 AA; 49597 MM; 8384F875E404777 CRC64;
 Query Match 49.2%; Score 1171.5; DB 1; Length 448;
 Best Local Similarity 53.6%; Pred. No. 1.3e-47;
 Matches 245; Conservative 46; Mismatches 105; Indels 61; Gaps 11;

27 PYSLOVTLTVCLAGLMLLVFGNVLIAVFTSRALAPONLFLVSLASADILVATLV 86
 6 PYSVQATAIAIAVITFLILFTIRGNALVILAVTSLSLPQNLFVSLAADIATLI 65
 87 IPRSLANEVGYWYKACETIYALDVLFCSSIVHLCAISLDKRYSTQVAVENLKR 146
 66 IPRSLANELLGWYFWRTCEVYALDVLFCSSIVHLCAISLDKRYSTQVAVENLKR 125
 147 PRIKAITTVAVISAPVSEPLTIEKGGGGPOAPAPCEINDOKWYVISCIGSPF 206
 126 PRIKAITTVAVISAPVSEPLTIEKGGGGPOAPAPCEINDOKWYVISCIGSPF 181
 207 APCLIMILVYVYIYAKRRTVPSRRGPDVAAPPGTERRPMLGPERSAGFGAEA 266
 182 APCLIMILVYVYIYAKRRTVPSRRGPDVAAPPGTERRPMLGPERSAGFGAEA 233
 267 EPLPQLNG---APGAPAGPRTDLDLESSSSDHAERPPGRPRGGRGKARA 323
 234 PPLASPLSTGEANGHPKPTGKE-----EETSDPEARTLPPSWAALPTSGGQAKA 287
 324 SQVCP-----GDSL-PRRPG-----ATGIGTPAAGPGE 351
 288 VYLAPEAE 346
 352 ERYGAAKASRMGR--QNRKRTFVLAVYIGVAVVCMPEFFETVLTAV---GCSVPT 406
 347 --VGAVDGGMWRRRQOMTREKRTFVLAVYIGVAVVCMPEFFETVLTAV---GCSVPT 404
 407 LKFEFFWFGYCNSSLNAPVYITTFNHPRAFKIICR 443
 405 LKFEFFWFGYCNSSLNAPVYITTFNHPRAFKIICR 441

```

RESULT 12
A2AC_DIDMA STANDARD: PRT: 469 AA.
ID A2AC_DIDMA PRT: 469 AA.
AC P35405;
DT 01-JUN-1994 (Rel. 29, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-2C adrenergic receptor (Alpha-2C adrenoceptor).
OS Dielphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
NCBI_TaxID=9267;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=94158793; PubMed=7509437;
RA Blaxall H.S., Cerulis D., Hass N.A., Iversen L.J., Bylund D.B.;
RT Cloning and expression of the alpha 2C-adrenergic receptor from the
RT OK cell line.";
RL Mol. Pharmacol. 45:176-181(1994).
RN [2]
RN REVISIONS TO 60; 75; 110; 143; 326-332; 365 AND 432.
RA Bylund D.B.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC or send an email to license@isb-sib.ch).
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DR EMBL: U04310; AAA17566.2; -.
DR HSP: P29274; 1MMH.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOODPSN.
DR PROSITE: PS00237; G-PROTEIN_RECPT_FL_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECPT_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation.
FT DOMAIN 1 41 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 42 62 1 (POTENTIAL).
FT DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 73 93 2 (POTENTIAL).
FT DOMAIN 94 109 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 110 130 3 (POTENTIAL).
FT DOMAIN 131 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 175 4 (POTENTIAL).
FT DOMAIN 176 195 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 196 216 5 (POTENTIAL).
FT DOMAIN 217 386 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 387 407 6 (POTENTIAL).
FT DOMAIN 408 427 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 428 448 7 (POTENTIAL).
FT DOMAIN 449 469 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 470 493 HIS-RICH (BASIC).
FT CAROHD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFD 109 187 BY SIMILARITY.
SQ SEQUENCE 469 AA; 53223 MW; 6F97D3718CC15C18 CRC64;
Query Match 48.2%; Score 1147; DB 1; Length 469;
Best Local Similarity 50.9%; Pred. No. 1.8e-46;
Matches 249; Conservative 52; Mismatches 106; Indels 82; Gaps 12;

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QY 7 DAGNANMGTEAPGCGARAP--YSLOVTLTLVCLAGLMLTFYGVNLVIAVTSRAL 64
DB 11 DSGDGGSSNESL---QKPPSYSPAEVAGLAIVVSEFLVTVGVNLVIAVLISRAL 67
QY 65 KAPONLEFLVSLASADIVATLVIPFSLANEWGYGKAMCEIYLADLVFCSTSYHL 124
DB 68 KAPONLEFLVSLASADIVATLVIPFSLANEWGYGKAMCEIYLADLVFCSTSYHL 127
QY 125 CAISLDRTWSTQALIEYNLAKTPRRKAIITTVWISAVISFPPLISEKGGGGCPQA 184
DB 128 CAISLDRTWSTQALIEYNLAKTPRRKAIITTVWISAVISFPPLISLUR-----DPE 180
QY 185 E---PRCINQKRWYVSSCGSFAPCLIMITVYVRYTOAKRRTPVPSRGRDAVAA 241
DB 181 DDLVPQCELDNEIWTYLISSCGSFFAPCLIMLVYVRYTAKRLRTLSKR-----T 234
QY 242 PPGSTERRPNCIG--PERSAGPGAEPPLPTOLGABEPAPAPR----- 286
DB 235 VPESSSQTEENGSLRPYAGAPSTAAAMASLRQ-----AGENGHYLHHHHHLH 286
QY 287 -----DTDALDESSSDHAERPRPRPRPRPRPRPRPRPRPRPRPRPRPRPR 332
DB 287 HHHHHHOLRKSALIEDIELESSTSENRR-----RSREBAARKSGRFSFS 336
QY 333 --PRRGPGATGIGTPAAGPGEERYGAAKASRWGR-----QNEKAPFPVLAIVIG 381
DB 337 FSTRKGOSAGASAELEDELESSTSENRR-----RSREBAARKSGRFSFS 386
QY 382 VFVVCWPFPEFTYTLAV--GCSVPRTLKFFKPFYGCNSLNIPVYITFNHFRAPK 438
DB 397 VFVVCWPFPEFTYTLAV--GCSVPRTLKFFKPFYGCNSLNIPVYITFNHFRAPK 436
QY 439 KIICRGDRK 447
DB 457 HILFKKKK 465
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RESULT 13
A2AR_LABOS STANDARD: PRT: 432 AA.
ID A2AR_LABOS PRT: 432 AA.
AC Q91081;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-1998 (Rel. 36, Last annotation update)
DE Alpha-2 adrenergic receptor (Alpha-2 adrenoceptor).
OS Labrus ossilagus (Cuckoo wrasse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidel;
OC Labridae; Labrus.
NCBI_TaxID=30800;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=94035926; PubMed=7693288;
RA Svensson S.P.S., Bailey T.J., Pepperl D.J., Grundstrom N.,
RA Ala-Dotolia S., Scheinin M., Karlsson J.O.G., Regan J.W.;
RT Cloning and expression of a fish alpha 2-adrenoceptor.;
RL Br. J. Pharmacol. 110:54-60(1993).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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RP	SEQUENCE FROM N.A.
RC	STRAIN-DBA/2; TISSUE=Liver;
RX	MEDLINE=93129625; PubMed=1336396;
RA	Chen W.-M., Chang A.C., Shie B.-J., Chang Y.-H., Chang N.-C.A.;
RL	"Molecular cloning and characterization of a mouse alpha 2C2
RT	adrenoceptor subtype gene,"
RT	Biochim. Biophys. Acta 1171:219-223(1992).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=92378586; PubMed=1354956;
RA	Chruscieliski A.J., Link R.E., Daut D.A., Barsh G.S., Koblika B.R.;
RL	"Cloning and expression of the mouse homolog of the human alpha 2-C2
RT	adrennergic receptor,"
RT	Biochem. Biophys. Res. Commun. 186:1280-1287(1992).
CC	-1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC	INDUCED INHIBITION OF ADENYLYLATE CYCLASE THROUGH THE ACTION OF G
CC	PROTEINS.
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC	-----
DR	EMBL; M94583; AAA73895.1; -
DR	EMBL; L00979; AAA57131.1; ALT_INIT.
DR	PIR; JH0693; JH0693.
DR	PIR; S28221; S28221.
DR	HSSP; P29274; 1MMH.
DR	MGI:87935; Adra2b.
DR	InterPro: IPR000276; GPCR_Rhodopsn.
DR	Pfam: PF00001; 7tm_1; 1.
DR	PRINTS; PRO0237; GPCR_RHODOPSN.
DR	PROSITE; PS00237; G_PROTEIN_RECPE_FL_1; 1.
DR	PROSITE; PS50262; G_PROTEIN_RECPE_FL_2; 1.
KW	G-protein coupled receptor; Transmembrane; Multigene family;
KW	Phosphorylation; Lipoprotein; Palmitate.
FT	DOMAIN 1 17
FT	TRANSMEM 18 42
FT	DOMAIN 43 54
FT	TRANSMEM 55 80
FT	DOMAIN 81 90
FT	TRANSMEM 91 113
FT	DOMAIN 114 135
FT	TRANSMEM 136 158
FT	DOMAIN 159 174
FT	TRANSMEM 175 198
FT	DOMAIN 199 377
FT	TRANSMEM 378 401
FT	DOMAIN 402 410
FT	TRANSMEM 411 434
FT	DOMAIN 435 455
FT	DISULFID 90 169
FT	LIPID 447 447
FT	DOMAIN 306 316
FT	SITE 97 97
FT	SITE 181 181
FT	SITE 185 185
FT	CONFLICT 202 202
FT	CONFLICT 229 230
SO	SEQUENCE 455 AA; 50615 MW; A3954AD76EDB6263 CRC64;
Query Match	47.0%; Score 1119.5; DB 1; Length 455;
Best Local Similarity	53.0%; Pred. No. 3.3e-45;
Matches 242; Conservative	49; Mismatches 107; Indels 59; Gaps 14;

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OM protein - protein search, using sw model

Run on: February 15, 2003, 14:14:47 ; Search time 13.5 Seconds

(without alignments)
1382.544 Million cell updates/sec

Title: US-09-636-259b-4

Perfect score: 2380

Sequence: 1 MGSLQPDAGNAGNMGTEAPG.....HDFRRAPKRLICRGDRKRIY 450

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2375	99.8	450	A2AA_HUMAN	P08913 homo sapien
2	2221	93.3	450	A2AA_PIG	P18871 sus scrofa
3	2193	92.1	450	A2AA_MOUSE	O01338 mus musculu
4	2182	91.7	450	A2AA_CAVPO	O60474 cavia porce
5	2160	90.8	450	A2AA_RAT	P22909 rattus norv
6	2114	88.8	452	A2AA_BOVIN	Q28838 bos taurus
7	1182	49.7	462	A2AC_HUMAN	P18825 homo sapien
8	1173.5	49.3	448	A2AC_CAVPO	O60475 cavia porce
9	1173	49.3	458	A2AC_MOUSE	O01337 mus musculu
10	1173	49.3	458	A2AC_RAT	P22086 rattus norv
11	1171.5	49.2	455	A2AC_CAVPO	O60476 cavia porce
12	1146	48.2	469	A2AC_DIDMA	P33405 didelphis m
13	1127.5	47.4	450	A2AB_HUMAN	P18089 homo sapien
14	1126.5	47.3	432	A2AR_LABOS	O91081 labrus ossi
15	1121.5	47.1	455	A2AB_MOUSE	P30545 mus musculu
16	1100.5	46.2	453	A2AB_RAT	P19328 rattus norv
17	1018.5	42.8	436	A2AR_CAVPO	P33251 carassius a
18	946	38.7	382	A2AB_DIDMA	O77713 didelphis m
19	934	39.2	384	A2AB_ELEMA	O19014 elephas max
20	931	39.1	386	A2AB_AMBHO	O18935 amblysomus
21	929	39.0	390	A2AB_DUGDU	O77713 dugong dugu
22	928	39.0	388	A2AB_ORYAF	O19032 oryctolopus
23	927	38.9	394	A2AB_RABIT	O77830 oryctolagus
24	925.5	38.9	389	A2AB_PROHA	O19054 procavia ca
25	921.5	38.7	387	A2AB_MACPR	O19025 macrotelid
26	921	38.7	389	A2AB_HORSE	O77700 bos taurus
27	920	38.7	392	A2AB_BOVIN	O19012 equus cabal
28	916.5	38.5	391	A2AB_ERIEU	O19012 erinaceus e
29	896	37.6	384	A2AB_ECHRE	O77723 echinops te
30	893.5	37.5	397	A2AB_TALEU	O19091 talpa europ
31	693.5	29.1	484	ORAL_LOCOM	O23321 locusta mig
32	692.5	29.1	484	ORAL_LOCOM	O23322 locusta mig
33	681.5	28.6	379	GRE2_BALAM	O93127 balanus amp

34	652	27.4	476	GRE1_BALAM	O93126 balanus amp
35	649	27.3	601	OAR_PROME	P22270 drosophila
36	640.5	26.9	477	OAR_HELVI	O25188 heliothia v
37	632.5	26.6	479	OAR_BOMO	O17232 bombyx mori
38	626.5	26.3	443	D2DR_CERAE	P52702 ceropithec
39	624	26.2	444	D2DR_BOVIN	P20288 bos taurus
40	624	26.2	463	D2DR_FUGRI	P53453 fugu rubrip
41	621.5	26.1	443	D2DR_HUMAN	P14416 homo sapien
42	613	25.8	444	D2DR_MOUSE	P13953 mus musculu
43	611	25.7	377	SHID_CANFA	P16164 canis famli
44	608.5	25.6	442	D2DI_XENLA	P24628 xenopus lae
45	605	25.4	376	SHID_CAVPO	O60484 cavia porce

ALIGNMENTS

RESULT 1
ID A2AA_HUMAN STANDARD; PRT; 450 AA.
AC P08913;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR subtype C10).
GN ADRA2A OR ADRA2R OR ADRAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89308571; PubMed=2568356;
RA Fraser C.M., Arikawa S., McCombie W.R., Venter J.C.;
RT "Cloning, sequence analysis, and permanent expression of a human alpha 2-adrenergic receptor in Chinese hamster ovary cells. Evidence for independent pathways of receptor coupling to adenylate cyclase attenuation and activation.";
RT J. Biol. Chem. 264:11754-11761(1989).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX TISSUE=Platelet;
RA MEDLINE=86042789; PubMed=2823383;
RA Koblika B.K., Matsui H., Koblika T.S., Yang-Feng T.L., Francke U.,
RA Caton M.G., Lefkowitz R.J., Regan J.W.;
RT "Cloning, sequencing, and expression of the gene coding for the human platelet alpha 2-adrenergic receptor.";
RT Science 238:650-656(1987).
RN [3]
RP REVISIONS TO 333-365.
RX MEDLINE=9109167; PubMed=2170371;
RA Guyer C.A., Horstman D.A., Wilson A.L., Clark J.D., Krage E.J. Jr.,
RA Limbird L.E.;
RT "Cloning, sequencing, and expression of the gene encoding the porcine alpha 2-adrenergic receptor. Allosteric modulation by Na⁺, H⁺, and aniloride analogs.";
RT J. Biol. Chem. 265:17307-17317(1990).
RN [4]
RP MUTAGENESIS OF PHE-412.
RX MEDLINE=91332079; PubMed=1678390;
RA Suvanyaratana S., Daunt D.A., von Zastrow M., Koblika B.K.;
RT "A point mutation in the seventh hydrophobic domain of the alpha 2 adrenergic receptor increases its affinity for a family of beta receptor antagonists.";
RT J. Biol. Chem. 266:15488-15492(1991).
RN [5]
RP MUTAGENESIS OF ASPARTIC ACID AND SERINE RESIDUES.
RX MEDLINE=91342598; PubMed=1678850;
RA Wang C.-D., Buck M.A., Fraser C.M.;
RT "Site-directed mutagenesis of alpha 2a-adrenergic receptors: Identification of amino acids involved in ligand binding and receptor activation by agonists.";

RL Mol. Pharmacol. 40:168-179(1991).

CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIANE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS. THE RANK ORDER OF POTENCY FOR AGONISTS OF THIS RECEPTOR
CC IS OXIMETAZOLINE > CLONIDINE > EPINEPHRINE > NOREPINEPHRINE >
CC PHENYLEPHRINE > DOPAMINE > P-SYNEPHRINE > P-TYRINE > SEROTONIN -
CC P-OCTOPAMINE. FOR ANTAGONISTS, THE RANK ORDER IS YOHIMBINE >
CC PHENOLAMINE = MANSERINE > CHLOROPRAMAZINE = SPIPERONE = PRAZOSIN
CC > PROPRANOLOL > ALPENOLOL = PINDOLOL.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC -----

DR EMBL; M23533; AAA51665.1; -.

DR EMBL; M18415; AAA51664.1; -.

DR PIR; A34169; A34169.

DR PIR; A40132; A40132.

DR HSSP; P29274; 1MMH.

DR Genew; HGNC:281; ADRA2A.

DR MIM; 104210; -.

DR InterPro: IPR000276; GPCR_Rhodopsn.

DR Pfam: PF00001; 7tm.1; 1.

DR PRINTS; PR00237; GPCRHOPOPSN.

DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.

DR PROSITE; PS50262; G-PROTEIN_RECEP_FL_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multisene family; Phosphorylation; Lipoprotein; Palmitate.
KW DOMAIN 1 33
FT DOMAIN 1 33
FT TRANSSEM 34 59
FT TRANSSEM 60 70
FT TRANSSEM 71 96
FT TRANSSEM 97 106
FT TRANSSEM 107 129
FT TRANSSEM 130 149
FT TRANSSEM 150 173
FT TRANSSEM 174 192
FT TRANSSEM 193 217
FT TRANSSEM 218 374
FT TRANSSEM 375 399
FT TRANSSEM 400 406
FT TRANSSEM 407 430
FT TRANSSEM 431 450
FT CARBOHYD 10 14
FT CARBOHYD 14 14
FT DISULFID 106 188
FT LIPID 442 442
FT SITE 113 113
FT SITE 200 200
FT SITE 204 204
FT SITE 79 79
FT MUTAGEN 113 113
FT MUTAGEN 130 130
FT MUTAGEN 200 200
FT MUTAGEN 204 204
FT MUTAGEN 412 412

FT FT ANTAGONIST YOHIMBINE, 3000X INCREASE FOR
FT FT BETA-ANTAGONIST ALPENOLOL.
FT FT CONFLICT 104 104 A -> T (IN REF. 2).
FT FT CONFLICT 157 157 V -> C (IN REF. 2).
FT FT CONFLICT 333 365 PRGGGATGGIGTPAGPEEREEVGAAKASRWGR ->
FT FT CONFLICT 368 368 PRGGRGSGRRLOGRRRSASGLPERRAGAG
FT FT CONFLICT 368 368 (IN REF. 1 AND 2).
FT FT CONFLICT 48956 MM; A703CG262F04E8AC CXC64;
SQ SEQUENCE 450 AA; 48956 MM; A703CG262F04E8AC CXC64;

Query Match 99.8%; Score 2375; DB 1; Length 450;
Best local Similarity 99.8%; Pred. No. 5.7e-103;
Matches 449; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSGLDQDAGNAGNNGTEAGGAGARATPYSLQVTLITVCLAGLMLTFEGNVLTIAFT 60
DB 1 MSGLDQDAGNAGNNGTEAGGAGARATPYSLQVTLITVCLAGLMLTFEGNVLTIAFT 60

QY 61 SRALKAPQNLFLVSLASADILVATVIPSFLANEVGYWFGKAWCEIYLALDVLFCYSS 120
DB 61 SRALKAPQNLFLVSLASADILVATVIPSFLANEVGYWFGKAWCEIYLALDVLFCYSS 120

QY 121 IYHLCASIDRWSTTQALEYMLKRPRIKAIITVWISAVISFPPLISTEKKGGGG 180
DB 121 IYHLCASIDRWSTTQALEYMLKRPRIKAIITVWISAVISFPPLISTEKKGGGG 180

QY 181 POPAEPCEINQKMWVISCIGSFAPCLIMILVYVRVYQAKRRTRVPSRRGPDAVA 240
DB 181 POPAEPCEINQKMWVISCIGSFAPCLIMILVYVRVYQAKRRTRVPSRRGPDAVA 240

QY 241 APPGTERPPKGLGPPRSAGPGAEAPLPTQNLNAPGEPADAGPRDIALDESSSSD 300
DB 241 APPGTERPPKGLGPPRSAGPGAEAPLPTQNLNAPGEPADAGPRDIALDESSSSD 300

QY 241 APPGTERPPKGLGPPRSAGPGAEAPLPTQNLNAPGEPADAGPRDIALDESSSSD 300
DB 241 APPGTERPPKGLGPPRSAGPGAEAPLPTQNLNAPGEPADAGPRDIALDESSSSD 300

QY 301 HAERPGRPPRRPGRPGKAKARASQYKPGDSIPRGGPATGTGCTAAGGEEVRVAAS 360
DB 301 HAERPGRPPRRPGRPGKAKARASQYKPGDSIPRGGPATGTGCTAAGGEEVRVAAS 360

QY 361 RMGRGRNRKRRTPYLAIVGVVCMPPFFTYLLTANAGSVPTLTKRFFWFEGCNS 420
DB 361 RMGRGRNRKRRTPYLAIVGVVCMPPFFTYLLTANAGSVPTLTKRFFWFEGCNS 420

QY 421 LNPVYITFNHDFRRAFKKILCRGDRKRV 450
DB 421 LNPVYITFNHDFRRAFKKILCRGDRKRV 450

RESULT 2
ID A2AA_PIG STANDARD; PRT; 450 AA.
AC P18871;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR).
GN ADRA2A OR A2AR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 212-232.
RC TISSUE=Liver;
RX MEDLINE=91009167; PubMed=2170371;
RA Guyer C.A., Horstman D.A., Wilson A.L., Clark J.D., Kragoe E.J. Jr.,
RA Limbird L.E.;
RT "Cloning, sequencing, and expression of the gene encoding the porcine
RT alpha-2-adrenergic receptor. Allosteric modulation by Na⁺, H⁺, and
RT aniloride analogs.";
RL J. Biol. Chem. 265:17307-17317(1990).
RN [2]
RP MUTAGENESIS OF CYS-442.
RX MEDLINE=93216775; PubMed=8385131;

RA Kennedy M.E., Limbird L.E.;
 RT *Mutations of the alpha 2A-adrenergic receptor that eliminate
 RT detectable palmitoylation do not perturb receptor-G-protein
 RT coupling".
 RL J. Biol. Chem. 268:8003-8011(1993).
 CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 CC PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- MISCELLANEOUS: ALPHA2-ADRENERGIC RECEPTOR SHOWS AN ALLOSTERIC
 CC MODULATION BY NA⁺, H⁺, AND AMLODIPINE ANALOGS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: J05652; AAA30984.1; -.
 DR PIR: A38316; A38316.
 DR HSP: P29274; IMM.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G-PROTEIN_RECP_FL_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 33
 FT TRANSMEM 34 59
 FT DOMAIN 60 70
 FT TRANSMEM 71 96
 FT DOMAIN 97 106
 FT TRANSMEM 107 129
 FT DOMAIN 130 149
 FT TRANSMEM 150 173
 FT DOMAIN 174 192
 FT TRANSMEM 193 217
 FT DOMAIN 218 374
 FT TRANSMEM 375 399
 FT DOMAIN 400 409
 FT TRANSMEM 410 430
 FT DOMAIN 431 450
 FT CARBOHD 10 10
 FT CARBOHD 14 14
 FT DISULFD 106 188
 FT LIPID 442 442
 FT SITE 113 113
 FT SITE 200 200
 FT SITE 204 204
 FT SITE 204 204
 FT MUTAGEN 442 442
 FT SEQUENCE 450 AA; 48975 MM; 79D75B47372074E CXC64;
 SO

Query Match 93.3%; Score 2221; DB 1; Length 450;
 Best Local Similarity 93.8%; Pred. No. 6.7e-96;
 Matches 422; Conservative 3; Mismatches 25; Indels 0; Gaps 0;

DB 121 IVHCAISLDKRWYSITQAEYENLKRTPRRIKAITVWVISAIVISFPPPLISTIEKKAGCGG 180
 QY 181 POPAPREINIDOKWYVSSCISGFAPCLMILVYRIYQIARRRVRPPSRGCPAVA 240
 DB 181 QOPAPREINIDOKWYVSSCISGFAPCLMILVYRIYQIARRRVRPPSRGCPAAA 240
 QY 241 APPGTERPPGLDPERSGAEEPLPTQLNGACGEPAPAPRPTDALDIESSSSD 300
 DB 241 ALPGAEERRPGLDPERGVGVGAEEPLPYQLNGACGEPAPAPRPTDALDIESSSSSE 300
 QY 301 HAERPGRPRERPRGCKGKARASQVKGDSLPRRGATGICGTPAAGCEERYGAAKAS 360
 DB 301 HAERPGRPRERPRGCKGKARASQVKGDSLPRRGATGICGTPAAGCEERYGAAKAS 360
 QY 361 RWRGQNERKFTVLAIVGVVCMFPFFFTYTLTAVGCVSRPTLKFPPWGYCNSS 420
 DB 361 RWRGQNERKFTVLAIVGVVCMFPFFFTYTLTAVGCVSRPTLKFPPWGYCNSS 420
 QY 421 LNPVYITFNHDFRRAFKILCRGDKRIY 450
 DB 421 LNPVYITFNHDFRRAFKILCRGDKRIY 450

RESULT 3
 A2AA_MOUSE STANDARD; PRT; 450 AA.
 ID A2AA_MOUSE
 AC 001338:
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR).
 GN ADRA2A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92342131; PubMed=1353249;
 RA Link R.E., Daut D.A., Barsh G., Chrusciński A.J., Koblika B.K.;
 RT "Cloning of two mouse genes encoding alpha 2-adrenergic receptor
 RT subtypes and identification of a single amino acid in the mouse alpha
 RT 2-C10 homolog responsible for an interspecies variation in
 RT antagonist binding.";
 RL Mol. Pharmacol. 42:16-27(1992).
 CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 CC PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M99377; AAA37213.1; -.
 DR HSP: P29274; IMM.
 DR MCD: MGI:87934; Adra2a.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G-PROTEIN_RECP_FL_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 33
 FT TRANSMEM 34 59
 FT DOMAIN 60 70
 FT TRANSMEM 71 96

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FT DOMAIN 97 106 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 107 129 3 (POTENTIAL).
FT DOMAIN 130 149 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 150 173 4 (POTENTIAL).
FT DOMAIN 174 192 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 193 217 5 (POTENTIAL).
FT DOMAIN 218 374 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 375 399 6 (POTENTIAL).
FT DOMAIN 400 409 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 410 430 7 (POTENTIAL).
FT DOMAIN 431 450 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 188 BY SIMILARITY.
FT LIPID 442 442 PALMITATE (BY SIMILARITY).
FT SITE 113 113 IMPLICATED IN LIGAND BINDING (BY SIMILARITY).
FT SITE 200 200 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
FT SITE 204 204 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
SQ SEQUENCE 450 AA; 48865 MW; F07E25393AFA93B CRC64;

Query Match 92.1%; Score 2193; DB 1; Length 450;
Best Local Similarity 92.0%; Pred. No. 1.3e-94;
Matches 414; Conservative 8; Mismatches 28; Indels 0; Gaps 0;

QY 1 MGSLOPDAGNASMNGTEAPGGARATPSLOYTLVLVCLAGLLMLTFVGNVLIIVFT 60
D 1 MGSLOPDAGNSMNGTEAPGGATRATPSLOYTLVLVCLAGLLMLTFVGNVLIIVFT 60
QY 61 SRAKAPQNLFLVSLASADILVATLVIPFSLANEMGWYFGRKWCETIYALDVFCTSS 120
D 61 SRAKAPQNLFLVSLASADILVATLVIPFSLANEMGWYFGRKWCETIYALDVFCTSS 120
QY 61 SRAKAPQNLFLVSLASADILVATLVIPFSLANEMGWYFGRKWCETIYALDVFCTSS 120
D 61 SRAKAPQNLFLVSLASADILVATLVIPFSLANEMGWYFGRKWCETIYALDVFCTSS 120
QY 121 IVHCAISLDRTYSITQATIEYNLKRTPRIKAIITVWVSAVISFPPLISIEKKGSGG 180
D 121 IVHCAISLDRTYSITQATIEYNLKRTPRIKAIITVWVSAVISFPPLISIEKKGSGG 180
QY 181 POPAEPCEINDOKWYVSSICSGFAPCLIMLVYVYIOIARRTVRPPSRGPDVA 240
D 181 QOPAPESCKINDOKWYVSSISGFFAPCLIMLVYVYIOIARRTVRPPSRGPDVA 240
QY 241 APGGTERPRKGLPERSAGGAEAPLPTOLNGAPGEPAPGRDGLDLESSSSD 300
D 241 APGGADRRPGLPERSAGGAEAPLPTOLNGAPGEPAPGRDGLDLESSSSD 300
QY 301 HAERPPGRRERPRGKARASQVKSQVPSLPRRGATGIGTPAAGPEERYGAAKAS 360
D 301 HAERPPGRRERPRGKARASQVKSQVPSLPRRGATGIGTPAAGPEERYGAAKAS 360
QY 361 RWRGRONERKFTFVLAVVIGVYVVCWPPFFTYTLTAVGCSVPRTLKFFPFWGYCNSS 420
D 361 RWRGRONERKFTFVLAVVIGVYVVCWPPFFTYTLTAVGCSVPRTLKFFPFWGYCNSS 420
QY 421 LNPVIYTFENHDFRRAFKILCRGDKRIY 450
D 421 LNPVIYTFENHDFRRAFKILCRGDKRIY 450

RESULT 4
A2AA_CAVPO STANDARD; PRT; 450 AA.
AC 0604/4;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR).
GN ADR2A.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
NCBI_TaxId=10141;
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RN [1]
SEQUENCE FROM N.A.
RP STRAIN-Hartley;
RC MEDLINE=96152573; PubMed=8573196;
RX Svensson S.P., Bailey T.J., Porter A.C., Richman J.G., Regan J.W.,
RT "Heterologous expression of the cloned guinea pig alpha 2A, alpha 2B,
and alpha 2C adrenoceptor subtypes. Radioligand binding and
functional coupling to a CAMP-responsive reporter gene.",
RL Biochem. Pharmacol. 51:291-300(1996).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-
INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U25722; AAA67074.1; -.
DR HSSP: P29274; 1MMH.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1.1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_REC_F1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_REC_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 34 59 1 (POTENTIAL).
FT DOMAIN 60 70 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 71 96 2 (POTENTIAL).
FT DOMAIN 97 106 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 107 129 3 (POTENTIAL).
FT DOMAIN 130 149 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 150 173 4 (POTENTIAL).
FT DOMAIN 174 192 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 193 217 5 (POTENTIAL).
FT DOMAIN 218 374 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 375 399 6 (POTENTIAL).
FT DOMAIN 400 409 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 410 430 7 (POTENTIAL).
FT DOMAIN 431 450 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 187 BY SIMILARITY.
FT LIPID 442 442 PALMITATE (BY SIMILARITY).
FT SITE 113 113 IMPLICATED IN LIGAND BINDING (BY SIMILARITY).
FT SITE 199 199 IMPLICATED IN AGONIST BINDING AND RECEPTOR ACTIVATION (BY SIMILARITY).
FT SITE 203 203 IMPLICATED IN AGONIST BINDING RECEPTOR ACTIVATION (BY SIMILARITY).
FT FT
SQ SEQUENCE 450 AA; 48910 MW; E6BBE9A1FFBDD1 CRC64;

Query Match 91.7%; Score 2182; DB 1; Length 450;
Best Local Similarity 92.2%; Pred. No. 4.1e-94;
Matches 416; Conservative 8; Mismatches 25; Indels 2; Gaps 2;

QY 1 MGSLOPDAGNASMNGTEAPGGARATPSLOYTLVLVCLAGLLMLTFVGNVLIIVFT 60
D 1 MGSLOPDAGNSMNGTEAPGGATRATPSLOYTLVLVCLAGLLMLTFVGNVLIIVFT 60
QY 61 SRAKAPQNLFLVSLASADILVATLVIPFSLANEMGWYFGRKWCETIYALDVFCTSS 120
D 61 SRAKAPQNLFLVSLASADILVATLVIPFSLANEMGWYFGRKWCETIYALDVFCTSS 120
QY 61 SRAKAPQNLFLVSLASADILVATLVIPFSLANEMGWYFGRKWCETIYALDVFCTSS 120
D 61 SRAKAPQNLFLVSLASADILVATLVIPFSLANEMGWYFGRKWCETIYALDVFCTSS 120
QY 121 IVHCAISLDRTYSITQATIEYNLKRTPRIKAIITVWVSAVISFPPLISIEKKGSGG 180
D 121 IVHCAISLDRTYSITQATIEYNLKRTPRIKAIITVWVSAVISFPPLISIEKKGSGG 180
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Db 121 IYHLCALISDRWYSITQALEYVNLKRTPRRIKAIITVWVISAIVISPPPLISFE-KAGGGG 179
Qy 181 POPAEPRCEINDOKWYVSSICGSFFAPCLIMLVYRIYQIAKRTTRVPSRGPDA-V 239
Db 180 QOPAEPRCEINDOKWYVSSICGSFFAPCLIMLVYRIYQIAKRTTRVPSRGPDA 239
Qy 240 AAPPGGTERPRKGLGERSAGPGAEAEPLPTQNLNAPCEPPAPAGRDADLDLESSSS 299
Db 240 AAPPGGTERPRKGLGERSAGPGAEAEPLPTQNLNAPCEPPAPAGRDADLDLESSSS 299
Qy 300 DHAERPPGRPRPERGPRGKAGKASQVKGDSLPFRGPGATGIGTPAAGPGEERYGAKA 359
Db 300 EHAERPPGARPRPERGLRAKSKASASQVKGDSLPFRAPGAGSGTSGSGPGEERGAKA 359
Qy 360 SRMRGQNRKRTFVLAVYIGVFYVVCWPPFFTYTLTAVGSGVPTLTKFFFWGYCNS 419
Db 360 SRMRGQNRKRTFVLAVYIGVFYVVCWPPFFTYTLTAVGSGVPTLTKFFFWGYCNS 419
Qy 420 SLNPVITYTFNHDFFRAFKKILCRGDRKRIY 450
Db 420 SLNPVITYTFNHDFFRAFKKILCRGDRKRIY 450

RESULT 5
A2AA_RAT STANDARD: PRT: 450 AA.
AC P22909:
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2a adrenergic receptor (Alpha-2a adrenoreceptor) (Alpha-2AAR)
DE (CA2-47) (Alpha-2b adrenergic receptor).
GN ADR2A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid-10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91244823; PubMed-1645350;
RA Lanier S.M., Downing S., Duzic E., Homcy C.J.;
RT Isolation of rat genomic clones encoding subtypes of the alpha 2-
RL adrenergic receptor. Identification of a unique receptor subtype.;
RL J. Biol. Chem. 266:10470-10478(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-91125329; PubMed-2177834;
RA Chaberg S.C., Duda T., Rhine J.A., Sharma R.K.;
RT Molecular cloning, sequencing and expression of an alpha 2-adrenergic
RL receptor complementary DNA from rat brain.;
RL Mol. Cell. Biochem. 97:161-172(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-95349560; PubMed-7623790;
RA Wyp1ewski K., Duda T., Sharma R.K.;
RT Structural, genetic and pharmacological identity of the rat alpha
RL 2-adrenergic receptor subtype CA2-47 and its molecular
RT characterization in rat adrenal, adrenocortical carcinoma and bovine
RL retina.;
RL Mol. Cell. Biochem. 144:181-190(1995).
RN [4]
RP FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL: M62372; AAA42034.1; -.
DR EMBL: U79031; AAC24959.1; -.
DR PIR: B40392; B40392.
DR PIR: JH0190; JH0190.
DR HSSP: P29274; 1MMH.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1.
DR PROSITE: PS0262; G-PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 33
FT TRANSMEM 34 59
FT DOMAIN 60 70
FT TRANSMEM 71 96
FT TRANSMEM 97 106
FT TRANSMEM 107 129
FT DOMAIN 130 149
FT TRANSMEM 150 173
FT TRANSMEM 174 192
FT TRANSMEM 193 217
FT DOMAIN 218 374
FT TRANSMEM 375 399
FT DOMAIN 400 409
FT TRANSMEM 410 430
FT DOMAIN 431 450
FT CARBOHYD 10 10
FT CARBOHYD 14 14
FT DISULFID 106 188
FT LIPID 442 442
FT SITE 113 113
FT SITE 200 200
FT SITE 204 204
FT SITE 204 204
FT CONFLICT 147 147
FT CONFLICT 154 158
FT CONFLICT 252 253
FT CONFLICT 264 264
FT CONFLICT 304 305
FT CONFLICT 333 333
FT CONFLICT 445 445
SQ SEQUENCE 450 AA; 48939 MM; AFA078DCA3D612AC CRC64;

Query Match 90.8%; Score 2160; DB 1; Length 450;
Best Local Similarity 90.7%; Pred. No. 4,2e-93;
Matches 408; Conservative 9; Mismatches 33; Indels 0; Gaps 0;

Qy 1 MSLQPDGNSMNGTTEAPGGGATPYSLQVTLTVCLAGLMLTFPGVLIYVFT 60
Db 1 MSLQPDGNSMNGTTEAPGGGATPYSLQVTLTVCLAGLMLTFPGVLIYVFT 60
Qy 61 SPALRAPQNLFLVSLASADIVATLVIPFSLANEVGYGKAMCEIYLAADVLECTSS 120
Db 61 SPALRAPQNLFLVSLASADIVATLVIPFSLANEVGYGKAMCEIYLAADVLECTSS 120
Qy 121 IYHLCALISDRWYSITQALEYVNLKRTPRRIKAIITVWVISAIVISPPPLISIEKKGGGG 180
Db 121 IYHLCALISDRWYSITQALEYVNLKRTPRRIKAIITVWVISAIVISPPPLISIEKKGGGG 180
Qy 181 POPAEPRCEINDOKWYVSSICGSFFAPCLIMLVYRIYQIAKRTTRVPSRGPDA 240
Db 181 POPAEPRCEINDOKWYVSSICGSFFAPCLIMLVYRIYQIAKRTTRVPSRGPDA 240
Qy 241 AAPPGGTERPRKGLGERSAGPGAEAEPLPTQNLNAPCEPPAPAGRDADLDLESSSSD 300
Db 241 AAPPGGTERPRKGLGERSAGPGAEAEPLPTQNLNAPCEPPAPAGRDADLDLESSSSD 300
Qy 301 HAERPPGRPRPERGPRGKAGKASQVKGDSLPFRGPGATGIGTPAAGPGEERYGAKAS 360
Db 301 HAERPPGRPRPERGPRGKAGKASQVKGDSLPFRGPGATGIGTPAAGPGEERYGAKAS 360

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Db 301 HAERQGGKPEGRPRANKTKASQVKGPSLPRRPGAAAGSAGSGGGERAGAKAS 360
QY 361 BRKGONREKRRTFLAVVIGVYVCMPEFFETTLTAVGSGVPTLTKFFFMGYCSS 420
Db 361 BRKGONREKRRTFLAVVIGVYVCMPEFFETTLTAVGSGVPTLTKFFFMGYCSS 420
QY 421 INPVTYITFNHDFRRAFKILCRGDKRRIV 450
Db 421 INPVTYITFNHDFRRAFKILCRGDKRRIV 450

RESULT 6
A2AA_BOVIN STANDARD: PRT; 452 AA.
AC 028838:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR)
GN ADRA2A.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98111113; PubMed=9450652;
RA Venkataraman V., Duda T., Sharma R.K.;
RT "The bovine alpha 2D-adrenergic receptor gene: structure, expression
RT in retina, and pharmacological characterization of the encoded
RT receptor";
RL Mol. Cell. Biochem. 177:113-123(1997).
RN [2]
RP SEQUENCE OF 171-210 FROM N.A.
RX MEDLINE=94018366; PubMed=8412494;
RA Blaxall H.S., Heck D.A., Bylund D.B.;
RT "Molecular determinants of the alpha-2D adrenergic receptor subtype.";
RL Life Sci. 53:9-9(1993).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: RETINA, BRAIN AND OLFACTORY LOBE.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U79030; AAC24958.1; -
DR EMBL; S66295; AAB28450.1; -
DR HSSP; P29274; IMM.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHDOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECPEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPEP_F1_2; 1.
KW G-protein coupled receptor; transmembrane; glycoprotein;
KW Multigene family; phosphorylation; lipoprotein; Palmitate.
FT DOMAIN 1 33 1 (POTENTIAL).
FT TRANSMEM 34 59 1 (POTENTIAL).
FT CYTOPLASMITC (POTENTIAL).
FT DOMAIN 60 70 2 (POTENTIAL).
FT TRANSMEM 71 96 2 (POTENTIAL).
FT DOMAIN 97 106 2 (POTENTIAL).
FT TRANSMEM 107 129 3 (POTENTIAL).
FT DOMAIN 130 149 3 (POTENTIAL).
FT TRANSMEM 150 173 4 (POTENTIAL).

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FT DOMAIN 174 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 217 5 (POTENTIAL).
FT DOMAIN 218 376 CYTOPLASMITC (POTENTIAL).
FT TRANSMEM 377 401 6 (POTENTIAL).
FT DOMAIN 402 411 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 412 432 7 (POTENTIAL).
FT DOMAIN 433 452 CYTOPLASMITC (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 188 BY SIMILARITY.
FT LIPID 444 444 PALMITATE (BY SIMILARITY).
SQ SEQUENCE 452 AA; 49252 MW; F10C1DD2860CD6F9 CRC64;

Query Match 88.8%; Score 2114; DB 1; Length 452;
Best Local Similarity 90.7%; Pred. No. 5 4e-91;
Matches 411; Conservative 4; Mismatches 34; Indels 4; Gaps 4;

QY 1 MGSLDPAGNASWNGTEAPGGARATPYSLOVTLTVCLAGLMLTLTVGNVLIATVFT 60
Db 1 MGSLDPAGNASWNGTEAPGGARATPYSLOVTLTVCLAGLMLTLTVGNVLIATVFT 60
QY 61 SRALKAPQNLFLVSLASADILVATLVIPSLANEWGWYFGKACEITLALDYFCISS 120
Db 61 SRALKAPQNLFLVSLASADILVATLVIPSLANEWGWYFGKACEITLALDYFCISS 120
QY 121 IVHLCATSLDRWYSITQATEYNLKRTPRIKATIIIVWISAVISPPPLISTEKKGGGG 180
Db 121 IVHLCATSLDRWYSITQATEYNLKRTPRIKATIIIVWISAVISPPPLISTEKKRSG 180
QY 181 POPAEPRCEINDQKWYVSISSCSFFAPCLIMLVYRTYQAKRRTRVPSRRGDAVA 240
Db 181 QPAEPRCEINDQKWYVSISSCSFFAPCLIMLVYRTYQAKRRTRVPSRRGDATA 240
QY 241 AP-PPGTEPRPKGLGPER-SAGGGAEPPLPQLNGACGEPAPGRPTDLDEESS 298
Db 241 AELPGSAERPNGLGPGRGVGVGAESLOQLNGACGEPAPG-ACADLDDEESS 299
QY 299 SDAERPPGRRERPRGRGKARASQVKGPSLPRPGATIGTPAAGEERY-GNA 357
Db 299 SEHAERPPGRRSERPRGKARASQVKGPSLPRPGATIGTPAAGEERSGGA 359
QY 358 KASRMGRONREKRRTFLAVVIGVYVCMPEFFETTLTAVGSGVPTLTKFFFMGYC 417
Db 360 KASRMGRONREKRRTFLAVVIGVYVCMPEFFETTLTAVGSGVPTLTKFFFMGYC 419
QY 418 NSSLNPIYITFNHDFRRAFKILCRGDKRRIV 450
Db 420 NSSLNPIYITFNHDFRRAFKILCRGDKRRIV 452

RESULT 7
A2AC_HUMAN STANDARD: PRT; 462 AA.
AC P18825; P35369; Q9HBA9;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Alpha-2C-adrenergic receptor (Alpha-2C adrenoceptor) (Subtype C4).
GN ADRA2C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Kidney.
RX MEDLINE=88320430; PubMed=2842764;
RA Regan J.W., Koblika T.S., Yang-Feng T.L., Caron M.G., Lefkowitz R.J.,
RA Koblika B.K.;
RT "Cloning and expression of a human kidney cDNA for an alpha
RT 2-adrenergic receptor subtype.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:6301-6305(1988).
RN [2]

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RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE-Brain:
 RX MEDLINE=98041882; PubMed=9371698;
 RA Schak S., Devedjian J.C., Cayla C., Sender Y., Paris H.;
 RT "Molecular cloning, sequencing and functional study of the promoter
 RT region of the human alpha2c-adrenergic receptor gene.";
 RL Biochem. J. 328:431-438(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Yano K., Takeda M., Sugimoto E., Sagai H.;
 RT "Molecular cloning and expression of a novel human alpha2c-adrenergic
 RT receptor, alpha2c1, gene";
 RL Submitted (Oct-1992) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT 322-GLY--PRO-325 DEL.
 RX MEDLINE=20390061; PubMed=10801795;
 RA Small K.M., Forbes S.L., Rahman F.F., Bridges K.M., Liggett S.B.;
 RT "A four amino acid deletion polymorphism in the third intracellular
 RT loop of the human alpha 2C-adrenergic receptor confers impaired
 RT coupling to multiple effectors.";
 RL J. Biol. Chem. 275:23059-23064(2000).
 CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 CC PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- POLYMORPHISM: The Del322-325 variant has a significant loss of
 CC function. It is approximately 10 times more frequent in African-
 CC Americans compared with Caucasians (allele frequencies 0.381
 CC versus 0.040).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: J03853; AAA35513.1; -;
 DR EMBL: U72648; AAC78723.1; -;
 DR EMBL: D13538; BAA02737.1; -;
 DR EMBL: AF280399; AAG28076.1; -;
 DR EMBL: AF280400; AAG28077.1; -;
 DR PIR: A31237; A31237.
 DR HSSP: P29274; 1MMH.
 DR GeneW: HGNC:283; ADRA2C.
 DR MIM: 104250; -;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHOPOPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECPEP_FL_1; 1.
 DR PROSITE: PS0262; G-PROTEIN_RECPEP_FL_2; 1.
 KM G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Multigene family; Phosphorylation; Polymorphism; Alternative splicing.
 FT DOMAIN 1 51
 FT TRANSSEM 1 51
 FT TRANSSEM 52 76
 FT TRANSSEM 77 88
 FT TRANSSEM 89 114
 FT TRANSSEM 115 124
 FT TRANSSEM 125 147
 FT TRANSSEM 148 168
 FT TRANSSEM 169 191
 FT TRANSSEM 192 207
 FT TRANSSEM 208 231
 FT TRANSSEM 232 239
 FT TRANSSEM 380 407
 FT TRANSSEM 408 420
 FT TRANSSEM 421 441
 FT TRANSSEM 442 462
 FT DOMAIN 294 308
 FT DOMAIN ARG-RICH (BASIC).

FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 124 202 BY SIMILARITY.
 FT VARSPLIC 270 300 AGENCHCAPPEAAOPDESSAAERRRRGA -> EARTGT
 FT VARIANT 322 325 ARPPPTWSTRAAOPRRGAPAP (IN ISOFORM 2).
 FT VARIANT 322 325 MISSING.
 FT CONFLICT 239 239 /FTID=VAR_012747.
 FT CONFLICT 329 329 L -> R (IN REF. 1 AND 2).
 FT CONFLICT 401 401 E -> Q (IN REF. 1 AND 2).
 FT CONFLICT 446 446 S -> I (IN REF. 1 AND 2).
 FT CONFLICT 446 446 R -> P (IN REF. 1 AND 2).
 SQ SEQUENCE 462 AA; 49522 MW; ELEF9CA1E7F6EDA CRC64;
 Query Match 49.7%; Score 1182; DB 1; Length 462;
 Best Local Similarity 52.7%; Pred. No. 3,2e-48;
 Matches 254; Conservative 40; Mismatches 102; Indels 86; Gaps 10;
 OY 10 NASMNGTEAPGGGARAT-----PISLOVTLTLCVLAAGLLMLVFGVAVTIYVT 60
 DB 19 NASGGERGSGGVANASGASWGPGRGOYSAGAVAGLAAVGFLLVTVGVAVIYAVLT 78
 OY 61 SRALKAPQNLFLVSLASADIIIVATLIPESLANEFGWYFGKAMCEIYALDVLCTSS 120
 DB 79 SRALKAPQNLFLVSLASADIIIVATLIPESLANEFGWYFGKAMCEIYALDVLCTSS 138
 OY 121 IVHLCAISLDRYWSTQAEYENLKRPRRIKAIITVWISAVISFPPLISIEKGGGG 180
 DB 139 IVHLCAISLDRYWSTQAEYENLKRPRRIKAIITVWISAVISFPPLISIEKGGGG 197
 OY 161 POPAPRCEINDQKWYVISCISGFAPCLIMLYVARIYIYAKRRRVPPSRGPDVA 240
 DB 198 --AVPQGLNDEWTYIISCSIGSEFFAPCLIMGYAVIRYAVAKRTTSEKRAP--V 251
 OY 241 APGGTERPPKGLGERASGPGCAEAPLPQNLGAPEPAPGRPDALDESSSSD 300
 DB 252 GPDGASPTTENGLGAAGAENGHCA-----PPPA-----DVEPDSSA 290
 OY 301 HAERPPGRPRPEGRGKARASQVKPDLSLPRKPGATIGTPAGPGEERYAAKAS 360
 DB 291 AAE-----RRRRGALRRGGRRRGAEGG-----AGADGG--AGPGAESGALTAS 336
 OY 361 RWRG-----RNRKRTFTVLAIVYGVVCF 388
 DB 337 RSPGPGGRSLRASRSRVFFLRRRRARRSVCRKRVAAQRKRFVLAIVGVVCF 396
 OY 389 PEEFTYTLAV---GCSVPRLTFKEFWGYGNSLVYITFHNDHRAFFKILCRGD 445
 DB 397 PEEFTSLYIGICRACQVGPPLKEFFWIGYCNSSLNPIVITVENODRRSFKHLFRRR 456
 OY 446 RK 447
 DB 457 RR 458
 RESULT 8
 A2AB_CAVPO STANDARD; PRT; 448 AA.
 ID A2AB_CAVPO
 AC 060475;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor).
 GN ADRA2B.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Hartley;
 RX MEDLINE=96152573; PubMed=8573196;
 RA Svensson S.P., Bailey T.J., Porter A.C., Richman J.G., Regan J.W.;
 RT "Heterologous expression of the cloned guinea pig alpha 2A, alpha 2B,

RT and alpha 2C adrenoceptor subtypes. Radioligand binding and functional coupling to a cAMP-responsive reporter gene.*;
 RL Biochem. Pharmacol. 51:291-300(1996).
 CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL: U25723; AAA67075.1; -.
 CC HSSP: P29274; IMM.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHOOPS.
 DR PROSITE: PS00237; G-PROTEIN_RECPT_FL_1; 1.
 DR PROSITE: PS0262; G-PROTEIN_RECPT_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Multigene family; Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 12 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 13 38 1 (POTENTIAL).
 FT DOMAIN 39 49 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 50 75 2 (POTENTIAL).
 FT DOMAIN 76 85 3 (POTENTIAL).
 FT TRANSSEM 86 108 3 (POTENTIAL).
 FT DOMAIN 109 130 4 (POTENTIAL).
 FT TRANSSEM 131 153 4 (POTENTIAL).
 FT DOMAIN 154 168 5 (POTENTIAL).
 FT TRANSSEM 169 192 5 (POTENTIAL).
 FT DOMAIN 193 370 6 (POTENTIAL).
 FT TRANSSEM 371 394 6 (POTENTIAL).
 FT DOMAIN 395 403 7 (POTENTIAL).
 FT TRANSSEM 404 427 7 (POTENTIAL).
 FT DOMAIN 428 448 7 (POTENTIAL).
 FT DISULFID 85 163 CYTOPLASMIC (POTENTIAL).
 FT LIPID 440 440 PALMITATE (POTENTIAL).
 FT DOMAIN 294 309 ASP/GLU-RICH (ACIDIC).
 FT SITE 92 92 IMPLICATED IN LIGAND BINDING (BY SIMILARITY).
 FT SITE 175 175 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
 FT SITE 179 179 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
 FT SITE 179 179 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
 SQ SEQUENCE 448 AA; 49597 MW; 8384f8757e404777 CRC64;
 Query Match 49.3%; Score 1173.5; DB 1; Length 448;
 Best Local Similarity 53.6%; Pred. No. 7.7e-48;
 Matches 245; Conservative 47; Mismatches 104; Indels 61; Gaps 11;
 QY 27 PYSLOVTLTVAGLLMLLTGVMVLIIVTSRAKPNQLFVLSASADILVATLV 86
 Db 6 PYSQATAAIAAVITFLIFTFGNALVLIIVLTSRLPAPQNLVLSLAADILVATLI 65
 QY 87 IIPSLANEVGVYFGKANCEIYLAADVLCSTSIYHLCAISLDRWSTQAEVYLRKT 146
 Db 66 IIPSLANEGLGVYFWMTWEVYLAADVLCSTSIYHLCAISLDRWAVSRALEVNSKRT 125
 QY 147 PRKATITVWVYAVISPEPLISTEKKGSGGPPAPARCEINOKWVVISGSGSFE 206
 Db 126 PRKRCITITVWVLIIVATISLPLI-----YKDGDPSPRPQCKINEAMVTLASISGSFE 181
 QY 207 APCILIMLVVRYTOAKRRTRVPSRKRPDAVAAPPGGTERPKGLGERSAGPGAGA 266
 Db 182 APCILIMLVVLRITLYLAKR-----SHRGRPRAGKPGEGESKSR--PSPGAPRASAV 233
 QY 267 EPLPTQUNG---APGEAPAGPDOTALDESSSSSDHAERPPGPRRPERGRGKAKA 323

Db 234 PPLASLSSTGEANGHPKRTGKE-----EGTSDPQAKLIPSPMALPISGGGOKKA 287
 QY 324 SQYKP-----GDSL-PRRGP-----ATGIGTPAAGPE 351
 Db 288 VVLAPAEAEAEAEDEEGDECEPOAPGLPASCPSLQPOGSRVLAIRGOVLLGRG- 346
 QY 352 ERGAKASRWRR--QNEKEFTFLAVVIGVFWCWPFFFTYTLAV---GGSVPT 406
 Db 347 --VGAVDGGMWRRRQMTTEKRTFVLAVIGVFWCWPFFFTYSLAICPQHKVPBG 404
 QY 407 LKFEFPGYCNSSLNPIYITFNHDFRAFKRICR 443
 Db 405 LKQFFWIGYCNSSLNPIYITFNDFRFRRIICR 441
 RESULT 9
 A2AC_MOUSE
 ID A2AC_MOUSE STANDARD; PRT; 458 AA.
 AC 001337;
 DT 01-APR-1993 (rel. 25, Created)
 DT 01-APR-1993 (rel. 25, Last sequence update)
 DT 01-NOV-1997 (rel. 35, Last annotation update)
 DE Alpha-2C adrenoergic receptor (Alpha-2C adrenoceptor) (Subtype C4).
 GN ADRA2C.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid:10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92342131; Pubmed-1353249;
 RA Link R.E., Daunt D.A., Barsh G., Chruscinski A.J., Koblika B.K.;
 RT Cloning of two mouse genes encoding alpha 2-adrenergic receptor subtypes and identification of a single amino acid in the mouse alpha 2-C10 homolog responsible for an interspecies variation in antagonist binding.*;
 RT Mol. Pharmacol. 42:16-27(1992).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN-DBA/2;
 RX MEDLINE-93250567; Pubmed-8387367;
 RA Chang Y.-H., Chang A.C., Chen W.-M., Chang N.-C.A.;
 RT Molecular characterization of a murine homologue of alpha 2C4 adrenoceptor subtype gene.*;
 RT Biochem. Mol. Biol. Int. 29:467-474(1993).
 RL -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL: M99376; AAA37212.1; -.
 DR EMBL: M97516; AAA37183.1; -.
 DR HSSP: P29274; IMM.
 DR MGD: MGI:87936; Adra2c.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHOOPS.
 DR PROSITE: PS00237; G-PROTEIN_RECPT_FL_1; 1.
 DR PROSITE: PS0262; G-PROTEIN_RECPT_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Phosphorylation.
 FT DOMAIN 1 51 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 52 76 1 (POTENTIAL).

FT DOMAIN 77 88 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 89 114 2 (POTENTIAL).
 FT DOMAIN 115 124 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 125 147 3 (POTENTIAL).
 FT DOMAIN 148 168 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 169 191 4 (POTENTIAL).
 FT DOMAIN 192 207 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 208 231 5 (POTENTIAL).
 FT DOMAIN 232 379 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 380 403 6 (POTENTIAL).
 FT DOMAIN 404 416 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 417 437 7 (POTENTIAL).
 FT DOMAIN 438 458 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 459 488 ARG-RICH (BASIC).
 FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 124 202 BY SIMILARITY.
 FT CONFLICT 196 196 G -> V (IN REF. 2).
 FT CONFLICT 296 296 G -> A (IN REF. 2).
 FT CONFLICT 298 298 L -> V (IN REF. 2).
 SQ SEQUENCE 458 AA: 49906 MW: 104800.00 COA8BDF0302BFLFB CRC64:

Query Match 49.3%; Score 1173; DB 1; Length 458;
 Best Local Similarity 53.5%; Pred. No. 8, 2e-48;
 Matches 251; Conservative 46; Mismatches 104; Indels 68; Gaps 11;
 14 NCTEA-----PGGGRAT-----PYSLOVTLTVCLAGLLMLTVGNVLTAVPT 60
 19 NSGDAEMSGGGANSGTDWVPPPGQYSAAGAVAGLAAGVGLVTVGNVLTAVLT 78
 61 SRLAKAPONLFLVSLASADILVATLVPFSLANEMVGYVFGKAMCEIYALDVLEFCTSS 120
 79 SRLAPAPONLFLVSLASADILVATLVPFSLANEMVGYVFGQVWGVLTADVLEFCTSS 138
 121 IYHLCALISLDRVYSTQALIEYLNKTRPRKAIITVWYISAVISPPPLISIEKGGGG 180
 139 IYHLCALISLDRVYSTQALIEYLNKTRPRKAIITVWYISAVISPPPLISIEKGGGG 197
 181 PQAEPRECEINDOKWVVISGSGFAPCLIMLVVRYLQAKRTRVPPSRGPDVA 240
 198 ---AYPGGLNDETWYILSCISGSPFAPCLIMLVVRYLQAKRTRVPPSRGPDVA 250
 241 APPGTERRRKGLGPRSGAGPGAEAPPLPTOLNG---APGEPAPAGPDDTALDEESS 297
 251 -----AGPDGAS-----PTTENGKGAENGHCAPPRTE-VEPDESS 287
 298 SSDHAERPEPPRRPERRGPRGKAKARASQVKGPDLSLRPRRGATGCTPRAAGEEERVGAA 357
 288 AARERRRRRGAALRRGGRRRRGAECDTGSADGPGGLAEOGARTASRSP--GFGGLSRAS 345
 358 KAS-----RMGR-----ONREKRFPFLVAVVIGVYVCEPPEFFTYTLAV-- 399
 346 SRKVERFLRRRRARRASSVCRKVAQAQRKRFTEFLVAVVIGVYVCEPPEFFTYTLAV 405
 400 -GCSVPRTLKFFEFMGYCNSSLNPIYITFNHDFRRAKFLICRDRK 447
 406 EACQLPEPLKFFEFMGYCNSSLNPIYITFNHDFRRAKFLICRDRK 454
 RESULT 10
 A2AC_RAT STANDARD; PRT; 458 AA.
 AC A2AC_RAT
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Alpha-2C adrenergic receptor (Alpha-2C adrenoceptor) (Subtype C4).
 GN ADRA2C.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCBL_TaxID=10116;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=91126047; PubMed=1704126;
 RA Flordellis C.S., Hardy D.E., Bresnahan M.R., Zannis V.I., Gavras H.;
 RT "Cloning and expression of a rat brain alpha 2B-adrenergic receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:1019-1023(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91130596; PubMed=1704314;
 RA Voigt M.M., McGuire S.K., Kanterman R.Y., Felder C.C.;
 RT "The rat alpha 2-C4 adrenergic receptor gene encodes a novel
 pharmacological subtype.";
 RL FEBS Lett. 278:45-50(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91244823; PubMed=1645350;
 RA Lanier S.M., Downing S., Duzic E., Homcy C.J.;
 RT "Isolation of rat genomic clones encoding subtypes of the alpha 2-
 adrenergic receptor. Identification of a unique receptor subtype.";
 RL J. Biol. Chem. 266:10470-10478(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Satoh M., Imai A., Shimomura H.;
 RT "Cloning of rat alpha-2-B-adrenergic receptor gene and expression in
 rat submandibular gland.";
 RL Shigaku 80:317-326(1992).
 CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-
 INDUCED INHIBITION OF ADENYLYLATE CYCLASE THROUGH THE ACTION OF G
 PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 or send an email to license@isb-sib.ch).
 CC EMBL; M58316; AAA40634.1; -;
 DR EMBL; X57659; CA440861.1; -;
 DR EMBL; M62371; AAA42033.1; -;
 DR EMBL; D00819; BAA00700.1; -;
 DR PIR; A37869; A37869.
 DR PIR; S13023; S13023.
 DR PIR; A40392; A40392.
 DR HSSP; P29274; IMMH.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Phosphorylation.
 FT DOMAIN 1 51 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 52 76 1 (POTENTIAL).
 FT DOMAIN 77 88 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 89 114 2 (POTENTIAL).
 FT DOMAIN 115 124 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 125 147 3 (POTENTIAL).
 FT DOMAIN 148 168 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 169 191 4 (POTENTIAL).
 FT DOMAIN 192 207 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 208 231 5 (POTENTIAL).
 FT DOMAIN 232 379 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 380 403 6 (POTENTIAL).
 FT DOMAIN 404 416 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 417 437 7 (POTENTIAL).
 FT DOMAIN 438 458 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 459 488 ARG-RICH (BASIC).
 FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 124 202 BY SIMILARITY.

RESULT 12

A2AC_DIDMA STANDARD: PRT: 469 AA.

ID A2AC_DIDMA PRT: 469 AA.

AC P35405;

DT 01-JUN-1994 (Rel. 29, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Alpha-2C adrenergic receptor (Alpha-2C adrenoceptor).

OS Didelphis marsupialis virginiana (North American opossum).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.

OX NCBI_Taxid=9267;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RA Blaxell H.S., Cerutis D., Hass N.A., Iversen L.J., Bylund D.B.;

RT "Cloning and expression of the alpha 2C-adrenergic receptor from the OK cell line";

RT Mol. Pharmacol. 45:176-181(1994).

RN [2]

RP REVISIONS TO 60; 75; 110; 143; 326-332; 365 AND 432.

RA Bylund D.B.;

RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.

CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G PROTEINS.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC -----

CC EMBL: U04310; AAA17566.2; -

DR HSSP: P29274; 1MMH.

DR InterPro: IPR000276; GPCR_Rhodpsn.

DR Pfam: PF00001; 7tm_1.1.

DR PRINTS: PR00237; GPCRHOPOPSN.

DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.

DR PROSITE: PS50262; G-PROTEIN_RECEP_FL_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Multigene family; Phosphorylation.

FT DOMAIN 1 41

FT TRANSMEM 42 62

FT DOMAIN 63 72

FT TRANSMEM 73 93

FT DOMAIN 94 109

FT TRANSMEM 110 130

FT DOMAIN 131 154

FT TRANSMEM 155 175

FT DOMAIN 176 195

FT TRANSMEM 196 216

FT DOMAIN 217 386

FT TRANSMEM 387 407

FT DOMAIN 408 427

FT TRANSMEM 428 448

FT DOMAIN 449 469

FT DOMAIN 274 293

FT CARBOHYD 8

FT CARBOHYD 20

FT DISULFID 109

FT SEQUENCE 469 AA; 53223 MW; 6F97D3718CC15C18 CRC64;

Query Match 48 2%; Score 1146; DB 1; Length 469;

Best Local Similarity 50.9%; Pred. No. 1.5e-46;

Matches 249; Conservative 52; Mismatches 106; Indels 82; Gaps 12;

QY 7 DAGNANNGTEAPGGGATAP--YSLOYTLTVLCLAGLLMLTVEGNVLTIAVTSRAL 64

DB 11 DSGDRGSSNESL---QRPSPQISPAEVAGLAAYVSLIFTVIGNLVIAVLTSRAL 67

QY 65 KAPQMLFLVSLASADILVATLVIPFSLANEVWYFGKACEIYLALDVCTSSIVHL 124

DB 68 KAPQMLFLVSLASADILVATLVIPFSLANEVWYFGKACEIYLALDVCTSSIVHL 127

QY 125 CAISIDRWSTQATIEVNLKTRPRRIKAIITVWVIAVISFPPLISTEKGGGGCPQPA 184

DB 128 CAISIDRWSTQATIEVNLKTRPRRIKAIITVWVIAVISFPPLISTEKGGGGCPQPA 180

QY 185 E---PRCEINQKMWIVISSGSPFAPCTIMLVYRITQYAKTRTPRPSRPG-PPAIVA 240

DB 181 DDLYPQCELNDETWTYLLSSCGISFPAPCTIMLVYRITQYAKTRTPRPSRPG-PPAIVA 240

QY 241 APPGTERRRPKGLSPERSAGPGCAEAPLPOLNGAPDEPAPAPR----- 286

DB 241 QTENGLSRPVGAGPSTAA---AAAASRLQ-----AGBNHYLHHHHNHLN 286

QY 287 -----DTDALDLESSSDHAERPPRRPRRRPRRRPRRRPRRRPRRRPRRRPRRR 332

DB 287 HHHHHHQLRKSAELEDEIELESSSTENRR-----RRSRERAAARKSGRGSFS 336

QY 333 --PRRGPGATGIGTPAGPGEERVGAAKASRRGR-----QNRKRTFLVAVYG 381

DB 337 FSSTGGGAGAGSLSANRSLFEFTHRRKRSSLCRRKYVQARKRTFLVAVYMG 396

QY 382 VEVVCMPEFFFTYTLTAV---GCSVPTLFFKFFWFGYNSLNPVITYTIPNDFRAFK 438

DB 397 VEVVCMPEFFFTYTLTAV---GCSVPTLFFKFFWFGYNSLNPVITYTIPNDFRAFK 456

QY 439 KILCGDKR 447

DB 457 HILFKRRK 465

RESULT 13

A2AB_HUMAN STANDARD: PRT: 450 AA.

ID A2AB_HUMAN PRT: 450 AA.

AC P18089;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Subtype C2).

CN ADR2B.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90311349; PubMed=2164221;

RA Lomasney J.W., Lorenz W., Allen L.F., King K., Regan J.W.,

RA Yang-Feng T.L., Caron M.G., Lefkowitz R.J.;

RT "Expansion of the alpha 2-adrenergic receptor family: cloning and characterization of a human alpha 2-adrenergic receptor subtype, the gene for which is located on chromosome 2.";

RL Proc. Natl. Acad. Sci. U.S.A. 87:5094-5098(1990).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=91042469; PubMed=2172775;

RA Weinshank R.L., Zgonick J.M., Meechl M., Adham N., Lichthblau H.,

RA Branchek T.A., Hartig P.R.;

RT "Cloning, expression, and pharmacological characterization of a human alpha 2B-adrenergic receptor.";

RT Mol. Pharmacol. 38:681-688(1990).

RN [3]

RP SEQUENCE FROM N.A.

RA Cayla C., Schack S., Bouloumie A., Devedjian J.C., Paris H.;

RL Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.

RN [4]

RP SEQUENCE OF 95-389 FROM N.A.
 RX MEDLINE=91054503; PubMed=2173582;
 RA Chang A.C., Ho T.F., Chang N.-C.A.;
 RT "In vitro amplification by polymerase chain reaction of a partial
 RT gene encoding the third subunit of alpha-2 adrenergic receptor in
 RT humans.";
 RL Blochem. Biophys. Res. Commun. 172:817-823(1990).
 CC -I- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-
 CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 CC PROTEINS. THE RANK ORDER OF POTENCY FOR AGONISTS OF THIS RECEPTOR
 CC IS CLONIDINE > NOREPINEPHRINE > EPINEPHRINE = OXMETAZOLINE >
 CC DOMAMINE > P-TYRAMINE = PHENYLEPHRINE > SEROTONIN > P-SYNEPHRINE /
 CC P-OCTOPAMINE. FOR ANTAGONISTS, THE RANK ORDER IS YOHIMBINE >
 CC CHLOROPHOLAMINE > PHENTOLAMINE > MINSERINE > SPIPERONE > PRAZOSIN
 CC > ALPENOLOL > PROCANOLOL > PINDOLOL.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M34041; AAA51666.1; -;
 DR EMBL: M38742; AAA62823.1; -;
 DR EMBL: AF005900; AAB62558.1; -;
 DR PIR: A36158; A36158.
 DR PIR: A37223; A37223.
 DR HSSP: P29274; 1MMH.
 DR GeneW: HGNC:282; ADRA2B.
 DR MIM: 104260; -;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G-PROTEIN_RECPT_FL_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECPT_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Multigene family;
 KW Phosphorylation; Lipoprotein; Palmitate;
 KW
 FT DOMAIN 1 12
 FT TRANSMEM 13 38
 FT DOMAIN 39 49
 FT TRANSMEM 50 75
 FT DOMAIN 76 85
 FT TRANSMEM 86 108
 FT DOMAIN 109 130
 FT TRANSMEM 131 153
 FT DOMAIN 154 169
 FT TRANSMEM 170 193
 FT DOMAIN 194 372
 FT TRANSMEM 373 396
 FT DOMAIN 397 405
 FT TRANSMEM 406 429
 FT DOMAIN 430 450
 FT DOMAIN 294 311
 FT DISULFID 85 164
 FT LIPID 442 442
 FT SITE 92 92
 FT SITE 176 176
 FT SITE 180 180
 FT CONFLICT 362 363
 FT SEQUENCE 450 AA; 49948 MW; A476817C8788E1FD CRC64;
 SO
 Query Match 47.4%; Score 1127.5; DB 1; Length 450;
 Best Local Similarity 53.2%; Pred. No. 9,9e-46;
 Matches 243; Conservative 51; Mismatches 104; Indels 59; Gaps 14;
 Oy 27 PYSIQVITLVAGLMLLTIVFGNVLIIVFTSRALKAPQNLFLVSLASADITLVATLV 86

DB PYSQVATAAIAAATFLIFTIFGNALVLIIVATLSRLAPQNLFLVSLAADITLVATLI 65
 Oy 87 IPSLSANEVGVYFPGKAMEIYLAIDYLFCTSSYIHLCAISDRWSTQIAEYLNKRT 146
 DB 66 IPFSLANELGIVYFRTWCEVYLAIDYLFCTSSYIHLCAISDRWAASRALEVNSKRT 125
 Oy 147 PRKATITIVWYISAVISPPPLISIEKKGGGGGPOP-AEPCEINDQKMYVISCIGSF 205
 DB 126 PRKTCITLVLIIVLAIVISPLPL----YKGDGPPRGRPOCKNLQEMAYIASISGSF 181
 Oy 206 FAPCLIMILVYRIYQIAKRTVPPSRKPPDAVAAPGCTERRPKGLGERSAGPGAE 265
 DB 182 FAPCLIMILVYRIYLAIAKR-----ANRRGPRAKGPGCGESKQPR--PDHGALASAK 233
 Oy 266 AEPPLPT-----QUNG---ANGEPAPA-GPRDTALDLES-----SS 298
 DB 234 LPALASVASAREVNGSHKSTGEKEEGETPEDTGTALPPSMALPNSGGGQEGVCGASP 293
 Oy 299 SDAERPPGRRERPRGKARASQVKGPD--SLPRKPG----ATGIGTPAAGPE 351
 DB 294 EDEAE-----EEEEEEECCEPQAVPVSPASCSFPLDQPGQSRVLAIRQVLLGRG- 348
 Oy 352 ERYGAKAASWKRGRON--REKRTFVLAIVGVVCMFPFFETVTLAV---GCSVPT 406
 DB 349 --VGAIGGQWRRRAHRTREKRTFVLAIVGVVCMFPFFESYSIGAICPKHCKVPHG 406
 Oy 407 LKFFFWGCGNSSLNPVITYITFNHDFRAFKITLR 443
 DB 407 LFOFFWIGCGNSSLNPVITYITFNODFRARFRILCR 443
 RESULT 14
 A2AR_LABOS
 ID A2AR_LABOS STANDARD; PRT; 432 AA.
 AC G91081;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Alpha-2 adrenergic receptor (Alpha-2 adrenoceptor).
 OS Labrus ossifagus (Cuckoo wrasse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidel;
 OC Labridae; Labrus.
 OX NCBI_TaxID=30800;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94035926; PubMed=7693288;
 RA Svensson S.P.S., Bailey T.J., Pepperl D.J., Grundstrom N.,
 RA Ala-Uotila S., Scheinin M., Karlsson J.O.G., Regan J.W.;
 RT Cloning and expression of a fish alpha 2-adrenoceptor.";
 RL Br. J. Pharmacol. 110:54-60(1993)
 CC -I- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-
 CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 CC PROTEINS.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U07743; AAA17386.1; -;
 DR HSSP: P29274; 1MMH.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PR00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G-PROTEIN_RECPT_FL_1; 1.

DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KM G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 33 57 1 (POTENTIAL).
 FT DOMAIN 38 69 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 70 95 2 (POTENTIAL).
 FT DOMAIN 96 105 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 106 128 3 (POTENTIAL).
 FT DOMAIN 129 149 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 150 172 4 (POTENTIAL).
 FT DOMAIN 173 188 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 189 212 5 (POTENTIAL).
 FT DOMAIN 213 356 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 357 380 6 (POTENTIAL).
 FT DOMAIN 381 393 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 394 413 7 (POTENTIAL).
 FT DOMAIN 414 432 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 432 453 BY SIMILARITY.
 FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 18 18 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 432 AA; 48563 MW; 0AA2FAF9849F8BA CRC64;

Query Match 47.3%; Score 1126.5; DB 1; Length 432;
 Best Local Similarity 53.0%; Pred. No. 1.9e-45;
 Matches 240; Conservative 50; Mismatches 108; Indels 55; Gaps 11;

OY 10 NASMNGTEAPGGGARAATPYSLQVTLVCLAGLMLTVFGNVLIAVTSRAKAPON 69
 DB 18 NASMS---ADSG-----YSLAAIASIALVSTLFTVAGNLVIAVTSRAKAPON 68
 OY 70 LFLVSLASADILVATLVIPFSLANEVGYFGKANCEIYALDVLCTSIYHLCALSL 129
 DB 69 LFLVSLATADILVATLVMPFSLANELMGVYFGKWCGLYALDVLCTSIYHLCALSL 128
 OY 130 DRWSTQALAEVYLKTPRKRIKAITTVAVISAVISFPLISIEKKGGGCPAPAPRCE 189
 DB 129 DRWSTQALAEVYLKTPRKRIKAITTVAVISAVISFPLISIEKKGGGCPAPAPRCE 184
 OY 190 INDKNVVSSICISGFPAFLIMILVVRITQAKRRTPVPSRRGPAVAPPGSTER 249
 DB 185 LNDTYITLSSMASFFACLIMILVIRITQAKRRTPVPSRRGPAVAPPGSTER 231
 OY 250 PKGL-----GPERAGP-----GGAEPLEPTQNGAPGAPAPRDTALDESS 297
 DB 232 PDGVQTENGANKANSPCHGRNGHCQCPPTPSQRTVIGQ-----QTDADADESF 284
 OY 298 SSDHAERPPRRPRRPRGPKGAKARASQVPRGDSLPFRPGATGCTPAAGGEERVGA 357
 DB 285 SSGKGRKPRRPRRPRGPKGAKARASQVPRGDSLPFRPGATGCTPAAGGEERVGA 343
 OY 358 KASRMGRONREKRFVLAIVGVVCMPPPEFTYTLAV---GCSVPRTLFKFEWF 414
 DB 344 KVS-----QAREKRFVLAIVGVVCMPPPEFTYTLAV---GCSVPRTLFKFEWF 397
 OY 415 GYCNSSLNPYITFINHDFRFAFKILCRGDR 447
 DB 398 GYCNSSLNPYITFINHDFRFAFKILCRGDR 430

RESULT 15
 A2AB_MOUSE
 ID A2AB_MOUSE STANDARD; PRT; 455 AA.
 AC P30545;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ALPHA-2B adrenergic receptor (Alpha-2B adrenoceptor).
 GN ADRA2B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN (1)

RP SEQUENCE FROM N.A.
 RC STRAIN=DBA/2; TISSUE=liver;
 RX MEDLINE=93128625; PubMed=1336396;
 RA Chen W.-W., Chang A.C., Shle B.J., Chang Y.-H., Chang N.-C.A.;
 RT "Molecular cloning and characterization of a mouse alpha 2c2
 RL adrenoceptor subtype gene.";
 RN Biochim. Biophys. Acta 1171:219-223(1992).
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92378586; PubMed=1354956;
 RA Chrusciński A.J., Link R.E., Daunt D.A., Barsh G.S., Kobilka B.K.;
 RT "Cloning and expression of the mouse homolog of the human alpha 2-C2
 RL adrenergic receptor.";
 RN Biochem. Biophys. Res. Commun. 186:1280-1287(1992).
 CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIANE THE CATECHOLAMINE-
 CC INDUCED INHIBITION OF ADENYLYLATE CYCLASE THROUGH THE ACTION OF G
 CC PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL; M94583; AAA73895.1; -.
 DR EMBL; L00979; AAA37131.1; ALT_INIT.
 DR PIR; JH06933; JH0693.
 DR PIR; S28221; S28221.
 DR HSSP; P29274; IMMH.
 DR MGP; MGI:87935; Adra2b.
 DR InterPro; IPR00276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KM G-protein coupled receptor; Transmembrane; Multigene family;
 KW Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 17 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 18 42 1 (POTENTIAL).
 FT DOMAIN 43 54 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 55 80 2 (POTENTIAL).
 FT DOMAIN 81 90 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 91 113 3 (POTENTIAL).
 FT DOMAIN 114 135 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 136 158 4 (POTENTIAL).
 FT DOMAIN 159 174 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 175 198 5 (POTENTIAL).
 FT DOMAIN 199 377 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 378 401 6 (POTENTIAL).
 FT DOMAIN 402 410 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 411 434 7 (POTENTIAL).
 FT DOMAIN 435 455 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 90 169 BY SIMILARITY.
 FT LIPID 447 447 PALMITATE (POTENTIAL).
 FT LIPID 306 316 ASP/GLU-RICH (ACIDIC).
 FT SITE 97 97 IMPLICATED IN LIGAND BINDING (BY
 FT SIMILARITY).
 FT SITE 181 181 IMPLICATED IN CATECHOL AGONIST BINDING
 FT (BY SIMILARITY).
 FT SITE 185 185 IMPLICATED IN CATECHOL AGONIST BINDING
 FT (BY SIMILARITY).
 FT CONFLICT 202 202 V -> L (IN REF. 1).
 FT CONFLICT 229 230 MISSING (IN REF. 2).
 SQ SEQUENCE 455 AA; 50615 MW; A3954AD76DE06263 CRC64;

Query Match 47.1%; Score 1121.5; DB 1; Length 455;
 Best Local Similarity 53.0%; Pred. No. 1.9e-45;
 Matches 242; Conservative 50; Mismatches 106; Indels 59; Gaps 14;

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 15, 2003, 14:30:52 : Search time 50 Seconds
(without alignments)
1854.424 Million cell updates/sec

Title: US-09-636-259b-3

Perfect score: 2381
Sequence: 1 MGSLOPDAGNSWNGTEAPG.....HDFRRAPKKILCRGDRRIIV 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*
15: sp-virus:*
16: sp-bacteriophage:*
17: sp-archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2375	99.7	450	Q9BZK1	Q9BZK1 homo sapien
2	1305.5	54.8	388	Q90WY4	Q90WY4 Brachydanio
3	1180.5	49.6	432	Q90WY6	Q90WY6 Brachydanio
4	1135	47.7	510	Q90WY5	Q90WY5 Brachydanio
5	1124	47.2	447	Q9BZK0	Q9BZK0 homo sapien
6	1115.5	46.9	448	11 Q925K6	Q925K6 mus musculus
7	1114.5	46.8	448	11 Q925K7	Q925K7 mus musculus
8	1110.5	46.6	453	11 Q925E4	Q925E4 ratu
9	967.5	40.6	393	11 Q9JWJ2	Q9JWJ2 ratu
10	941	39.5	392	6 Q95N90	Q95N90 tadrida br
11	940	39.5	390	6 Q9GKZ6	Q9GKZ6 trichechus
12	940	39.5	390	6 Q9GLI9	Q9GLI9 cynocephalu
13	938.5	39.4	395	6 Q9GLI2	Q9GLI2 maris sp. a
14	937.5	39.4	379	6 Q9GLI3	Q9GLI3 macropus ru
15	937.5	39.4	391	6 Q8SOA0	Q8SOA0 emballonura
16	936.5	39.3	389	6 Q9GKZ5	Q9GKZ5 tupia tana

17	934.5	39.2	393	6 Q9GLI1	Q9GLI1 nycticebus
18	932.5	39.2	395	6 Q95N91	Q95N91 tonatia bid
19	932	39.1	390	6 Q95N89	Q95N89 taphozous s
20	931	39.1	388	6 Q9GLI8	Q9GLI8 diceros blic
21	930.5	39.1	383	6 Q9GLI20	Q9GLI20 cynopterus
22	930.5	39.1	387	6 Q9GLI7	Q9GLI7 felis silve
23	930.5	39.1	389	6 Q9GLI07	Q9GLI07 phoca vitul
24	929.5	39.0	393	6 Q95N92	Q95N92 myotis daub
25	927.5	39.0	393	6 Q9GLI5	Q9GLI5 macrotus ca
26	926	38.9	392	6 Q9GLI3	Q9GLI3 balenopter
27	925.5	38.9	385	6 Q9GLI4	Q9GLI4 microptero
28	925.5	38.9	393	6 Q9GLI6	Q9GLI6 hippopotamo
29	923.5	38.8	385	6 Q9GKZ7	Q9GKZ7 tenrec ecau
30	922.5	38.7	391	6 Q9GLI06	Q9GLI06 sus scrofa
31	922	38.7	388	6 Q8SO21	Q8SO21 nycteris th
32	921.5	38.7	389	6 Q95N94	Q95N94 hipposidero
33	920.5	38.7	391	6 Q8SOB3	Q8SOB3 antrozous p
34	920	38.6	388	6 Q8SOQ3	Q8SOQ3 nyctereis gr
35	919	38.6	396	6 Q8SO87	Q8SO87 rhogoesa t
36	914.5	38.4	395	6 Q8SO94	Q8SO94 noctilio al
37	914	38.4	392	6 Q95N95	Q95N95 megaderma l
38	912	38.3	394	6 Q8SOQ1	Q8SOQ1 desmodus ro
39	911.5	38.3	389	6 Q8SO95	Q8SO95 nyctimene a
40	909.5	38.2	383	6 Q95N93	Q95N93 pteropus ra
41	909	38.2	398	6 Q8SO92	Q8SO92 natalus str
42	908.5	38.2	383	6 Q9GLI28	Q9GLI28 bradypus tr
43	902	37.9	365	6 Q8SO88	Q8SO88 rhinopoma h
44	900.5	37.8	389	6 Q8SO89	Q8SO89 rhinolophus
45	684.5	28.7	419	5 Q77254	Q77254 boophilus m

ALIGNMENTS

RESULT 1

Q9BZK1 ID Q9BZK1 PRELIMINARY; PRT; 450 AA.
AC Q9BZK1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Alpha 2A adrenergic receptor.
GN ADRA2A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20556293; PubMed=10948191;
RA Small K.M., Forbes S.L., Brown K.M., Liggett S.B.;
RT "An asn to lys polymorphism in the third intracellular loop of the
RT human alpha 2A-adrenergic receptor imparts enhanced agonist-promoted
RT Gi coupling";
RL J. Biol. Chem. 275:38518-38523(2000).
CC -! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -! SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF316894; AKR01634.1; .
DR HSSP; P29274; IMM.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G-PROTEIN_RECPT_FL_1; 1.
DR PROSITE; PS50262; G-PROTEIN_RECPT_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT VARIANTS 251 K -> N.
SQ SEQUENCE 450 AA; 48970 MW; 94E02E227CE5ECPE CRC64;

Query Match 99.7%; Score 2375; DB 4; Length 450;
Best Local Similarity 99.8%; Pred. No. 7.4e-165;
Matches 449; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGSLOPDAGNSWNGTEAPGGGARATPYSLQVTLVCLAGLMLTFVGNVLIIVAVT 60

```
|||||
Db 1 MSLQPDGNSMNGTEPAGGARATPSLQVTLTVCLAGLMLTLVFGNVLIIVFT 60
Oy 61 SRALAPQNLFLVSLASADIIIVATLVIPESLANEMGWGKAMCEIYALDVLEFCTSS 120
Db 61 SRALAPQNLFLVSLASADIIIVATLVIPESLANEMGWGKAMCEIYALDVLEFCTSS 120
Oy 121 IVHCAISLDRYWSTIQAIEYNLKRTPRIKAIITVWVISAIVSPPLISIEKKGCGG 180
Db 121 IVHCAISLDRYWSTIQAIEYNLKRTPRIKAIITVWVISAIVSPPLISIEKKGCGG 180
Oy 181 POPAPRCEINDQKWYVIVSSCIGSFAPCLIMIIYVYRIYQIARRRVRPPSRGPPAVA 240
Db 181 POPAPRCEINDQKWYVIVSSCIGSFAPCLIMIIYVYRIYQIARRRVRPPSRGPPAVA 240
Oy 241 APPGTERPNSGLPERGAGGAEAPLPTOLNGAPCEPAPAPRDTALDEESSSSD 300
Db 241 APPGTERPNSGLPERGAGGAEAPLPTOLNGAPCEPAPAPRDTALDEESSSSD 300
Oy 301 HAERPGRPERGPRGKARASQVKGDSLPRRGPGATIGTPAAGPGEERYGAAKAS 360
Db 301 HAERPGRPERGPRGKARASQVKGDSLPRRGPGATIGTPAAGPGEERYGAAKAS 360
Oy 361 RWRGQNEKREFTVLAIVGVVWCWPFPTTTLTAAGSVRTLFKFFWFGYCNSS 420
Db 361 RWRGQNEKREFTVLAIVGVVWCWPFPTTTLTAAGSVRTLFKFFWFGYCNSS 420
Oy 421 LNPVYITFNHDFRAFKIILCRGDKRRIY 450
Db 421 LNPVYITFNHDFRAFKIILCRGDKRRIY 450
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RESULT 2

090WT4 PRELIMINARY; PRT; 388 AA.

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AC 090WT4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Alpha2A-adrenergic receptor.
GN ADRA2A.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Ruuskanen J., Xhaard H., Marjamaki A., Salaneck E., Salminen T.,
RA Yan Y.L., Postlethwait J.H., Johnson M.S., Larhammar D., Schein M.;
RT "Origin of Alpha2-Adrenergic Receptor Subtypes as Revealed by Cloning
RT and Mapping of Three Receptor Subtype Genes in the Zebrafish (Danio
RT rerio).";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY048971; ALU07510.1; -.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
KW Receptor.
SQ
SEQUENCE 388 AA; 43996 MW; 431965A04E1986DD CRC64;
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Query Match 54.8%; Score 1305.5; DB 13; Length 388;
Best Local Similarity 60.5%; Pred. No. 3.3e-87;
Matches 266; Conservative 37; Mismatches 78; Indels 59; Gaps 8;

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Oy 15 GTEAPGGAATPSLQVTLTVCLAGLMLTLVFGNVLIIVFTSRALAPQNLFLVS 74
Db 4 GANNTNGNATKEYTLLVALPLSLAVGLLILIFGNVLIIVFTSRALAPQNLFLVS 63
Oy 75 LASADIIIVATLVIPESLANEMGWGKAMCEIYALDVLEFCTSSIVHCAISLDRYWS 134
Db 64 LASADIIIVATLVIPESLANEMGWGKAMCEIYALDVLEFCTSSIVHCAISLDRYWS 123
```

```
Oy 135 ITOAIEYNLKRTPRIKAIITVWVISAIVSPPLISIEKKGCGGPPAPRCEINDQK 194
Db 124 ITOAIEYNLKRTPRIKAIITVWVISAIVSPPLISIEKKGCGGPPAPRCEINDQK 175
Oy 195 WYIVSSCIGSFAPCLIMIIYVYRIYQIARRRVRPPSRGPPAVAAPPGETERRPNIG 254
Db 176 WYIVSSCIGSFAPCLIMIIYVYRIYQIARRRVRPPSRGPPAVAAPPGETERRPNIG 213
Oy 255 PESSAGGAEAPLPTOLNGAPCEPAPAPRDTALDEESSSSDHARPPGRRP 311
Db 214 DHKKNVEYKENDP-HEKLGION---AEPDDKDEINGDHESSSDHKKNPCSLKK 268
Oy 312 ERPRGKARASQVKGDSLPRRGPGATIGTPAAGPGEERYGAAKASRWRGQNRKR 371
Db 269 K---SSKGRKILSQIKPGD-----GDKTEACQYTKASRWRGQNRKR 308
Oy 372 FTTVLAIVGVVWCWPFPTTTLTA-VGCSVPRTLFKFFWFGYCNSSLNPVYITFN 430
Db 309 FTTVLAIVGVVWCWPFPTTTLTAFCDCVETLKFKEFWFGYCNSSLNPVYITFN 368
Oy 431 HDFRAFKIILCRGDKRRIY 450
Db 369 NDFRRSFKILCRDKRRVY 388
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RESULT 3

090WT6 PRELIMINARY; PRT; 432 AA.

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AC 090WT6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Alpha2C-adrenergic receptor.
GN ADRA2C.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Ruuskanen J., Xhaard H., Marjamaki A., Salaneck E., Salminen T.,
RA Yan Y.L., Postlethwait J.H., Johnson M.S., Larhammar D., Schein M.;
RT "Origin of Alpha2-Adrenergic Receptor Subtypes as Revealed by Cloning
RT and Mapping of Three Receptor Subtype Genes in the Zebrafish (Danio
RT rerio).";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY048969; ALU07508.1; -.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
KW Receptor.
SQ
SEQUENCE 432 AA; 49137 MW; 1A52F0283C663DA7 CRC64;
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Query Match 49.6%; Score 1180.5; DB 13; Length 432;
Best Local Similarity 56.6%; Pred. No. 4.5e-78;
Matches 243; Conservative 45; Mismatches 112; Indels 29; Gaps 8;

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Oy 20 GGGARATPSLQVTLTVCLAGLMLTLVFGNVLIIVFTSRALAPQNLFLVSLASAD 79
Db 22 GNSTNSTSPATITIGLAGLVSLFIFTGVNVLIIVFTSRALAPQNLFLVSLASAD 81
Oy 80 IIVATLVIPESLANEMGWGKAMCEIYALDVLEFCTSSIVHCAISLDRYWSTIQA 139
Db 82 IIVATLVIPESLANEMGWGKAMCEIYALDVLEFCTSSIVHCAISLDRYWSTIQA 141
Oy 140 EYNLKRTPRIKAIITVWVISAIVSPPLISIEKKGCGGQAPRCEINDQKWYVYS 199
Db 142 EYNLKRTPRIKAIITVWVISAIVSPPLISMDR---NTVDERRPMQQLNDHTWYLLY 197
Oy 200 SCIGSFAPCLIMIIYVYRIYQIARRRVRPPSRGPPAVAAPPGETERRPNIGPERS 258
```



```

Db 234 LPALASVASAREVNGHSGKSTGEKEGEPTPEDTGRALPSPMALPNSGOGKEGVCASGP 293
QY 299 SDHAERPPGPRRRPRRGKGAARASQVPGD--SLPRRPG-----ATGIGTPAAGPGE 351
Db 294 EDAEAE-----EEEEECEPOAVFVSPASCSPLPQPOGSRVLAITLRGQVLLGRG- 345
QY 352 ERVGAARASRWGRQ--NREKRTFVLAVYIGVVCWMPPEFTYTLAV---GGSVPRT 406
Db 346 --VGAIGGQWMMRRRAQLTREKRTFVLAVYIGVVCWMPPEFTYSLGAIQPKCKVPHG 403
QY 407 LKFEFFWFGYCNSSLNPVYITITFNHDFRRAFKIICR 443
Db 404 LFOEFFWIGYCNSSLNPVYITITFNHDFRRAFKIICR 440

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```

RESULT 6
Q925K6 PRELIMINARY; PRT; 448 AA.
AC Q925K6:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Adrenergic receptor alpha 2B.
GN ADRA2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ISS;
RA Ehlinger M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikelia J.M.,
RT "High-throughput Sequence Identification of Gene Coding Variants
RT within Alcohol-Related QTLs."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332050; AAK56079.1; -.
DR MGD; MGI:87935; Adra2b.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF000237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.
DR Receptor.
SQ SEQUENCE 448 AA; 49998 MW; B37E5E21B0EC4625 CRC64;

```

Query Match 46.9%; Score 1115.5; DB 11; Length 448;
 Best Local Similarity 52.7%; Pred. No. 2,3e-73;
 Matches 241; Conservative 50; Mismatches 105; Indels 61; Gaps 14;

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QY 27 PYSLOYTLVLCAGLMLITVFGNVLYIAVFTSRALKAPONFLVSLASADILVATLV 86
Db 6 PYSVOATAIASAIFLILFTIFGNALVTLAVTSRSLRAQONFLVSLAADILVATLI 65
QY 87 IPFSLANEVGYWYFGKACEIYALDVLFCSTIVHCAISLDKRWYSITQAIYENLRT 146
Db 66 IPFSLANEELGTYWYFWRACVEYIALDVLFCSTIVHCAISLDKRWYSITQAIYENLRT 125
QY 147 PRRIKAIITTVWVAVISFPLISIEKKGGGGPOP--AEPRCEINQKWTYVSSICISGF 205
Db 126 PRRIKAIITTVWVAVISFPLISIEKKGGGGPOP--AEPRCEINQKWTYVSSICISGF 205
QY 147 PRRIKAIITTVWVAVISFPLISIEKKGGGGPOP--AEPRCEINQKWTYVSSICISGF 205
Db 126 PRRIKAIITTVWVAVISFPLISIEKKGGGGPOP--AEPRCEINQKWTYVSSICISGF 205
QY 206 FAPCLIMILVYRIQIKRRTVPPSRGPDVAAAPPGERTERRPNGLGERSAGPGAG 265
Db 182 FAPCLIMILVYRIQIKRRTVPPSRGPDVAAAPPGERTERRPNGLGERSAGPGAG 265
QY 266 AEPLEPTQUNG---APGEPAAPRDTDALDLEESSSDHAER---PPG-----PRRERGP 315
Db 234 VPTLVSPSLSSVGEANGHKRP--PREK-----EEGETPEDEEARALPPNMSALPRSVQDOK 286
QY 316 RKGKARASQVKKPGD-----SLPRRPGATGIGTPAAGPGEER----- 353
Db 287 KGTSGATAEKAEDDEEBEVECEPQITLP--ASPASVFNPLPQOPQTSRVLATLRGQVLLS 344

```

```

QY 354 --VGAARASRWGRQ--NREKRTFVLAVYIGVVCWMPPEFTYTLAV---GGSVPRT 406
Db 345 KNGVVASGQWMMRRRTQLSREKRTFVLAVYIGVVCWMPPEFTYSLGAIQPKCKVPHG 404
QY 407 LKFEFFWFGYCNSSLNPVYITITFNHDFRRAFKIICR 443
Db 405 LFOEFFWIGYCNSSLNPVYITITFNHDFRRAFKIICR 441

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RESULT 7
Q925K7 PRELIMINARY; PRT; 448 AA.
AC Q925K7:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Adrenergic receptor alpha 2B.
GN ADRA2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ISS;
RA Ehlinger M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikelia J.M.,
RT "High-throughput Sequence Identification of Gene Coding Variants
RT within Alcohol-Related QTLs."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332049; AAK56078.1; -.
DR MGD; MGI:87935; Adra2b.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PSS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.
DR Receptor.
SQ SEQUENCE 448 AA; 50018 MW; 1B5ED9456C0B2B73 CRC64;

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Query Match 46.8%; Score 1114.5; DB 11; Length 448;
 Best Local Similarity 52.7%; Pred. No. 2,9e-73;
 Matches 241; Conservative 49; Mismatches 106; Indels 61; Gaps 14;

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QY 27 PYSLOYTLVLCAGLMLITVFGNVLYIAVFTSRALKAPONFLVSLASADILVATLV 86
Db 6 PYSVOATAIASAIFLILFTIFGNALVTLAVTSRSLRAQONFLVSLAADILVATLI 65
QY 87 IPFSLANEVGYWYFGKACEIYALDVLFCSTIVHCAISLDKRWYSITQAIYENLRT 146
Db 66 IPFSLANEELGTYWYFWRACVEYIALDVLFCSTIVHCAISLDKRWYSITQAIYENLRT 125
QY 147 PRRIKAIITTVWVAVISFPLISIEKKGGGGPOP--AEPRCEINQKWTYVSSICISGF 205
Db 126 PRRIKAIITTVWVAVISFPLISIEKKGGGGPOP--AEPRCEINQKWTYVSSICISGF 205
QY 147 PRRIKAIITTVWVAVISFPLISIEKKGGGGPOP--AEPRCEINQKWTYVSSICISGF 205
Db 126 PRRIKAIITTVWVAVISFPLISIEKKGGGGPOP--AEPRCEINQKWTYVSSICISGF 205
QY 206 FAPCLIMILVYRIQIKRRTVPPSRGPDVAAAPPGERTERRPNGLGERSAGPGAG 265
Db 182 FAPCLIMILVYRIQIKRRTVPPSRGPDVAAAPPGERTERRPNGLGERSAGPGAG 265
QY 266 AEPLEPTQUNG---APGEPAAPRDTDALDLEESSSDHAER---PPG-----PRRERGP 315
Db 234 VPTLVSPSLSSVGEANGHKRP--PREK-----EEGETPEDEEARALPPNMSALPRSVQDOK 286
QY 316 RKGKARASQVKKPGD-----SLPRRPGATGIGTPAAGPGEER----- 353
Db 287 KGTSGATAEKAEDDEEBEVECEPQITLP--ASPASVFNPLPQOPQTSRVLATLRGQVLLS 344
QY 354 --VGAARASRWGRQ--NREKRTFVLAVYIGVVCWMPPEFTYTLAV---GGSVPRT 406
Db 345 KNGVVASGQWMMRRRTQLSREKRTFVLAVYIGVVCWMPPEFTYSLGAIQPKCKVPHG 404
QY 407 LKFEFFWFGYCNSSLNPVYITITFNHDFRRAFKIICR 443

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Db 405 LFOFFWIGYCNSSLNPIYITTFNODFRARFRILICR 441

RESULT 8
Q925E4 PRELIMINARY: PRT: 453 AA.
AC Q925E4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Alpha2B-adrenergic receptor.
GN Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Schaak S., Cusack D., Paris H.;
RT Cloning and characterization of the rat alpha2B-adrenergic receptor
RT gene promoter";
RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF366899; AAK53388.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECPEP_FL_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECPEP_FL_2; 1.
KW Receptor
SQ SEQUENCE 453 AA: 50369 MW: CBA69CE23EAC8511 CRC64;

Query Match 46.6%; Score 1110.5; DB 11; Length 453;
Best Local Similarity 52.5%; Pred. No. 5.8e-73;
Matches 240; Conservative 50; Mismatches 106; Indels 61; Gaps 14;

Qy 27 PYSQVLTLLVCLAGLMLTFVGNVLIYAVTSRALKAPONLFLVSLASADIVATLV 86
Db 11 PYSQVATPAALASATITFLITFTFGNALVILAVITSLRPNQLFLVSLAADIVATLI 70
Qy 87 IFSLANEVMGYVYFGKACEIYALDVLFCTSSIVHLCAISIDRYWSTOAEVNLKRT 146
Db 71 IFSLANELLGYVYFMRACEVYALDVLFCTSSIVHLCAISIDRYWAVSALEVNSKRT 130
Qy 147 PRRIKAITITVWVSAVISPPPLISIEKKGGGGGPOP-AEPCEINDQKMYVSSCIGSF 205
Db 131 PRRIKICILITVWLIAAVISLPLI---YKGDQPEPRGILPOCELNDEAMYLIIASSIGSF 186
Qy 206 FAPCLIMILVVRITVYQIAKRTVRVPSRRGPDVAAPPGCTERRPNGLGERSAGPGAE 265
Db 187 FAPCLIMILVLRITVIAKR-----SHCRGLGAKRGSGEGESKPPQ---PVAGCVPTSAK 238
Qy 266 AEPITQING---APGEPAAGPRDPTALDLESSSSDAHER---PPG-----PRRPERGP 315
Db 239 VPTLVSPILSVGEANGHKP---PREK-----EEGETPEDEARALPTWSALPRSOGOK 291
Qy 316 RCKGKARASQVKKPD-----SLPRGPGATGIGTPAAGGEER----- 353
Db 292 KGTSGATAEDEDEDEEVECEPQTLP--ASPAVSCNPILQDPQTSRVLATLRGQVILG 349
Qy 354 --VGAAKASRMGRG--NRKRRTFVLAIVGVVCMFPFFTYTLTAV---GCSVPRT 406
Db 350 KAVGVAASQGMWRRTQLSREKRRTFVLAIVGVVCMFPFFTSYSLGALCPQCKVPHG 409
Qy 407 LKFFFWYGYCNSLNPIYITTFNIDFRARFKILICR 443
Db 410 LFOFFWIGYCNSSLNPIYITTFNODFRARFRILICR 446

RESULT 9
Q9JWJ2 PRELIMINARY: PRT: 393 AA.
ID Q9JWJ2;
AC Q9JWJ2;

DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Alpha adrenergic receptor 2B (Fragment).
GN AAR2B.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA Madsen O.;
RT Molecular evolution of alpha adrenergic receptor 2B.";
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
CC 1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC 1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AJ271336; CAB6895.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECPEP_FL_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECPEP_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT NON_TER 1 393
FT NON_TER 1 393
SQ SEQUENCE 393 AA: 42921 MW: 5399B7175A53BD48 CRC64;

Query Match 40.6%; Score 967.5; DB 11; Length 393;
Best Local Similarity 52.2%; Pred. No. 1.2e-62;
Matches 214; Conservative 41; Mismatches 86; Indels 69; Gaps 13;

Qy 43 IMLTVEGNVLIYAVTSRALKAPONLFLVSLASADIVATLVIPFSLANEVMGYVTFG 102
Db 9 ILFTFGNALVILAVITSLRPNQLFLVSLAADIVATLIIPFSLANELLGYVTFW 68
Qy 103 KACEIYALDVLFCTSSIVHLCAISIDRYWSTOAEVNLKRTPRRIKAITITVWVISA 162
Db 69 RTWCEVYALDVLFCTSSIVHLCAISIDRYWAVSALEVNSKRTPRRIKICILITVWLI 128
Qy 163 VISPPPLISIEKKGGGGGPOP-AEPCEINDQKMYVSSCIGSFAPCLIMILVVRITV 221
Db 129 VISLPLI---YKGDQGPQPSQCKINQDEAMYLIIASSIGSFAPCLIMILVLRITV 184
Qy 222 IAKRTRVPSRRGPDVAAPPGCTERRPNGLGERSAGPGAE---PLPTQING-- 275
Db 185 IAKR-----SNRRGPRAKGPGEGESKESRPL-----PGAPASAKYVPLASPLSTG 232
Qy 276 -APEPAAGPRDPTALDLESSSSDAHERPPGRRPERGPRGKARASQVKKP----- 328
Db 233 EANGPKPTGEKE-----EGETSEDGARTLPSSMALPTSGOGKKAVVLAPAEAE 286
Qy 329 ----GDSL-PRRPG-----ATGIGTPAAGGEERVGAAKASRMGR 363
Db 287 EEEEGDCECPQAPAGLPASWCSPSLQPOGSRVLATLRGQVILGR---VGVVDQGMWR 343
Qy 364 GR--ONREKRTFVLAIVGVVCMFPFFTYTLTAV---GCSVPRT 408
Db 344 RRTQMTREKRRTFVLAIVGVVCMFPFFTYSLGALCPQCKVPHGLF 393

RESULT 10
Q9SN90 PRELIMINARY: PRT: 392 AA.
ID Q9SN90;
AC Q9SN90;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Alpha adrenergic receptor 2B (Fragment).
GN AAR2B.
OS Tadarida brasiliensis (Brazilian free-tailed bat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Molossidae; Tadarida.
OX NCBI_TaxID=9438;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21267399; PubMed=11353869;
RA Springer M.S., Teeling E.C., Madsen O., Stanhope M.J., de Jong W.W.;
RT "Integrated fossil and molecular data reconstruct bat echolocation.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:6241-6246(2001).
DR EMBL; AF37342; AAK5307.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 392 AA; 42771 MW; 8DA9B78A13C5997E CRC64;

Query Match
Best Local Similarity 39.5%; Score 941; DB 6; Length 392;
Matches 206; Conservative 45; Mismatches 105; Indels 38; Gaps 11;

QY 43 LMLTFVGNVLTIAVFTSRALKAPQNLFLVSLASADILVATLVTFSLANVMGYWFG 102
DQ 9 LILFTFGNVLAVLTSLRPAQNLFLVSLAADILVATLVTFSLANELLGYWYFR 68
QY 103 KANCEIYALADVLCSTSIYHCAISLDRYWSTQAIENYLNKRPRIKAIITVWVISA 162
DQ 69 RTWCEYIALADVLCSTSIYHCAISLDRYWAVSRALEVNSKRPRIKRIITVWMLIA 128
QY 163 VISFPLISIEKKGGGGGPOP-AEPCETINDQKWTIVSSIGSFAPCLMILVYVRIYQ 221
DQ 129 AILSPLI-----YKDGQGPQPRGRPOCKLNQAWIILSSIGSFAPCLMILVYLRIV 184
QY 222 IAKRRTRVPPSRGPDVAAPPGGTERRPNGL-GEPSAGPGAEAPLTQNG---- 275
DQ 185 IAKR-----SHRGGPAGKAPRKESKQPHSLDSGPSALN-----LPTLASLAVA 231
QY 272 ---QLNGAGEPA-PAGRPDIDL-----DLESSSSDHAERPGRPRPERGPKGKAR 322
DQ 240 GEKEXGTEDPDONALPSPWFLPAAGQKEGVCEASPEDVDGEEDDEEDCEFOAL 299
QY 323 ASQVKGDSLPRRGATGICTPAAGPG--EEYVGAAKASRW---RGHONREKRTFVLA 377
DQ 300 PASPASACSPPLQOPGSGSLATLRGOVLNLSGVGA-GGMWLKRAQLTTEKRTFVLA 358
QY 378 VYIGVYVWCMPEFFTYTLTAV---GCSVPRTLF 408
DQ 359 VVIGVFLCMPEFFSYSLGALCPQHCKVPHGLF 392

RESULT 11
Q9GKZ6 PRELIMINARY; PRT; 390 AA.
AC Q9GKZ6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Alpha adrenergic receptor, subtype 2B (Fragment).
GN AAR2B.
OS Trichechus manatus (Caribbean manatee) (West Indian manatee).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Sirenia; Trichechidae; Trichechus.
OX NCBI_TaxID=9778;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., Madsen O., Catzefflis F., Stanhope M., de Jong W.W.;
RT "Probing the protein sequence support for the 'African clade' of
mammals.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ251109; CAC16418.1; -.
DR HSPSP; P29274; 1MMH.
DR InterPro; IPR000276; GPCR_Rhodpsn.

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DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHOOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 390 AA; 42713 MW; 06D90A8DICE912A3 CRC64;

Query Match
Best Local Similarity 39.5%; Score 940; DB 6; Length 390;
Matches 212; Conservative 37; Mismatches 95; Indels 60; Gaps 14;

QY 43 LMLTFVGNVLTIAVFTSRALKAPQNLFLVSLASADILVATLVTFSLANVMGYWFG 102
DQ 9 LILFTFGNVLAVLTSLRPAQNLFLVSLAADILVATLVTFSLANELLGYWYFR 68
QY 103 KANCEIYALADVLCSTSIYHCAISLDRYWSTQAIENYLNKRPRIKAIITVWVISA 162
DQ 69 RTWCEYIALADVLCSTSIYHCAISLDRYWAVSRALEVNSKRPRIKRIITVWMLIA 128
QY 163 VISFPLISIEKKGGGGGPOP-AEPCETINDQKWTIVSSIGSFAPCLMILVYVRIYQ 221
DQ 129 AILSPLI-----YKDGQGPQPRGRPOCKLNQAWIILSSIGSFAPCLMILVYLRIV 184
QY 222 IAKRRTRVPPSRGPDVAAPPGGTERRPNGL-GEPSAGPGAEAPLTQNG---- 275
DQ 185 IAKR-----SHRGGPAGKAPRKESKQPHSLDSGPSALN-----LPTLASLAVA 231
QY 276 --APGEPAPGPDIDLLESSSSDHAERPGR--PRPERGPKGK--CKAASQVKGDS 331
DQ 232 GEADGHSMPGPKER-----ETSEDPGTPTLPSPVFLPNSGQCKEYVCALEEADK 286
QY 332 LPRR--GP-----GATGIGTPAAGPGEER-----VGAKASRWGRQ--N 367
DQ 287 EEEDECGPAVPASPAATACSPPLQOPGSRVLAFLRGVFLRGVGAAGGWMRRRAQLT 346
QY 368 REKRTFVLAIVYIGVYVWCMPEFFTYTLTAV---GCSVPRTLF 408
DQ 347 REKRTFVLAIVYIGVFLCMPEFFSYSLGALCPQHCKVPHGLF 390

RESULT 12
Q9GLI9 PRELIMINARY; PRT; 390 AA.
AC Q9GLI9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Alpha adrenergic receptor 2B (Fragment).
GN AAR2B.
OS Cynocephalus variegatus.
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Dermoptera; Cynocephalidae; Cynocephalus.
OX NCBI_TaxID=9457;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082081; PubMed=11214318;
RA Madsen O., Scally M., Douady C., Kao D., Debry R., Adkins R.,
RA Amrine H., Stanhope M., de Jong W., Springer M.;
RT "Parallel adaptive radiations in two major clades of placental
mammals.";
RL Nature 409:610-614(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ251182; CAC16685.1; -.
DR HSPSP; P29274; 1MMH.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHOOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.

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0Y 43 IMLLTVFEGVLYITIAVFTSSRLAKAPQNFVLSASADILVATVIPSILANEWGYWYFG 102
Db 9 LLLFFIFGNAVLIAVLVLSRSLRAPQNFVLSAAADILVGTLLIPSLANELLGWYFR 68
0Y 103 KAMECEIYALDVLCTSSIVHCAISIDRWYSIOALEYNNKPRPRKAIITTWAVISA 162
Db 69 HWCVEYIALDVLCTSSIVHCAISIDRWYSRALEYNSKPRPRKIKIITVWLIIA 128
0Y 163 VISPEPLISIEBKGGGGGPOAPBRCETINDQKWVVISCSIGSEFAPCLMIIVYVRYOI 222
Db 129 FLSLPELI---YKGDKKKSGRGPOCKLNEAWVILSSIGSEFAPCLMIIVLYLIIYL 185
0Y 223 AKRRIRVPSRRGCDYAAAPGCGTERRPNGLGPBRASGPEGABA-BPLPTQLGABGE-- 279
Db 186 AKRR---NRQGHGRKALSDG----DTGP---SGPGASAIKLPSSVLSAVGEAN 231
0Y 280 --PAPAGRDJDALDLESSSSDAERPG--PRRPRGPRG-----GKAR 322
Db 232 GHSKPAGRE-----GGEIDGPPSTTPMQSSVSGEDVSHROEEBEEDEGEDEC 281
0Y 323 ASQYKPGDSLPRRPGATIGITPAAG-----GERRYGAARKS---RWGR-- 365
Db 282 GSPALPTSSSQ-----GTPXQGPQGSQMLATLIRQVLLARQPAISLGQPMWRKRIQ 333
0Y 366 QNRKRRTVLAIVYIGVFWCWPFFFTYITLV---GCSVPETLF 408
Db 334 MNRKRRTVLAIVYIGVFWCWPFFFSYIGVHCIOHCKVPPGLR 379

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RESULT 15			
08SOAO			
ID	08SOAO	PRELIMINARY;	PRT; 391 AA.
AC	08SOAO;		
DT	01-JUN-2002 (TREMBLREL, 21, Created)		
OC	01-JUN-2002 (TREMBLREL, 21, Last sequence update)		
DT	01-JUN-2002 (TREMBLREL, 21, Last annotation update)		
DE	Alpha 2B adrenergic receptor (Fragment).		
OS	ADRA2B.		
GN	Emballonura atrata (Peters's sheath-tailed bat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Chiroptera; Microchiroptera; Emballonuridae;		
OC	Emballonura.		
OX	NBIL_TaxID=110940;		
RN	[1]		
RN	SEQUENCE FROM N.A.		
RP	MEDLINE=21819367; PubMed=11805285;		
RX	Teeling E.C., Madsen O., Van Den Bussche R.A., de Jong W.W.,		
RA	Stanhope M.J., Springer M.S.,		
RA	"Microbat paraphyly and the convergent evolution of a key innovata		
RT	in Old world rhinolophoid microbats.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:1431-1436(2002).		
DR	EMBL; AJ419810; CAD11977.1; "-.		
KW	Receptor.		
FT	NON_TER	1	1
FT	NON_TER	391	391
SEQUENCE	391 AA;	42656 MW;	E9EDCFOC2426672F CRC64;

Query Match	39.4%;	Score 937.5;	DB 6;	Length 391;
Best Local Similarity	52.1%;	Pred. No. 1.9e-60;		
Matches 208; Conservative	45;	Mismatches 97;	Indels 49;	Gaps 13;

DQ 43 LMJTVGNVNIIVAVTSRRLAKAPQULEVLVSADILVALTVIPSLANEWGYYFC 102
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 9 LILTIFGNAIYLIIVATSRSLRAPQLFYLISLAADIIVALTILIPSANELLGWYER 68
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DQ 103 KAMEIYIALDVLFCTSSIIYHLCASIDRWSTIQALEYNLKTPTRIKAIITTWVTSA 162
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 69 RTMCEVVIADVLTFTCSIYIHLCASIDRWAAVASRALEYNSKRTPPRIKCIITLVMLIAA 128
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DQ 163 VISEPPIISIEKKGGGGPPD-APRECEINDOKMYIASISCIGSFAPCLIMLYVKRIO 221
|| || | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 129 VISLPPLV-----TKNGNPGDPGRGPCKKLQEWEMTIASSIGFFNPCLMIIMLYVRITY 184

QY	222	IAKRTRVPPSRGDAVAAPPGTERRPNCGLGEBRSAGEGAEPLPLQINGAPGEPA	261
Db	185	IAKR-----SHRRGPRAGCGPGVDSDKSPREY- GGRSAKLPTLASHLATS-GEANGHSK	237
QY	282	PAGPRDTDALDLEESSSDHAREPPGPRRPRGRGK-GKARAS-QYKPRD-----	330
Db	238	PTGEEGGGTADDEGSP---ALPPSWPALPHAGGGGKGVCAGASPEVEVEEEDDECE	294
QY	331	--SLPRRGPGATGIGTPAAGGEERV-----	
Db	295	POALP--ASPASACSPPLQCPQGSRLVATLRGVLTLGRGMAASGGMRRRAOLTEKRF	352
QY	373	TEVLAVTVGVGVNCGMPPEFFTYITLAV---GCSYPRLEF	408
Db	353	TEVLAVTVGVVLCWMPPEFFSYSGALCQPOHCKVPHLE	391

Search completed: February 15, 2003, 18:07:00
Job time : 53 secs


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Db 606 CAACCGCAGAGCTCCAGGCCAAGG--GGGGCTGGGCGAGGTGATCCAAAGCAGCCC 663
OY 738 CGAGCGCAGGCCCAAGGGTCTGGGCCCCGAGCCGAGCGCGGGCCCCGGG-----GGCGCA 792
Db 664 CGACCGCAGCATGGTGGGGCTTTGGGCTCAGCCAAACTGCAGCCCTTGCGCTTG6CT 723
OY 793 GAGCGCGAACCCTGCCACCTCAGCGCGCCCTGGCGAGCCCGCGCGCGCGGG 852
Db 724 TCTGCCAAGAGGTCAGGACACTCGAAGTCCACTGGGAGAGAGAGGAGGAGACC 783
OY 853 CCGCGCAGACGACGACGCGCTGGACCTGGAGGAGAGCTGCTTCCGACACAGCCGAGCGG 912
Db 784 CCTGAAGATACGGGAGCCGGGCTTGCCACCCAGTTGGGCTGCCCTTCCCACTCAGGC 843
OY 913 C-----CTCCAGGGCCCCGCGAGACCAGCGCG 940
Db 844 CAGGGCCAGAGAGAGGGGTGTTGTGGGCACTCCAGAGGATGAAGCTGAAGAGAGAGAG 903
OY 941 GTCCCCGGGGCAAGGCAAGGCCGAGCGAGCCAGGTGAAGCGGGCGACAGCTGCGCC 1000
Db 904 GAGGAGAGAGAGAGTGTGAACCCAGGCAAGTGTCTCCGGGCTCAGCTTGACG 963
OY 1001 GCGCGGCGCGGGGCGAGCGGGGATCGGG-----ACGCGGCTGCAAGGGC 1045
Db 964 CCCCGCTGCAGAGCCACAGGGGCTCCGGGTGCTGGCCACCCCTACGTGGCCAGGTGCTC 1023
OY 1046 CGGGGGAGAGCGCGTGG-----GGCTGCCAAGGCGTGCCTGGCGCGGGCGCAGAAC 1101
Db 1024 CTGGGCAAGGGGCTGGGTCTATAGTGGGAGTGGTGGCGTGAAGGGCGCAGCTGACG 1083
OY 1102 CGCGAGAGCGCTTCACGTTGCTGGTGGCGCGGTGATCGAGTGTGCTGCTGG 1161
Db 1084 CGGAGAGAGCGCTTCACGTTGCTGGTGGTGTATGCGCTTTTGTGCTGCTGG 1143
OY 1162 TTCCCTTCTTCACTACGCTACGCTACGCGCGTGG-----GTGCTCGTGCA 1212
Db 1144 TTCCCTTCTTCACTACGCTACGCTACGCGCGCTGCGCCGAGCAGCTGCAAGGTGCC 1203
OY 1213 CGCAGCGCTTCAATTTCTTCTGTTGGTGTACTGCAACAGCTGTTGAACCGGTC 1272
Db 1204 CATGGCTCTTCCAGTCTTCTTGTGATGGCTACTGCAACAGCTGACTGAACCTGTT 1263
OY 1273 ATCTACACCATCTTCAACACAGATTTCCGCGCGCTTCAAGAAGATCCTGTG 1328
Db 1264 ATCTACACCATCTTCAACACAGACTTCGCGCTTCCGAGAGATCCTGTGCG 1319
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Search completed: February 15, 2003, 14:30:30
Job time : 443.817 secs

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QY 1053 GGAGCGCGCGGGGCTGCCA-----AGCCCTCCGCTGGCGCGGCGGCGCAGAACCG 1103
Db 1026 GGGCAGGGGCGCTGGGTGTATAGTGGGAGTGGGTGGCTGCAGCGGGCGAGCTGACCG 1085
QY 1104 CGAGAAAGCGCTTACGTTCTGCTGCGCGGTCATCGAGTGTGTGTGTGTGTGTGTGTGT 1163
Db 1086 GGAGAAAGCGCTTACGTTCTGCTGCGCGGTCATCGAGTGTGTGTGTGTGTGTGTGTGT 1145
QY 1164 CCCCTCTCTCTCCACCTACACGCTCAGCGCGCTGGG-----TGCCTCGTGCACG 1214
Db 1146 CCCCTCTCTCTCCACCTACACGCTCAGCGCGCTGGGCGCCATCTCCGAAAGCACTGCAAGTGTGCCA 1205
QY 1215 CACGCTCTTCAAAATCTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1274
Db 1206 TGGCCTCTCTCCAGTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1265
QY 1275 CTACACATCTTACACGAGATTTCCGCGCGCTTCAAGAGATCTGTGTGTGTGTGTGTGTGT 1328
Db 1266 CTACACATCTTACACGAGATTTCCGCGCGCTTCCGAGAGATCTGTGTGTGTGTGTGTGTGT 1319

RESULT 15
AA199906
XX AA199906 standard; DNA; 1344 BP.
XX
AC AA199906;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human alpha-2BAR third intracellular loop variant encoding DNA.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2BAR; chromosome 2; ds.
XX
OS Homo sapiens.
XX
FH Key 1..1344 Location/Qualifiers
FT CDS /product= "alpha-2BAR"
FT /tag= a
FT /note= "sequence is deleted for a 9 nucleotide
FT polymorphic site found at nucleotides 901-909
FT of the wildtype alpha-2BAR protein (AA199905)"
XX
PN WO200179561-A2.
XX
XX 25-OCT-2001.
XX
PD 17-APR-2001; 2001WO-US12575.
XX
PF 17-APR-2000; 2000US-0551744.
XX
PR 10-AUG-2000; 2000US-0636259.
XX
PR 19-OCT-2000; 2000US-0692077.
XX
PA (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
PI Liggett SB, Small KM;
XX
DR WPI; 2001-611728/70.
DR P-PSDB; AAM52118.
XX
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
XX determining whether an individual is at increased risk of developing a
XX disease associated with the corresponding receptor comprises detecting
XX a polymorphic site .
XX
XX Claim 5; Page 144-145; 163pp; English.
XX
XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
XX

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CC receptor gene (I)-(III) by detecting a polymorphic site, comprising;
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (II)
CC or a site comprising (A) (999gg99ggcg) or (B) (999gg9ggcga) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2C, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. ephedrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC ranolazine, idazoxan, tolazoline, phenolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the third intracellular loop of
CC the human alpha-2BAR variant, the sequence is deleted for a 9 nucleotide
CC polymorphic site found at nucleotides 901-909 of the wildtype gene
CC (AA199905).
XX
SQ Sequence 1344 BP; 220 A; 458 C; 400 G; 266 T; 0 other;
XX

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Query Match 33.0%; Score 446; DB 23; Length 1344;
Best Local Similarity 63.4%; Pred. No. 1.6e-61;
Matches 835; Conservative 0; Mismatches 405; Indels 76; Gaps 7;
QY 78 CCTTACTCTCCAGGTGACGCTGACGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 137
Db 15 CCCCTACTCTCCGTCAGGCGCAGGCGGCGCATAGCGGCGGCGCATACCTTCTCTATCTCTT 74
QY 138 CACGNGTTCGGAACGCTGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 197
Db 75 TACCATCTTCGGACAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 134
QY 198 GCCCAAAACCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 257
Db 135 CCCCTAGAACCTGTCTCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 194
QY 258 CATCCCTTTCGCTGCGCAACAGAGTATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 317
Db 195 CATCCCTTTCGCTGCGCAACAGAGTATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 254
QY 318 CAGATCTACCTGCGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 377
Db 255 CGAGGTGTACTGCGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 314
QY 378 CATACGCTTGACCGCTTACTGTGTATCATCACAGGCTATGAGTACATCAAGCTGAAGCGAC 437
Db 315 CATACGCTTGACCGCTTACTGTGTATCATCACAGGCTATGAGTACATCAAGCTGAAGCGAC 374
QY 438 GCCGCGCGCATCAAGGCTATCATCAAGGCTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGT 497
Db 375 CCGCGCGCGCATCAAGGCTATCATCAAGGCTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGT 434
QY 498 CCGCGCGCTCATCTCATGAGAGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 557
Db 435 GCCGCGCGCTCATCT-----ACAAGGCGACCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 485
QY 558 GCGCTGCGAGATCAAGACAGACAGAGTGTGTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 617
Db 486 CCACTGCAAGCTCAACAGAGGCTGTGTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 545
QY 618 CGCTCCCTGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 677
Db 546 TGTCTCTTGCCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 605
QY 678 CACCGCGCTGACCCAGCGCGGCGGCTCGAGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 737

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AA064890
ID      AA064890 standard: DNA; 1382 BP.
XX
AC      AA064890;
XX
DT      01-FEB-1995 (first entry)
XX
DE      Human derived adrenaline alpha 2CII receptor DNA.
XX
KW      adrenaline receptor; alpha CII; screening; detection; pharmacology;
KW      drugs; ds.
XX
OS      Homo sapiens.
XX
FH      Key
FT      5'UTR
FT      Location/Qualifiers
FT      1..2
FT      /*tag= a
FT      /note= "5'-non translated region"
FT      CDS
FT      3..1376
FT      /*tag= b
FT      /product= adrenaline alpha CII receptor
FT      3..5
FT      /*tag= b
FT      /note= "encodes Met; this codon may or may not be
FT      present, but can only be present if
FT      nucleotides 6-53 are also present"
FT      misc_feature
FT      6..53
FT      /*tag= c
FT      /note= "this sequence may or may not be present"
FT      3'UTR
FT      1377..1382
FT      /*tag= c
FT      /note= "3'-non-translated region"
XX
PN      JF06121686-A.
XX
XX
PD      06-MAY-1994.
XX
XX
PF      12-OCT-1992: 92JP-0272744.
XX
XX
PR      12-OCT-1992: 92JP-0272744.
XX
PA      (ASAH ) ASahi KASEI Kogyo KK.
XX
DR      WPI; 1994-185923/23.
XX
DR      P-PSDB; AAR54834.
XX
XX
PT      Adrenaline receptor gene encoding alpha 2CII receptor - for
PT      screening drugs reactive to the alpha 2CII receptor
XX
PS      Claim 1; Page 9-11; 13pp; Japanese.
XX
XX
CC      This sequence encodes the amino acid sequence of a polypeptide
CC      (AAR54834) that constitutes human derived adrenaline alpha 2CII
CC      receptor. this can be used for the study of the pharmacological
CC      importance of the gene expression in humans.
XX
SQ      Sequence 1382 BP; 165 A; 480 C; 497 G; 240 T; 0 other;
Query Match 38.0%; Score 512.4; DB 15; Length 1382;
Best Local Similarity 64.7%; Pred. No. 6.3e-72;
Matches 866; Conservative 0; Mismatches 421; Indels 51; Gaps 5;
QY      19 GACGCGGCAACGAGCTGAGACGAGACGAGCGCGCGGGGCGCGCGGCGGCGACG 78
DB      || ||||| || || || || || || || || || || || || || || || ||
QY      79 CTTACTCCCTGACAGGTGACGTGACGTGCTGCTGCGCGCGCGCTGCTCATGCTGTC 138
DB      | ||||| || || || || || || || || || || || || || || || ||
QY      135 CAGTATCGGCGGCGCGGCGGCGGCGAGGCTGCTGCGGTGAGGCTTCCTCATGCTCTTC 194
DB      || ||||| || || || || || || || || || || || || || || || ||
QY      139 ACCGTGTCGCAACGCTGCTGTCATCATGCGCGGTTCACGAGCGCGCGCTCAAGCGC 198
DB      || ||||| || || || || || || || || || || || || || || || ||
QY      195 ACCGTGTCGCAACGCTGCTGTCATCATGCGCGGTTCACGAGCGCGCGCGCTGCGCGG 254
DB      || ||||| || || || || || || || || || || || || || || || ||
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QY      199 CCCCAAAACCTTCTCTGCTGCTCTGCGCTGCGCGCAATCTGTCGCGACGCTGTC 258
DB      || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      255 CCACAGAAACCTTCTCTGCTGCTGCTGCGCTGCGCGCAATCTGTCGCGACGCTGTC 314
QY      259 ATCCCTTCTGCGTGGGCGCAAGAGGTGATGGGCTACTGTAATCTTCCGCAAGCTTGTCG 318
DB      || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      315 ATGCCCTTCTGCTTGGCGCAAGAGCTGATGGGCTACTGTAATCTTCCGCAAGCTTGTCG 374
QY      319 GAGATCTACGTCGGGCTGCGAGTCTCTTCTGCAAGTCTGTCATGTCGACCTGTCGTCGCG 378
DB      || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      375 GCGGTGTACTGGGCGCTGATGTCTGTTTGCACCTGTCATCTGTCATCTGTCGTC 434
QY      379 ATCAGCCTGAGCGCTACTGCTGCTGCTCATACAGAGCCATGAGTAACTGAAGCGCAGC 438
DB      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      435 ATCAGCCTGAGCGCTACTGCTGCTGCTCATACAGAGCCATGAGTAACTGAAGCGCAGC 494
QY      439 CCGGCGCGCATCAAGGCCATCATCATCAGCGTGTGGTATCTGCGCGCTGCTGCTGTC 498
DB      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      495 CCACGCGCGCTCAAGGCCATCATCATCAGCGTGTGGTATCTGCGCGCTGCTGCTGTC 554
QY      499 CCGCGCTCATCTTCATCAGAGAAAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 558
DB      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      555 CCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
QY      559 CGCTGCAGATCAACGACGAGAGTGTATGTCATCTGTCGTCGTCGTCGTCGTCGTCGTC 618
DB      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      603 CAGTGGCGCTCAACGACGAGACCTGTGATCTGTCATCTGTCGTCGTCGTCGTCGTCGTC 662
QY      619 GCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 678
DB      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      663 GCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 722
QY      679 ACCCGGTGTCACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 738
DB      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      723 ACAGCGACGCTGACGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 782
QY      739 GACGCGAGCGCCAGAGGCTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 798
DB      || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      783 GA-----AAGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 824
QY      799 GAACGCTGCTCCACCGACGCTCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 838
DB      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      825 ----CACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 880
QY      859 GACACCGAGCGCTGACCTGAGAGAGAGCTGCTTCCGACCGCGCGCGCGCGCGCGCTCA 918
DB      || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      881 GAGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 940
QY      919 GGGCGCGCGACGACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 978
DB      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      941 GGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1000
QY      979 AAGCGCGCGACAGAGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1038
DB      || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      1001 GTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1060
QY      1039 GCAGGCGCGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1098
DB      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      1061 GTCCGCGCG-----GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1112
QY      1099 AACCAGGAGAGCGCTTACGCTTCTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1158
DB      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      1113 GCGCGCGAGAGCGCTTACGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1172
QY      1159 TGGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1209
DB      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      1173 TGGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1232
QY      1210 CCAGCGACGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1269
DB      || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      1233 CCGGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1292
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17-APR-2001; 2001WO-US12575.
 17-APR-2000; 2000US-0551744.
 10-AUG-2000; 2000US-0636259.
 19-OCT-2000; 2000US-0692077.
 (LIGGETT) LIGGETT S B.
 (SMALL) SMALL K M.
 Liggett SB, Small KM;
 WPI: 2001-611728/70.
 P-PSDB: AAM52126.
 Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting a polymorphic site -
 Claim 103; Page 158; 163pp; English.

The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising:
 (a) obtaining a sample having a polynucleotide encoding an alpha-2B, alpha2A or alpha2C or fragment or complement of; and
 (b) detecting a polymorphic site comprising nucleotide positions 901-909 or (I), a site comprising cytosine or guanine at position 753 of (II) or a site comprising (A) (ggggcgggccc) or (B) (ggggcggcggc) at positions 961-972 of (III). The method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor gene and further used to determine whether an individual is at increased risk of developing a disease associated with alpha2B, alpha2A or alpha2C, comprising detecting a polymorphic site which correlate to disease and combinations of these. In addition, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and combinations of these) or antagonist (e.g. yohimbine, prazosin, AKC 239, rauvolfine, idazoxan, tolazoline, phenolamine and combinations of these) by detecting the polymorphic site and correlating the site to a predetermined response (where the response is correlating to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol phosphate levels). The present sequence is that of the human alpha-2CAR variant, the sequence is deleted for a 12 nucleotide polymorphic site at nucleotides 961-972 of the wildtype gene (AA19931).

Sequence 1371 BP; 164 A; 479 C; 491 G; 237 T; 0 other;

Query Match 38.2% Score 516; DB 23; Length 1371;
 Best Local Similarity 64.9%; Pred. No. 1.7e-72;
 Matches 869; Conservative 0; Mismatches 415; Indels 54; Gaps 5;

19 GACGGGGGCAACGAGTGGAGGACGAGCGCGGGGGGGCGCGCGCCAGC 78
 73 GAGAGGGGAGGCGGGGGTTCATGCTTCGGGGCTTCGGGGCGCGCGGGC 132
 79 CCTTACTCCCTGACAGTACGCTGAGCTGGTGGCTTCGCGCGCTTCATGCTTC 138
 133 CAGTACTGGGGGGGGGGGGTGGCAGGCTGGCGGCTGGCTTCATGCTTC 192
 139 ACCGCTTGGGCAAGTGTCTCATTCATCCGCGGTTCAGAGCGCGCGCGCAAGGC 198
 193 ACCGCTTGGGCAAGTGTCTCATTCATCCGCGGTTCAGAGCGCGCGCGCAAGGC 252
 199 CCCCAAAACCTCTCTGCTGTCTGCTGGCGCGCATCTGCTGGCGCGCGCTGC 258
 253 CCACAAACCTCTCTGCTGTCTGCTGGCGCGCATCTGCTGGCGCGCGCTGC 312
 259 ATCCCTTCTCGCTGGCGCAAGTGTCTCATTCATCCGCGGTTCAGAGCGCGCTGC 318
 313 ATGCCCTTCTCGCTGGCGCAAGTGTCTCATTCATCCGCGGTTCAGAGCGCGCTGC 372
 319 GAGATCTACTGGCGCTGACAGTGTCTTCTGACAGTGTCTCATCTGACACTGTGC 378

373 GCGGCTACCTGGGGCTGATGTCTGTTCGACCTTCGATCTGATCTGTGTC 432
 379 ATGACCTTGAGACCGCTTACTGTGCTCATCAGAGCGCGCATGAGTACAGCGCAGC 438
 433 ATGACCTTGAGACCGCTTACTGTGCTCATCAGAGCGCGCATGAGTACAGCGCAGC 492
 439 CCGCGCGCATCAGAGCGCGCATGATCAGCGCTGGGTTCATCTGCGCGCTTCCTTC 498
 493 CCACGCGCGCATCAGAGCGCGCATGATCAGCGCTGGGTTCATCTGCGCGCTTCCTTC 552
 499 CCGCGCGCATCAGAGCGCGCATGATCAGCGCTGGGTTCATCTGCGCGCTTCCTTC 558
 553 CCGCGCGCATCAGAGCGCGCATGATCAGCGCTGGGTTCATCTGCGCGCTTCCTTC 600
 559 CCGCGCGCATCAGAGCGCGCATGATCAGCGCTGGGTTCATCTGCGCGCTTCCTTC 618
 601 CAGTGGGGCTCAGAGCGCGCATGATCAGCGCTGGGTTCATCTGCGCGCTTCCTTC 660
 619 GCTCCCTGCTCATCTATGATCTGCTTACGCTGCGCATCTACAGATGCGCAAGCTTCG 678
 661 GCGCCCTGCTCATCTATGATCTGCTTACGCTGCGCATCTACAGATGCGCAAGCTTCG 720
 679 ACCGCGTGCACACCGC 738
 721 ACCGCGTGCACACCGC 780
 739 GACGCGAGCGCCCAAGGCTGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 798
 781 GAAAGCGGCTGTGGGC 827
 799 GACGCGTGCACACCGC 858
 828 GC 887
 859 GACGCGTGCACACCGC 918
 888 GC 935
 919 GC 978
 936 GC 995
 979 AAGC 1038
 996 GTCGCCGGGGCGCGGTGGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 1055
 1039 GCAGGGCGCGGGGAGAGCGCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 1098
 1056 GTCGCCGGGGCGCGGTGGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 1107
 1099 AAGC 1158
 1108 GC 1167
 1159 TGGTTCCT 1209
 1168 TGGTTCCT 1227
 1210 CCAGCGAGCGCTTCAAGTGTCTGCTGGGTTCAGTACAGCGCGCGCGCGCGCGCGC 1269
 1228 CCGC 1287
 1270 GTCATCTACAGCGCTTCAAGTGTCTGCTGGGTTCAGTACAGCGCGCGCGCGCGCGC 1329
 1288 GTCATCTACAGCGCTTCAAGTGTCTGCTGGGTTCAGTACAGCGCGCGCGCGCGCGC 1347
 1330 GGGGAGAGGAGCGGATC 1347
 1348 CCGAGGAGGAGGCGCTTC 1365

RESULT 13

CC positions 961-972 of (III). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2C, comprising detecting a
 CC polymorphic site which correlates to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2A, alpha2A, or alpha2C agonist (e.g. epinephrine, the
 CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
 CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
 CC rauwolfine, idazoxan, tolazoxan, phenolamine, and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC levels). The present sequence is that of the human alpha-2CAR, the
 CC sequence includes a 12 nucleotide polymorphic site at nucleotides
 CC 961-972, absent in the alpha-2CAR variant (AA199933).

SO Sequence 1383 BP; 164 A; 482 C; 500 G; 237 T; 0 other;

Query Match 39.2%; Score 529; DB 23; Length 1383;
 Best Local Similarity 65.3%; Pred. No. 1.6e-74;

Matches 875; Conservative 0; Mismatches 420; Indels 44; Gaps 5;

QY 19 GAGCGGGGCAACGAGCTGGAACGGGACCGCGGGGGGGCGCGCCGGGCCACG 78
 Db 73 GAGAGGGGCAACGCGGGGTTGCCAATGCCGCGGGGCTTCTGGGGGGCGCGCGCGC 132
 QY 79 CTTACTCCTCAGAGTGAAGCTGAGCGTGGTGTGCTGGCGCGCGCTGCTATGCTGTC 138
 Db 133 CAGTACTCGCGGGGGCGCGGGGAGAGGCTGCTGCGGTGGGGCTTCTATGCTGTC 192
 QY 139 ACCGTGTGGGCAAGCTGCTGCTATGATGCGCGTGTTCAGAGCGCGCGCTCAAGGCG 198
 Db 193 ACCGTGTGGGCAAGCTGCTGCTGATGATGCGCGTGTTCAGAGCGCGCGCTCAAGGCG 252
 QY 199 CCCCAAAACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 258
 Db 253 CCAGAAACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 312
 QY 259 ATCCCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 318
 Db 313 ATGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 372
 QY 319 GAGATCTACCTGGGCTGAGCGTGTCTTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCT 378
 Db 373 GGGCTGTACCTGGGCTGAGCGTGTCTTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCT 432
 QY 379 ATCAAGCTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 438
 Db 433 ATCAAGCTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 492
 QY 439 CGGCGCGCATCAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 498
 Db 493 CGGCGCGCATCAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 552
 QY 499 CGGCGCGCATCTCATGAGAAAGAGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 558
 Db 553 CGGCGCGCATCTCATGAGAAAGAGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
 QY 559 CGGTGCGAGATCAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 618
 Db 601 CAGTGGCGCGCATCAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 QY 619 GCTCCCTGCTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 678
 Db 661 GCGGCTGCTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 QY 679 ACCGCGCTGCGACCG 738
 Db 721 ACCGCGCTGCGACCG 780
 QY 739 GAGCGAGGCGCAAGGGTCTGGGCGCGGAGCGGCGGCGCGCGGCGCGCGGCGCGCAAGGCG 798

Db 781 GAAAGCGGCTGGGGCG 831
 QY 799 GAACGCTGCG 857
 Db 832 -----CCCCCG 883
 QY 858 CGACACGAGCGCGCTGGACGCTGGAGGAGAGCTGCTTCCAGCCAGCGCGCGCGCGCTTC 917
 Db 884 GCG 943
 QY 918 AGGCG 977
 Db 944 GCGGTGCGGAGCG 1003
 QY 978 GAACCG 1037
 Db 1004 CCAAGTCCCG 1063
 QY 1038 TGCAGGCG 1097
 Db 1064 TCCGTGCG 1118
 QY 1098 GAACCGCGGAGAGCGCTTACGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1157
 Db 1119 GCGCGCGGAGAGCGCTTACGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1178
 QY 1158 CTGCTCCCTCTTCTTACCGACGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1208
 Db 1179 CTGCTCCCTCTTCTTATCTACAGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1238
 QY 1209 GCGACGCGCGCTTCAATTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1268
 Db 1239 GCG 1298
 QY 1269 GGTGATCTACACATCTTCAACGAGATTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1328
 Db 1299 GGTGATCTACAGGCTTCAACGAGATTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1358
 QY 1329 GGGGAGAGAGAGCGGATC 1347
 Db 1359 ACGGAGAGAGAGGCGCTTC 1377

RESULT 12
 AA199933
 ID AA199933 standard; DNA; 1371 BP.
 XX
 AC AA199933;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Human alpha-2CAR variant encoding DNA.
 XX
 DE Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
 KW polymorphic site; allelic variant; cardiovascular disease;
 KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
 KW phosphorylation; inositol phosphate; alpha-2CAR; chromosome 4; ds.
 XX
 OS Homo sapiens.
 XX
 XX
 FT key Location/Qualifiers
 FT CDS 1..1371
 FT /tag- a
 FT /product= "alpha-2CAR"
 FT /note= "sequence is deleted for a 12 nucleotide
 FT polymorphic site at nucleotides 961-972 of the
 FT wildtype sequence (AA199933)."
 XX
 PN W0200179561-A2.
 XX
 PD 25-OCT-2001.
 XX

Oy	241	CTGCTGGCCAGCCTCTGATCCCTTTCTCGTGGCCAAAGAGGTCATGGGCTACGGTAC	300
Db	1233	TTGGTGGTTACCTTCGTATATTTTTTTTTTTCGTTGGTTAAAGAGTTATGGTTATTGGTAT	1174
Oy	301	TTGGGCAAGGCTTTGGGGAGATCATACCTGGCGCTGACAGCTGCTCTTCTGCAAGTCTCC	360
Db	1173	TTTCGGTAAGGTTTGGTGGAGATTTATTTGGCGTTGACAGCTGTTTTTTTGTACGTGCTTT	1114
Oy	361	ATCGCTACACTGTGGCCATCAGCCTGGACCGCTACTGTGCATCACACAGGCCATCGAG	420
Db	1113	ATCGTGATTTTGGCGTTATTTAGTTTGGATCGTTATTTGGTTTATTTATAGGTTATCGAG	1054
Oy	421	TACAACTTAAGCGCAGCGCGCGCGCATCAAGGCAATCATCATACCGTGGGTCATC	480
Db	1053	TATTAATTTAAGAGGTAACGTGCGCTGTATTAGGTTATTTATTTATATACGTGGGTTATT	994
Oy	481	TGGGCGTCATCTCTTCCCGGCTCATCTCATCGAAGAAAGGCGGCGCGCGC	540
Db	993	TGGGTGGTTATTTTTTTTCGTGCTTATTTTATTCGAAGAAAGGCGCGCGCGCGGT	934
Oy	541	CCGCAAGCCGCGCAGCGCGCGCTGGAGATCAACAGCAAGATGCTACATCTGTG	600
Db	933	TTCGATGCTGCTGAGTGCAGTGTGCAAGATTAACTGATTTGAAGTGTGATTTTGTGTC	874
Oy	601	TGCATCGGCTCTTCTTTCGCTCCCTGCTCATCATGATCTGATCTACGTGCCATCTAC	660
Db	873	TGTATCGGTTTTTTTTTTCGTTTTTTGTTTTTATTTATGATTTTGGTTTACGTGCGATTTAT	814
Oy	661	CAGATCGCCAAAGCGTGCACCCGCGTGGCCACCACCCGCGCGGGTCCGGAGCGCGTCC	720
Db	813	TAGATCTTAAAGCGTGTATTCGCGGTTATTTATCTCTCGGGGTTCGGAGCTGCTGTC	754
Oy	721	GGCGCGCGGGGGGCAACCGACGCAAGCGCCCAAGGGTCTGGGCCCCGAGCGCAGCGCGGC	780
Db	753	GGCTGCTCGGGGGGTATCGACGCTTACGGTTTACGGTTTGGGTTTCGACGCGTACGCGGT	694
Oy	781	CCGGGGGGCGCAAGGCGCAACCGCTGCCCCACCAGCTCAACGGCGCCCTCGGCGAGCC	840
Db	693	TCCGGGGGCGTAGAGGTCGATGCTTGTATTTAGTTTAAAGCGGTTTTGGCGAGTTC	634
Oy	841	GGCGGGCGGGGGCGCGCGACACGACGCGCTGGACCTGGAGAGAGCTCTCTTCCGAC	900
Db	633	GGGTGGGTGGGTGCGCCGATTCGACGCGGTGGATTTGGAGAGAAAGTTGCTTTTCGAT	574
Oy	901	CACGCGAGCGGCGCTCCAGGGCCCCGACAGCCGAGCGCGGCTCCCGGGCGAAAGCAAG	960
Db	573	TACGTGAGCGGTTTTTAGGTTTCTAGATTTCGAGCCGCGGTTTTCCGGGCTAAAGCTAAG	514
Oy	961	GCCCGAGGCAACGATGAAGCCGGGCGAAGCTGCGCGCGCGGGCGGGGCGGGGGCGAG	1020
Db	513	GTTCGAGGGAATTTAGTGAAGATCGGGGAGATTTTTCGCGGCGCGGCTCGGGGGCGAG	454
Oy	1021	GGGATTCGAGAGCGCGGCTGCAGGGCGGGGGAGAGACCGGTGCGGAGCTCG	1080
Db	453	GGGATTCGGAGCGTGGTTTGAAGGTCGGGGAGAGACCGGTGCGGAGCTCG	394
Oy	1081	CGCTGGCGCGCGCGCGCAGAACCGCGAGAACCTTACACTGTGCTGCGCGTGTCTATC	1140
Db	393	CGTTGGCGCGGGCGGTAAATTCGCGAAMACGTTTTACCTGTGTGTGGTCTGCTGTTATC	334
Oy	1141	GGAGTTCGTGAGTGTGCTGCTTCCCTTCTTCTTACCTACAGCTCAAGGCGCTCGGG	1200
Db	333	GGAGTTCGTGAGTGTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG	274
Oy	1201	TGCTCGTGCACGCGAGCGCTCTCAATCTTCTCTGTTGGGCTACTGCAACGCTCG	1260
Db	273	TGTTTCGTGCTACGACGTTTTTAAATTTTTTTTTTGTGCTGATTTATGATGTTCTG	214
Oy	1261	TTGAACCCGCTCATCTACACATCTTACACAGATTTCCGCGCGCTTCAAGAAAGATC	1320
Db	213	TGTAACTCGGTTATTTATTTATTTTATTTATTTACGATTTTGTGCGCTTTTAAAGAAAT	154

QY	1321	C	T	C	T	G	T	C	G	G	G	G	G	A	C	A	G	A	G	C	G	A	T	C	T	G	1350
Db	153	T	T	T	T	G	T	C	G	G	G	G	G	A	T	A	G	A	A	C	G	A	T	C	T	G	124

RESULT 9
ABL32072
ID ABL32072 standard; DNA; 7353 BP.

AC ABL320727

DT 26-MAR-2002 (first entry)

Human immune system associated gene SEQ ID NO: 45.

KW Human; immune system disease; cytosine methylation; antisthmatic;
 KW antiarteriosclerotic; antiamebic; cytosatic; nootropic;
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
 KW antirheumatic; antiarthritic; antididiabetic; antiparasitic;
 KW antinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
 KW gene; ds-.

OS Homo sapiens.

PN W0200200928-A2.

PD 03-JAN-2002.

02-JUL-2001; 2001WO-EP07537.

PR 30-JUN-2000; 2000DE-1032529.

XX
XX
01 SEP 2000, 10:00
10:00

PA (EP16-) EPIGENOMICS AG-
YV

PI Olek A, Plepenbrock C, Berlin K;

DR WPI; 2002-130909/17.

Nucleic acid comprising fragment of chemically modified gene, useful

cytosine methylation -

aa
ps Claim 1: SEO ID NO 45; 32pp + Sequence Listing; German.

XX
CC The present invention provides a number of human immune system associated

genes which are modulated by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders,

CC Including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid

leukaemia, Alzheimer's disease, AIDS, epilepsy, neuroblastoma, CC

CC diseases. The present sequence is a gene of the invention.

sq Sequence 7353 BP; 1544 A; 384 C; 1956 G; 3469 T; 0 other;

Query Match	Score	DB	Length
62.08;	836.4;	24;	7353;

Matches	1029;	Conservative	0;	Mismatches	321;	Indels	0;	Gaps	0;
---------	-------	--------------	----	------------	------	--------	----	------	----

1 ATGGGCTCCCTGCAGCCGGACGGGCAACGCGAGCTGGAACGGGACCGAGGCCGGGG 60

5001 ATCCGTTTCTGAGTCCGACCGGTTACCGCACTTGGAAACGGGATCGAGGCGTCGGGG 50

5' **AGGTTGGTGGCCCTGGCC** 12

[illegible]

Abstract

5190

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OY 421 TACAACCTGAGCGACGCGCGCGCATCAAGGCATCATCATCAGCTGTGGCTATC 480
    || || || || || || || || || || || || || || || || || || || ||
Db 681 TAAATTTTAAACGCTACGCTCGCTGTATTAATTAATTAATTAATTAATTAATTA 740
OY 481 TCGGCGGTATCTCTTCCCGCGCTCATCTCAATCGAAGAGGCGGCGGCGGCGG 540
    || || || || || || || || || || || || || || || || || || || ||
Db 741 TCGGCTGTAATTTTTCGCTTATTTTATCGAAGAGAGGCGGCGGCGGCGGCT 800
OY 541 CCGCAGCGCGCGCGCGCGCGGTGAGATCAACAGCAAGAGTGTACATCTGCTG 600
    || || || || || || || || || || || || || || || || || || || ||
Db 801 TGTATGTCGTGTCAGTCCGTTGCGAGATTACGATTAGAGTGTATTCGCTG 860
OY 601 TGCATCGGCTCTTCTCTCTCTCTCTCATCATCTGCTGCTACGCTGCGCATC 660
    || || || || || || || || || || || || || || || || || || || ||
Db 861 TGTATCGGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTT 920
OY 661 CAGATCGCAGACGCTGCGACCGCTGCGACCCAGCGCGGCGGCTCGGACGCG 720
    || || || || || || || || || || || || || || || || || || || ||
Db 921 TGAATCGTTAAAGCGCTGATTCGCTGTTATTTAGTGTGCGGCGTTCGCGT 980
OY 721 GCGCGCGCGCGCGCGCGCGCGACCGCGCTGAGTGTGAGAGAGTGTCTTCG 780
    || || || || || || || || || || || || || || || || || || || ||
Db 981 GCGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1040
OY 781 CCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
    || || || || || || || || || || || || || || || || || || || ||
Db 1041 TCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1100
OY 841 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
    || || || || || || || || || || || || || || || || || || || ||
Db 1101 GCGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1160
OY 901 CAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
    || || || || || || || || || || || || || || || || || || || ||
Db 1161 TACGTCAGCGGCTTTTATTCGATTCGATTCGATTCGATTCGATTCGATTCG 1220
OY 961 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
    || || || || || || || || || || || || || || || || || || || ||
Db 1221 GTTGCAGCGATTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1280
OY 1021 GCGATCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
    || || || || || || || || || || || || || || || || || || || ||
Db 1281 GCGATCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1340
OY 1081 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
    || || || || || || || || || || || || || || || || || || || ||
Db 1341 CGTTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1400
OY 1141 GGAATGTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200
    || || || || || || || || || || || || || || || || || || || ||
Db 1401 GGAATGTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1460
OY 1201 TGTCTCGGTGCGACGACGCTCTTCAAAATCTCTCTGTGTGTGTGTGTGTGT 1260
    || || || || || || || || || || || || || || || || || || || ||
Db 1461 TGTCTCGGTGCGACGCTCTTCAAAATCTCTGTGTGTGTGTGTGTGTGTGTGT 1520
OY 1261 TTGAACCGCGGTATCTTACACCATCTTCAACACGATTTCCGCGCGCTTCA 1320
    || || || || || || || || || || || || || || || || || || || ||
Db 1521 TTGAATTCGTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1380
OY 1321 CTCTGTGCGGCGGACGAGAGCGGATCGTG 1350
    || || || || || || || || || || || || || || || || || || || ||
Db 1581 TTTTGTGCGGCGGATAGAGAGCGGATCGTG 1610

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RESULT 8
 ABQ47499/c
 ID ABQ47499 standard; DNA; 1733 BP.
 XX
 AC ABQ47499;
 XX
 DT 12-JUL-2002 (first entry)

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XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 34090.
DE Human: cytosine methylation; 5'-CpG-3', uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW gastr. cell differentiation; ds.
XX Homo sapiens.
OS WO200218632-A2.
XX
XX 07-MAR-2002.
XX
XX 01-SEP-2001; 2001WO-EP10074.
XX
XX 01-SEP-2000; 2000DE-1043826.
XX
XX 05-SEP-2000; 2000DE-1044543.
XX
XX (EPIC-) EPICENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
XX WPI: 2002-371829/40.
XX
XX Determining the degree of cytosine methylation in genomic DNA, useful
XX for diagnosis and prognosis, comprises selective hybridization of
XX amplicons from chemically treated DNA.
XX
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
XX This invention describes a novel method for determining the degree of
XX methylation of a particular cytosine in a motif 5'-CpG-3', present in a
XX genomic sample of DNA. The sample is treated chemically to convert
XX cytosine (C) but not methylated C, to uracil, then part of the genomic
XX DNA that contains the target C is amplified to form a labeled amplicon.
XX The amplicon is hybridised to two classes, each with at least one
XX member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
XX and the degree of hybridisation to both classes is determined from the
XX label on the amplicon. From the ratio of labels hybridised to the two
XX classes of oligomers, the degree of methylation is calculated. The method
XX is used: (i) for diagnosis and/or prognosis of side effects of
XX therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
XX of the central nervous, cardiovascular, gastrointestinal and respiratory
XX systems etc., particularly by detecting mutations or single nucleotide
XX polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
XX types and for investigating cell differentiation. The method allows the
XX methylation status of many C residues to be determined simultaneously.
XX ABQ1410-ABQ54121 represent genomic DNA sequences used to illustrate the
XX method for determining the degree of cytosine methylation described in
XX the disclosure of the invention.
XX
XX Sequence 1733 BP; 685 A; 585 C; 211 G; 252 T; 0 other:
XX
XX Query Match 62.0%; Score 836.4; DB 24; Length 1733;
XX Best Local Similarity 76.2%; Pred. No. 1.2e-122;
XX Matches 1029; Conservative 0; Mismatches 321; Indels 0; Gaps 0;

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OY 1 ATGAGGCTCCCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
    || || || || || || || || || || || || || || || || || || || ||
Db 1473 ATGAGGCTTTTGTATGCGACGCGGCGGTAACGGAATTTGAAACGCGGATCGCGGG 1414
OY 61 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
    || || || || || || || || || || || || || || || || || || || ||
Db 1413 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1354
OY 121 GCGCTGCTCATGCTGCTACCGCTGTTCGCAACGTCGTCTCATCATCGCGCTTCACG 180
    || || || || || || || || || || || || || || || || || || || ||
Db 1353 GGTTCGTTATGTTGTTATGCGTGTTCGTAACGTCGTCTCATCATCGCGCTTCACG 1294
OY 181 AGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
    || || || || || || || || || || || || || || || || || || || ||
Db 1293 AGTCGCGCGGTTAAAGCGTTTAAATTTTTCGTTGCTTTGCTTCGCGCATAT 1234

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QY	601	TGCATGCGCTCTTCTTGCTCTCCCTGCTCATATGATCCCGGTCTACGAGGCATCTAC	660
Db	1753	TACATCGACTCTCTTCTTGCTCTCCCTACCTCATTAATCTTAATCTAGTACGATCTAC	1694
QY	661	CAGATGCGCCAAAGGTGTCACCCGCTGTCACCCAGCGCGCCGGGTCCGGACGCGCTGCC	720
Db	1693	CAATGCGCCAAAGGTGTCACCCGCTGTCACCCAGCGCGCGCGGAAATCCGAAACGCGCTGCC	1634
QY	721	GCGCGCGCGGGGGGCGACGCGAGCGCAGGCCCAAGGCTCTGGGCGCCCGAGCGCAGCGGCG	780
Db	1633	GCGCGCGCGGGGGGCGACGCGAGCGCAGGCCCAAGGCTCTGGGCGCCCGAGCGCAGCGGCG	1574
QY	781	CGCGGGGGGGGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	840
Db	1573	CGGAAAAACCGAAAAACCGAACCGCTACCGCACCCTACCGCACCCTACCGCACCCTACCGCACC	1514
QY	841	GCGCGCGCGCGGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	900
Db	1513	GCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	1454
QY	901	CAGCGCGAGGGGCGCTCCAGGGCGCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	960
Db	1453	CAGCGCGAGGGGCGCTCCAGGGCGCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	1394
QY	961	GCGCGAGCGGAGGTGAAAGCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	1020
Db	1393	ACCGGAAAGGAAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1334
QY	1021	GCGATCGGGAGCGCGCGGTGCGAGGGCGGGGGGAGGAGCGCGGTGCGGCGGCGGCGGCGGCGG	1080
Db	1333	AAATATCGAAAGCGCGGACTACAAAACGAAAAAAGCGGTGGAATACCAAAAGCGTG	1274
QY	1081	CGCTGCGCGCGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	1140
Db	1273	CGCTGCGCGCGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	1214
QY	1141	GAGAGTCTCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1200
Db	1213	GAAATATTCGAAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1154
QY	1201	TGCTTCGTCGACGACGCGCTTCCTCAATTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT	1260
Db	1153	TACCTCGTACACGACGCGCTTCCTCAATTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT	1094
QY	1261	TTCGAAACCGCGGCTATCTACACATTCCTACACAGATTCCTGCGCGCGCTTCGAAAGATC	1320
Db	1093	TTCGAAACCGCGGCTATCTACACATTCCTACACAGATTCCTGCGCGCGCTTCGAAAGATC	1034
QY	1321	CTCTGTCGGGGGAGCAGGAAACGCGGATGCT	1349
Db	1033	CTCTATTCGAAAAACAAAAACGAAATGCT	1005
RESULT 7			
ABQ47498			
ID	ABQ47498 standard; DNA; 1733 BP.		
XX	ABQ47498;		
XX	12-JUL-2002 (first entry)		
DT	Oligonucleotide for detecting cytosine methylation SEQ ID NO 34089.		
DE	Human: cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;		
KM	drug; side effect; cancer; central nervous system; cardiovascular;		
KM	gastrointestinal; respiratory system; single nucleotide polymorphism;		
KM	SNP; cell differentiation; ds.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	WO200218632-A2.		
PN			

PD	07-MAR-2002.
XX	
PF	01-SEP-2001; 2001WO-EPI0074.
XX	
PR	01-SEP-2000; 2000DE-1043826.
XX	
PR	05-SEP-2000; 2000DE-1044543.
XX	
PA	(EPIC-) EPIDENOMICS AG.
XX	
PI	Olek A, Piepenbrock C, Berlin K, Guetig D;
DR	WPI; 2002-371829/40.
XX	
PT	Determining the degree of cytosine methylation in genomic DNA, useful
PT	for diagnosis and prognosis, comprises selective hybridization of
PS	amplicons from chemically treated DNA -
XX	
PS	Claim 12; 56pp + Sequence Listing; 56pp; German.
XX	
CC	This invention describes a novel method for determining the degree of
CC	methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC	genomic sample of DNA. The sample is treated chemically to convert
CC	cytosine (C) but not methylated C, to uracil, then part of the genomic
CC	DNA that contains the target C is amplified to form a labeled amplicon.
CC	The amplicon is hybridised to two classes, each with at least one
CC	member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC	and the degree of hybridisation to both classes is determined from the
CC	label on the amplicon. From the ratio of labels hybridised to the two
CC	classes of oligomers, the degree of methylation or side effects of
CC	is used: (i) for diagnosis and/or prognosis of side effects of
CC	therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC	of the central nervous, cardiovascular, gastrointestinal and respiratory
CC	systems etc., particularly by detecting mutations or single nucleotide
CC	polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC	types and for investigating cell differentiation. The method allows the
CC	methylation status of many C residues to be determined simultaneously.
CC	ABQ1410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC	method for determining the degree of cytosine methylation described in
XX	the disclosure of the invention.
XX	
SQ	Sequence 1733 BP; 252 A; 211 C; 585 G; 685 T; 0 other;
	Query Match 62.0%; Score 836.4; DB 22; Length 1733;
	Best Local Similarity 76.2%; Pred. No. 1.2e-122;
	Matches 1029; Conservative 0; Mismatches 321; Indels 0; Gaps 0;
QY	1 ATGGCGTCCTGTGCAGCCGACGCCGGCAACGACTGAAACGGACCGAGCCCGGGG 60
DB	
	261 ATGGGTTTTTTTGTATAGTCGGGAACGGGGTAGCGAGTGTAACGGAGATCGAGCGTGGCG 320
QY	61 GCGCGGCCCGGGCCACCCTTACTCCCTCAGGTATACGCTGACGCGGTGCTCGGCC 120
DB	
	321 GCGCGCGCTGGGGCTATTATTTTATTTTATTTTATTTAGGTGACGTGGACGTGGTGTGGTC 380
QY	121 GGCGTGCATAGTCGTACACGCTTTCGGCAACGTCGCTCATCATCACGCCGTTCACG 180
DB	
	381 GGTTTGTTTATAGTTGTTTATTCGTTCGTTCGTTAACGTATTCGTTATATTCGTGTTACG 440
QY	181 AGCCGCGCGCTCAAGCGCCGCCAACAACCTCTCTCGTGTCTCTGCGCTCGGCCGCATC 240
DB	
	441 AGTCGCGGTTTAAAGGGGCTTTTAAATTTTATTTTATTTTGGTGGTTTGGTTCGTGATATT 500
QY	241 CTGGGGCCACAGCGTCGTCATCCCTTTCGCTGGTGGCCCAACGAGTCAAGGGCTACTGTTAC 300
DB	
	501 TTGGTGGTATTCGTTATTTTATTTTTCGTTGGTTTAAACGAGGTTAAGGGTTATGGTAT 560
QY	301 TTCGCAAGAGCTTGGTGGAGATCTACCTGGCGCTCGACGTGCTCTTCGTGACGTCGCC 360
DB	
	561 TTCGTTAAGCTTGGTGGAGATTTATTTTGGCTTCGACGAGTGTATTTTGTACGTGTTT 620
QY	361 ATCTGCAACGTGGCGCATCAGCGTCGACGCGTACTGTCATCACACAGCGCATCGAG 420
DB	
	621 ATCTGTTATTTGGGTATTAGTTAGTTGGATCGTTATTCGTTATTTATATAAGTATACGAG 680

Db	1693	CAAAATGGCCAAACGTCGACCCCGGCTACCAACCCAGCCGGAATTCGAAACCGCGTCGCC	1634
QY	721	GGCCGCCGGGGGGACCAGAGCGCAGAGGCCCCAAGGGTCTGGGGCCCGAGCGACGCGGGC	780
Db	1633	GGCGCGCCGAAAAAACACCGAAACCGAAACCCCAAGATCTTAACCCCGAAGCCAGCGCAAC	1574
QY	781	CGGGGGGGCGAGAGGGCGGAACCGCTGCGCCAGCTAACGGCGCCCCGTGGAGGCC	840
Db	1573	CGGAAAAACGGAAAAACCGAACCGGCTATCCACCAACTACAGAGCGCCCTACGAAACC	1514
QY	841	GGCGGGCGGGGGCGCGCGACACCGAGCGGCTTGACCTGGAGAGAGGTCGCGCTTCGAC	900
Db	1513	GGCGCGACCGAACC GGCGCGACCGAGCGCGCTTAACCTTAATAAAAAAAACTCGTCTTCGAC	1454
QY	901	CACGCGGAGGGGCTCCAGGGGCCCGAGACCCGAGCGGCTCCCGGGGGCAAAAGCAG	960
Db	1453	CACGCGAAGCACTCCAAAAACCCCGCAAAACCGAAGCGATCCCGCAACAAAAACAA	1394
QY	961	GCCGACGACGACGAGTGAAGCCGGGGCGACAGCTGCGCGCGCGCGGGGCGGGGGCGACG	1020
Db	1393	ACCGGAACGACCAATATAAACCGAACGCAACTTACCGCGAGCGGAACCGAAAAACGACG	1334
QY	1021	GGATGCGGAGCGCCGGCTGCAAGGGCCGGGGGAGAGCGCGTGGGGGCTGCCAAGCGCTCG	1080
Db	1333	AAAAATCGAAACGCGCTACAAAAACCGAAAAAAAACGGGTGGAACACTACAAAAAGCTCG	1274
QY	1081	CGCTGGGGGGGGGGGAGAAACCGCGAGAGCGCCTTACGTTCTGTCGTGGCTGTGTCATC	1140
Db	1273	CGCTAACGCGCAACGACAAAAACCGCGAAAAACGCTTCACTGATCAACCGTAAATCATC	1214
QY	1141	GGAGTGTTCGTGTGCTGTGCTTCCTCCCTCTTCACTACAGCGTACAGCGCGCTGGGG	1200
Db	1213	GAATATATCTGATATATATAATTTCCCTCTTCTTCACTACAGCGTACAGCGCGTGGAA	1154
QY	1201	TGCGTCGTGCACAGCAGCGCTTTCAATTTCTTCTTGCTTGCGCTACTCGAACAGCTCG	1260
Db	1153	TACTCGGTACACGACGCGTCTTCAAAATCTTCTTCAATTCGACTACTACAACTCG	1094
QY	1261	TTCAGCCGGTCACTACACATCTTCAACACAGATTTCCGCGCGGCTTCAAGAAGATC	1320
Db	1093	TTAAACCGCATCTACACATCTTCAACCAACAGATTTTCGCGCGGCTTCAAAAAAATC	1034
QY	1321	CTCTGTGCGGGGACAGAGCGGATCGT	1349
Db	1033	CTCTATCGAAAAAACAAAAAGATTCGT	1005

RESULT 6
AAD28363/c
ID AAD28363 standard; DNA; 7353 BP.

AC AAD28363;

DT 22-APR-2002 (first entry)

Human chemically treated genomic DNA #4.

Human; cytosolic; antidepressant; neuroleptic; neurotoxic; antidiabetic
 adrenergic alpha-1C-receptor; cytosine methylation; therapy; alcoholism;
 behavioural disorder; neurological; psychiatric; cancer; schizophrenia;
 Tourette's syndrome; smoking; human immunodeficiency virus dementia;
 drug abuse; migraine; ds.

OS Homo sapiens.

PN WO200202809-A2

PD 10-JAN-2002.

02-JUL-2001; 2001WO-EP07540.

PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.

XX
PA (EPiG-) EPIGENOMICS AG

PI Olek A, Piepenbrock C, Berlin K;

WPI; 2002-154759/20.

PT Novel nucleic acid useful for diagnosis and therapy of behavioral
PT disorder, neurological disorder and cancer, comprises a sequence of a
PT segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
PT gene -
XX
PS Claim 1; Page 36-40; 100pp: English.

Claim 1; Page 36-40; 190pp; English.

CC The invention relates to nucleic acids comprising a segment of chemically
CC pretreated DNA of adrenergic alpha-1c-receptor gene. The invention also
CC relates to oligonucleotides or peptide nucleic acid (PNA) oligomers
CC useful for detecting tyrosine methylations. The pretreated DNA is useful
CC for the diagnosis or therapy of behavioural disorders, neurological
CC disorders and cancer, in particular major depressive disorder, Tourette's
CC syndrome, schizophrenia, psychiatric and neurological disorders, smoking,
CC drug abuse, alcoholism, personality traits, compulsive gambling, human
CC immunodeficiency virus dementia, migraine, behaviours in schizophrenic
CC and schizoaffective patients, and suicidal behaviour in patients with
CC schizophrenia. The nucleic acid is useful for detecting the methylation
CC state of all CpG dinucleotides and/or single nucleotide polymorphisms
CC (SNPs). The present sequence is human chemically treated genomic DNA.

Sequence 7353 BP; 1713 A; 384 C; 2140 G; 3116 T; 0 other;

Query Match	67.88;	Score 915.4;	DB 24;	Length 7353;
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Matches 1078; Conservative 0; Mismatches 271; Indels 0; Gaps 0;

2Y 1 ATGGGCTCCCTGCAGCCGGACCGGGCAACCGAGCTGGAACGGGACCGAGCGCGGGG 60

Db 2353 ATAACTCCCTACCAACCGAACGCGAACTAAACGAAACCGAAGCCGAAA 2294

61 GCGGCGCCGACCCCTTACTCCCTGCAGGTGACGCTGCTGCTGCC 120

Db 2293 AACGAGCGCCGAACCAACCCCTTACTCCCTACAATAACGCTAACGCTAATATACCTAAC 2234

121 GGCCTGCTCATGCTGCTCACC GTTGGCAACGTGCTCGTCATCATCGCCGTTACAG 180

Db 2233 GACCTACTACTCACCCTATTGACAACGTA CTCTCGTCATCATCGCCGATTCACG 2174

181 AGCGCGCGCTCAAGCGCGCCCAAAACCTCTTCCGTGTCTCTGGCCTCGGCCGACATC 240

DB 21 / 3 AACCGCGCTCAAAACGCCCAAAACCTCTTCTAATATCTCTAACCTCGACCGACATC 2114

241 C TGGGACACGCTCATCCCTTTCTCGCTGGCCACGAGGTCATGGGCTACTGGTAC 300

2113 CTAATACCCAGCGTCATCCCTTTCTCGCTAACCAACGAATCATAACTACTAATAC 2054

501 TCCGACGGCTTGGTGCAGATCTACCTGGCCGCTCGACGTGCTCTTCTGCACGTCGTC 360

2053 T TCGACAAACCTTAAATACGAAATCTACCGCTCGACGTACTCTTCTACACGTCGTCC 1994

301 ATGAGACCTGTGGCCATCAGCCTGGACCGTACTGCTCCATCACACAGGCCATCGAG 420

1933 A G G A C C C I A I A G C C A T C A A C C I A A C C G C T A C T A T C C A T C A C A C A A A C C A T G G A A 1934

*21 TACATCCGAGCGCAGCCGCCCAICAAAGGCCAICATCACCGTGTGGGCATC 480

1555 TACATCCATTAACGCACGCCGCCGCAICAAACCATCATCATCACCCTATAATCATC 1874

540

1875 1CGACCG1CA1CTCTTCCCGCGTCA1TCTCCAT1CGAAAAAAAACGACGACGACGAC 1814

241 CCGAGCCGGCCGAGCTGGAGATCAACGACCAGAGTGGTACGTCTCGTCG 600

1013 CCGCATTGATCGAACGGCTACGAATTCACGACCAAAATATACGTCACTCTGTCG 1754

DT	18-FEB-2002	(first entry)
XX	Human alpha-2AAR encoding DNA.	
DE	Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;	
XX	polymorphic site; allelic variant; cardiovascular disease;	
KW	central nervous system disease; adenylyl cyclase; MAP kinase activity;	
KW	phosphorylation; inositol phosphate; alpha-2AAR;	
KW	GenBank Accession AF281308; chromosome 10; ds.	
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	1..1353
FT		/tag= a
FT		/product= "alpha-2AAR"
PN	WO200179561-A2.	
XX		
PD	25-OCT-2001.	
XX		
PF	17-APR-2001; 2001WO-US12575.	
XX		
PR	17-APR-2000; 2000US-0551744.	
PR	10-AUG-2000; 2000US-0636259.	
PR	19-OCT-2000; 2000US-0692077.	
XX		
PA	(LIGG/) LIGGETT S B.	
PA	(SMAL/) SMALL K M.	
XX		
XX	Liggett SB, Small KM;	
PI	WPI: 2001-611728/70.	
DR	P-PSDB: AAM52122.	
XX		
PT	Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for	
PT	determining whether an individual is at increased risk of developing a	
PT	disease associated with the corresponding receptor comprises detecting	
PT	a polymorphic site -	
XX		
PS	Example 7: Page 151; 163pp; English.	
XX		
CC	The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic	
CC	receptor gene (I)-(III) by detecting a polymorphic site, comprising;	
CC	(a) obtaining a sample having a polynucleotide encoding an alpha-2B,	
CC	alpha2A or alpha2C or fragment or complement of; and	
CC	(b) detecting a polymorphic site comprising nucleotide positions 901-909	
CC	of (I), a site comprising cytosine or guanine at position 753 of (IIIV)	
CC	or a site comprising (A) (999gcg99gcg) or (B) (99gcgcctcga) at	
CC	positions 961-972 of (III). The method may be used for genotyping an	
CC	alpha2B, alpha2A or alpha2C receptor gene and further used to determine	
CC	whether an individual is at increased risk of developing a disease	
CC	associated with alpha2B, alpha2A or alpha2, comprising detecting a	
CC	polymorphic site which correlate to disease selected from cardiovascular	
CC	disease, central nervous system disease and combinations of these. In	
CC	addition, the technique may be used to predict an individual's response	
CC	to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,	
CC	norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and	
CC	combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,	
CC	rauwolscine, idazoxan, tolazoline, phenolamine and combinations of	
CC	these) by detecting the polymorphic site and correlating the site to a	
CC	predetermined response (where the response is correlated to adenylyl	
CC	cyclase, MAP kinase activity, phosphorylation or inositol phosphate	
CC	levels). The present sequence is that of the human alpha-2AAR gene	
CC	(GenBank Accession AF281308).	
XX		
XX	Sequence 1350 BP; 199 A; 490 C; 441 G; 220 T; 0 other;	
XX		
XX	Query Match	99.9%; Score 1348.4; DB 23; Length 1350;
XX	Best Local Similarity	99.9%; Pred. No. 8.3e-203;
XX	Matches 1349; Conservative	0; Mismatches 1; Indels 0; Gaps 0;

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QY	61	GGCGCGCGCGCGGGCCACCCCTTACTCCCTCAGGTGACGCTGACGCTGGTGTGTCGGGC	120
Db	61	GGCGCGCGCGGGCCACCCCTTACTCCCTCAGGTGACGCTGACGCTGGTGTGTCGGGC	120
QY	121	GGCGCTCATGTGCTACCGGTGTCGCAACGCTGCTCATCATCGCCGTGTTCACG	180
Db	121	GGCGCTCATGTGCTACCGGTGTCGCAACGCTGCTCATCATCGCCGTGTTCACG	180
QY	181	AGCGCGCGCTCAAGGGGGCCCAAAACCTTCTGTCGTGTCGTGGCCCTCGGCCGACATC	240
Db	181	AGCGCGCGCTCAAGGGGGCCCAAAACCTTCTGTCGTGTCGTGGCCCTCGGCCGACATC	240
QY	241	CTGGTGGCCACGCTGCTATCCCTTCTCGCTGGCCACAGAGTCAATGGGCTACTGTATC	300
Db	241	CTGGTGGCCACGCTGCTATCCCTTCTCGCTGGCCACAGAGTCAATGGGCTACTGTATC	300
QY	301	TTCCGCAAGGCTTGTGTCGAGATCTACCTTGGCCCTGACGTGCTTCTTGCAGCTGTC	360
Db	301	TTCCGCAAGGCTTGTGTCGAGATCTACCTTGGCCCTGACGTGCTTCTTGCAGCTGTC	360
QY	361	ATCTGTGACCTGTGCGGCATCAGCTTGGACCGCTACTGTGCTATCACAAGGCATCGAG	420
Db	361	ATCTGTGACCTGTGCGGCATCAGCTTGGACCGCTACTGTGCTATCACAAGGCATCGAG	420
QY	421	TACAACCTGAAGGCCACGCGCGCGCGGATCAAGGCCATCATCTACCGTGTGGGCTATC	480
Db	421	TACAACCTGAAGGCCACGCGCGCGCGGATCAAGGCCATCATCTACCGTGTGGGCTATC	480
QY	481	TCGGCGCTCATCTCTTCCGCGCGCTATCTCCATCGAGAGAAGGGCGCGCGCGCGC	540
Db	481	TCGGCGCTCATCTCTTCCGCGCGCTATCTCCATCGAGAGAAGGGCGCGCGCGCGC	540
QY	541	CCGCAAGCCGGCCAGCGCGCTGCGAGATTAACGACCAAGAAGTGGTACGTATCTTCGTC	600
Db	541	CCGCAAGCCGGCCAGCGCGCTGCGAGATTAACGACCAAGAAGTGGTACGTATCTTCGTC	600
QY	601	TGCATCGGCTCTTCTTGCGTCCCTGGCTCATCATATCTGGTACGTGGGCAATTCAC	660
Db	601	TGCATCGGCTCTTCTTGCGTCCCTGGCTCATCATATCTGGTACGTGGGCAATTCAC	660
QY	661	CAGATCGCAAGCGCTCGCACCCGCGGTGTCACCCAGCGCGCGGGGTCTCGAACCCGTCGC	720
Db	661	CAGATCGCAAGCGCTCGCACCCGCGGTGTCACCCAGCGCGCGGGGTCTCGAACCCGTCGC	720
QY	721	GGCGCGCGGGGGGACCGAGCGCAAGGGTCTGAGCCCGAGCGCAGCGCGGAGC	780
Db	721	GGCGCGCGGGGGGACCGAGCGCAAGGGTCTGAGCCCGAGCGCAGCGCGGAGC	780
QY	781	CGGGGGGGGCGAGAGGGCGGAAGCGCTGGCCACCACCTCAAGGGGCCCTTGGGAGGCC	840
Db	781	CGGGGGGGGCGAGAGGGCGGAAGCGCTGGCCACCACCTCAAGGGGCCCTTGGGAGGCC	840
QY	841	GGCGCGCGCGGGCCGCGCGACCGACCGCGCTTGAAGAGAGAGCTGCTTCCGAC	900
Db	841	GGCGCGCGCGGGCCGCGCGACCGACCGCGCTTGAAGAGAGAGCTGCTTCCGAC	900
QY	901	CAGCGCGAGCGGCTCCAGGGGCCCGAGACCCGAGCGCGTCCCGGGGCAAGAGCCAG	960
Db	901	CAGCGCGAGCGGCTCCAGGGGCCCGAGACCCGAGCGCGTCCCGGGGCAAGAGCCAG	960
QY	961	GGCGGACCGAGGCGAGGAGCGGGGCGACGCTGCGCGCGCGGGCGCGGGGGCGAG	1020
Db	961	GGCGGACCGAGGCGAGGAGCGGGGCGACGCTGCGCGCGCGGGCGCGGGGGCGAG	1020
QY	1021	GGGATCGGAGAGCGCGCTGCAAGGGCGGGGAGAGAGCGCTGGGGGTCTCCAAAGCGTCG	1080
Db	1021	GGGATCGGAGAGCGCGCTGCAAGGGCGGGGAGAGAGCGCTGGGGGTCTCCAAAGCGTCG	1080
QY	1081	CGGTGGGCGGGGCGAGAACCGCGAGAAAGCGTTTCAGCTTGTGCTGGCGTGGTCAATC	1140

PR 19-OCT-2000, 2000US-0692077.
 XX (LIGG/) LIGGETT S B.
 PA (SMAL/) SMALL K M.
 XX
 PI Liggett SB, Small KM;
 DR WPI: 2001-611728/70.
 DR P-PSDB: AAM52123.
 XX
 PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 PT determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting
 PT a polymorphic site -
 XX
 XX Disclosure; Page 152; 163pp; English.
 XX
 CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
 CC or a site comprising (A) (99ggcg9ggcg) or (B) (99ggcg9gctgag) at
 CC positions 961-972 of (III). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
 CC polymorphic site which correlate to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
 CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK1304, BHT933 and
 CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
 CC rauvolfisine, idaroxan, tolazoline, phenolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC levels). The present sequence is that of the human alpha-2Aa variant
 CC gene.
 XX
 XX
 XX Sequence 1350 BP; 199 A; 489 C; 442 G; 220 T; 0 other:
 S0
 Query Match 100.0%: Score 1350; DB 23; Length 1350;
 Best Local Similarity 100.0%: Pred. No. 4.7e-203;
 Matches 1350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 361 ATGTGACACTGTGTGGCCATCAGCCTGGACCGCTACTGTCTCATCACAGAGCCATCGAG 420
 Qy TACAACCTGAAGCGAGCGCGCGCGCATCAAGGCCATCATCAGCTGTGGTCAATC 480
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 Db 421 TACAACCTGAAGCGAGCGCGCGCGCATCAAGGCCATCATCAGCTGTGGTCAATC 480
 Qy TCGGCGGTCAATCTCTTCCCGCGCTCATCTCAATCAGAAAGGCGGCGGCGGCG 540
 Db TCGGCGGTCAATCTCTTCCCGCGCTCATCTCAATCAGAAAGGCGGCGGCGGCGG 540
 Qy 541 CCGCAGCCGCGCGAGCGCGCGCTGCGAGATCAAGACCAAGAAATGTGATCATCTCTG 600
 Db CCGCAGCCGCGCGAGCGCGCGCTGCGAGATCAAGACCAAGAAATGTGATCATCTCTG 600
 Qy 601 TGCATCGGCTCTTCTTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCG 660
 Db TGCATCGGCTCTTCTTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCG 660
 Qy 661 CAGATCGCCAAAGCGTTCGACACCGCGGTGACACCCAGCCGCGGCGTCCGAGCGCGT 720
 Db CAGATCGCCAAAGCGTTCGACACCGCGGTGACACCCAGCCGCGGCGTCCGAGCGCGT 720
 Qy 721 GCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
 Db GCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
 Qy 781 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 840
 Db CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 840
 Qy 841 GCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
 Db GCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
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 Db CAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 960
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 ID AA199917 standard; DNA: 1350 BP.
 XX
 AC AA199917;

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 11:01:28 ; Search time 387.567 Seconds
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Title: US-09-636-259b-2

Perfect score: 1350

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues 4370478

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1350	100.0	1350	23	AA19918 Human alpha-2AR v
2	1348.4	99.9	1350	23	AA19917 Human alpha-2AR e
3	915.4	67.8	1733	24	ABQ47500 Oligonucleotide fo
4	915.4	67.8	1733	24	ABQ47501 Oligonucleotide fo
5	915.4	67.8	1733	24	ABL32073 Human immune syste
6	915.4	67.8	1733	24	AA28363 Human chemically t
7	836.4	62.0	1733	24	ABQ47498 Oligonucleotide fo
8	836.4	62.0	1733	24	ABQ47499 Oligonucleotide fo
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ALIGNMENTS

10	836.4	62.0	7353	24	AA28362 Human chemically t
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17	443	32.8	1353	23	AA19905 Human alpha-2BAR t
18	423.8	31.4	2064	12	AA04151 Human alpha-2 beta
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25	225	16.7	1140	18	AA18392 Corn barnacle G-pr
26	202	15.0	1845	21	AA298400 Dog betai-betadreno
27	202	15.0	1845	21	AA298404 Rhesus monkey beta
28	188.6	14.0	4401	21	AA298404 Monkey betai-betadreno
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34	187	13.9	1637	22	AA161186 Human betai-betadreno
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37	187	13.9	1637	22	AA161189 Human betai-betadreno
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41	187	13.9	1723	24	ABK40731 Human betai-betadreno
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RESULT 1
AA19918
ID AA19918 standard; DNA; 1350 BP.
AC AA19918;
XX 18-FEB-2002 (first entry)
DT Human alpha-2AR variant encoding DNA.
XX
AC
XX
DE Human alpha-2AR variant encoding DNA.
DE
XX
XX Human; genotyping; alpha-2B; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2AR; chromosome 10; ds.
KW
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FH 1.1353
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PN WO200179561-A2.
PN
XX 25-OCT-2001.
XX
PD
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XX 17-APR-2001; 2001WO-US12575.
PF
XX 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR

JOURNAL REFERENCE AUTHORS TITLE JOURNAL COMMENT	Unpublished 3 (bases 1 to 896) Genoscope. Direct Submission Submitted (12-APR-2000) This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon .

JOURNAL REFERENCE AUTHORS	TITLE
Unpublished 2 (bases 1 to 966)	Characterization and repeat analysis of the compact genome of the freshwater pufferfish <i>Tetraodon nigroviridis</i>
Roest-Crollius,H., Jallou,O., Dasilva,C., Fikames,C., Fisher,C., Bouneau,L., Billault,A., Queller,F., Saurin,W., Bernot,A. and Weissenbach,J.	

```

QY 348 CTGACGTCATCGTCACCTGTGGCCATCAAGCCGTCGCTACTGTCATCAC 407
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QY 408 ACAGGCGCATCGATACACCTGAAGGCGACGCCGCGCCGATCAAGGCCATCATCAC 467
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QY 468 CGGTGGGTCATCGCGCGCTCATCTCTCCCGGCTCATCTCATCTGAGAGAGAGG 527
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 319 CGTGGGTCATCTCGCGCTGTATCTCTCCGCTCTGCTGCTCTTACCGCGGCC 378
QY 528 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGTA 587
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 379 CGACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGTA 426
QY 588 CCGTCATCTGTCGTGTCATCGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGTA 647
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 427 CATCTGTCCTCTGCTGCTGCTCTCTCTCTGCGCGCTGCTGCTGCTGCTGCTGTA 486
QY 648 CGTGGCATCTACAGATCGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGTC 707
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 487 TCGCGGCGATCTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 546
QY 708 GGACGCGCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 748
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 547 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 587

```

RESULT 12

```

BO302172      297 bp  mRNA  linear  EST 16-MAY-2002
LOCUS        QV0-BF0263-101299-072-n10 BF0263 Homo sapiens cDNA, mRNA sequence.
DEFINITION   BO302172
ACCESSION    BO302172.1 GI:20817694
VERSION       EST.
KEYWORDS
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
               1 (bases 1 to 297)

```

REFERENCE

```

AUTHORS      Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
               Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
               Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
               Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
               M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
               Simpson, A.J.
TITLE         Shotgun sequencing of the human transcriptome with ORF expressed
               sequence tags
JOURNAL       Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE       20202663
COMMENT       Contact: Simpson A.J.G.
               Laboratory of Cancer Genetics
               Ludwig Institute for Cancer Research
               Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
               Brazil
               Tel: +55-11-2704922
               Fax: +55-11-2707001
               Email: asimpson@ludwig.org.br

```

```

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV0&t2=QV0-BF0263-
101299-072-n10&t3=1999-12-10&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 26
High quality sequence stop: 205.
Location/Qualifiers

```

FEATURES

```

source
1..297
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BF0263"
/dev_stage="Adult"
/Note="Organ: Breast; Vector: puc18; Site_1: SmaI; Site_2:

```

SmaI: A mini-library was made by cloning products derived from ORFESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions." 57 t

Query Match 20.2%; Score 272.6; DB 14; Length 297;
 Best Local Similarity 98.6%; Pred. No. 6, 8e-40;
 Matches 275; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

QY 1 ATGGGCTCCCTGACAGCCGGAGCGGGCAACGCGAGCTGGAACGAGGAGCGCGGGG 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11 ATAGGCTCCCTGACAGCCGGAGCGGGCAACGCGAGCTGGAACGAGGAGCGCGGGG 70
QY 61 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGTC 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 71 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGTC 130
QY 121 GCGCTGCTCATGCTGCTACACCGTTCGCGCAAGCTGCTCATATCGCGCGTTCACG 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 131 GCGCTGCTCATGCTGCTACACCGTTCGCGCAAGCTGCTCATATCGCGCGTTCACG 190
QY 181 AGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGTC 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 191 AGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGTC 250
QY 241 CTGGTGGCACGCTCGTATCCCTTCTGCTGCTGCGGCAAC 279
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 251 CTGGTGGCACGCTCGTATCCCTTCTGCTGCTGCGGCAAC 289

```

RESULT 13

```

BO923710      935 bp  mRNA  linear  EST 20-AUG-2002
LOCUS        AGENCOURT 8803211 lupskl_sciatic_nerve Homo sapiens cDNA clone
DEFINITION   IMAGE:6198830 5', mRNA sequence.
ACCESSION    BO923710
VERSION       BO923710.1 GI:22338741
KEYWORDS
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
               1 (bases 1 to 935)

```

```

REFERENCE     NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS       National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE         Unpublished (1999)
JOURNAL
COMMENT       Contact: Robert Strausberg, Ph.D.
               Email: cgabbs-remail.nih.gov
               Tissue Procurement: Dr. James R. Lupski
               cDNA Library Preparation: Life Technologies, Inc.
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

```

```

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LHAM13611 row: b column: 15
High quality sequence stop: 535.
Location/Qualifiers

```

FEATURES

```

source
1..935
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:6198830"
/clone_lib="lupskl_sciatic_nerve"
/sex="male"
/tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
/Note="Vector: PCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.

```

```

Db      58  TCGGGGGGACAGAGCGGAT 38
|||||
RESULT 10
AL530418
LOCUS      AL530418      867 bp      mRNA      linear      EST 13-FEB-2001
DEFINITION AL530418 LTI_NFL001_NBC4 Homo sapiens cDNA clone CSDD007YE02 5
prime, mRNA sequence.
ACCESSION  AL530418
VERSION     AL530418.1  GI:12793911
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 867)
AUTHORS     L.I.W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source
1..867
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSDD007YE02"
/clone_lib="LTI_NFL001_NBC4"
/sex="male"
/risue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(df) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT      98 a      315 c      286 g      143 t      25 others
ORIGIN
Query Match      23.5%; Score 317.6; DB 9; Length 867;
Best Local Similarity 76.8%; Pred. No. 5.4e-48;
Matches 407; Conservative 8; Mismatches 102; Indels 13; Gaps 2;

QY 105 GCTGGTGCTGGCGCGCTGCTCATGCTGCTCACCAGTTCGCGCAACGTCGTGCAT 164
|||||
Db 351 GCTGGTTCCTGTTGGCTCTCTCATGCTTCATCCGTTGTGGCAACGTCGTGCTGT 410

QY 165 CATGGCGGTGTTACAGAGCGCGGCTCAAGGGCGCCCAAACTCTTCTGCTGCTCT 224
|||||
Db 411 GATGCGGCTTGTGACACAGCGGGGCT-GCGCCCCACAAACCTCTTCTGCTGCTGT 469

QY 225 GGCCTGCGGACATCTCTGTGGCCAGCTGTCATCCCTTCTGCTGCGCAACGAGGT 284
|||||
Db 470 TGCCTTGCAGACATCTGCTGGCCAGCTGTCATCCCTTCTGCTGTCGCAACGAGCT 529

QY 285 CATGGGCTACTGTTACTTCGGCAAGGCTTGGTGAGAGATCTACTGGCGCTGCAGTCT 344
|||||
Db 530 CATGGCTACTGGTACTTGGGAGGTGTGTGTGGGGGTGTACTTGGCGCTGCATGCTCT 589

QY 345 CTCTTGACAGTCTGTCATCTGTCACCTGTGCGCATCAGCTGAGCGGCTACTGTCAT 404
|||||
Db 590 GTTTTGACACTCGTCGATCTGTCATCTGTTCACACAGCTTGAGCCGCTACTGTCGCT 649

QY 405 CACACAGCATGATGATACACTGAAGCGCAGCGCGCGCATCAAGGCGATCATCAT 464
|||||
Db 650 GACGACAGCGCTGAGTACAACTGAAGCGCACACACGCGCGCTCAAGGCGACATCGT 709

```

```

QY 465 CACGCTGGTATCTCGGCGGCTCAATCTCTCCGCGGCTCATCTCCATGAGAA 524
|
Db 710 GCGGTGTGCTCAATCGGCGGCTGTATCTCTCCGCGGCTGCTCTTACCGCA 769

QY 525 GGGCGGCGGCGGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 584
|
Db 770 GCGCGAGCGG-----CCGCTACCGCGAGTGGGSCCTCAAGACAGACCGCG 817

QY 585 GTACATCTCTGCTGTCATCGGCTCTCTTCTGCTCCCTGCTCATCA 634
|||||
Db 818 GTACATCTCTGCTGTCATCGGCTCTCTTCTGCTCCCTGCTCATCA 867

RESULT 11
B0887729
LOCUS      B0887729      988 bp      mRNA      linear      EST 16-AUG-2002
DEFINITION AGENCOURT_8764335 NIH_MGC_129 Mus musculus cDNA IMAGE:6313133
5', mRNA sequence.
ACCESSION  B0887729
VERSION     B0887729.1  GI:22279743
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 988)
AUTHORS     NIH-MGC http://mgi.mcl.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
Email: cgrabbs-remail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
cDNA Library Preparation: Resgen, Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: LLM13739_row: m column: 06
High quality sequence start: 8
High quality sequence stop: 509.
Location/Qualifiers
1..988
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:6313133"
/clone_lib="NIH_MGC_129"
/lab_host="DH10B (phage-resistant)"
/note="Organ: olfactory epithelium; Vector:
pCMV-SPORT6.1.cdb; Site.1: EcoRV; Site.2: NotI; Cloned
unidirectionally. Primer: Oligo df. Average insert size
2.2 kb. Constructed by Resgen, Invitrogen Corp. Note: This
is a NIH_MGC Library."

BASE COUNT      158 a      349 c      300 g      181 t
ORIGIN
Query Match      23.5%; Score 317.4; DB 14; Length 988;
Best Local Similarity 74.4%; Pred. No. 5.9e-48;
Matches 432; Conservative 0; Mismatches 136; Indels 13; Gaps 2;

QY 169 GCGGTGTTACAGAGCGCGGCTCAAGCGCCCAAACTCTTCTGCTGCTGCGC 228
|||||
Db 19 GCTGTGTTACAGAGCGGCTGCGCGCGCGCGCAACTCTTCTGCTGCTGCGC 78

QY 229 TCGGCGG-ACATCTGCTGCGGCGGCTGCTCAATCCCTTCTGCGGCGCAAGAGTAT 287
|||||
Db 79 TCACTACACATCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 138

QY 288 GGGCTACTGCTGCTGCGGAGGCTTGTGCGAGATCTACTGCGGCTGCGAGCTGCT 347
|||||
Db 139 GGCCTACTGCTGCTGCGGAGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 198

```


[illegible]

Db	480	C6G6GCCT -GCCCGCCACAGAACTCTTTCGTGGTGTCGCTGAGCCTCGGCCAGATCCTG	538
Oy	244	GTTGGCACCCCTGTCAATCCCTTTCGTGCTGGCCAACGAGGTATGAGGTAATGTAATTTC	303
Dd	539	GTTGGCACCCCTGTATATGACCCTTCTGTTGGCCAAGACTCATGGCCATCTAGTAATTTC	598
Oy	304	GGCAGGCTTGTGGAGATCTAATCTGGCGCTGACGTCCTCTTTCGACGTCGTCATTC	363
Dd	599	GGGACAGTGTGGTGGCGGCTGTACCTGGCGCTGATGTGCTGTTTTGACATCTGTGATTC	658
Oy	364	GTTGCACCTGTGGCCATATGACCTGGACCGGCTACTGGTCCATACACAGGCCATCGATTC	423
Dd	659	GTTGATCTTGTGGCAATTCAGCCCTGGACCGCTACTGGTCCGTTGACGACGACCGCTCGATTC	718
Oy	424	AACCTGAACGGACGCGCGCGCCGATCAAGGCATATCATATCAGCT -GTGGATCATTC	482
Dd	719	AACCTGAACGGACGACGCGCGCCGATCAAGGCATATCATATGTCGCTCTATCTTC	778
Oy	483	GGCGCTCATCTCTTCCGCGCGCTCATCTCATCGAAGAAGAGGCGGCGCGCGGCC	542
Dd	779	GGCGCTCATCTCTTCCGCGCGCTCATCTCATCGAAGAAGAGGCGGCGCGGCC	831
Oy	543	GCAGCGCGCGGACCGCGCGCTGGAGATCAACGACGAGTAGTATCTCTCTGTCG	602
Dd	832	-----CCGCTACCCGCACTGGCGGCTCAGACGAGACCTGTATATCTTCTCTTCG	886
Oy	603	CATCGGCTCTTCTTTCGCTCCCTGCTCATCATGATCTGTCTACGTGCGATCAACA	662
Dd	887	CATCGGCTCTTCTTTCGCGCCCTGCTCATCATGGGCTGTGTCTACGCGCATCTACCG	946
Oy	663	GATCGCAAAGCTGCGACCCGCGGTGCGAACCCAGCCGCGGGTCCGGAGCCGTCGCGC	722
Dd	947	AGTGGCAAGCTGCGACCGCGACGCTGACGAGAAGCGCGCCCGTGGCGCCGACCG	1006
Oy	723	GGCGCC 728	
Dd	1007	TGCGTC 1012	
RESULT 8			
LOCUS	GGAA2AAR	855 bp	DNA linear GSS 14-SEP-2001
DEFINITION	Chicken alpha2 adrenergic receptor gene fragment probably subtype		
ACCESSION	AL606540		
VERSION	AL606540.1 GI:15591915		
KEYWORDS	GSS; Alpha2 adrenergic receptor gene.		
SOURCE	chicken.		
ORGANISM	Gallus gallus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;		
	Phasianine; Gallus.		
REFERENCE	1 (bases 1 to 855)		
AUTHORS	Hunter,C. and Elgar,G.		
JOURNAL	Alpha2 adrenergic receptor gene		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 855)		
TITLE	Hunter,C.		
JOURNAL	Direct Submission		
	Submitted (14-SEP-2001) MRC Human Genome Mapping Project Resource		
	Centre Hinxton, Cambridge, CB10 1SB. UK Email:		
	biohelp@hmp.mrc.ac.uk		
FEATURES	Location/Qualifiers		
source	1..855		
	/organism="Gallus gallus"		
BASE COUNT	201 a 248 c 245 g 161 t		
ORIGIN			
Query Match	23.8%	Score 321;	DB 17; Length 855;
Best Local Similarity	64.6%;	Pred. No. 1,3e-48;	
Matches 614; Conservative	0; Mismatches 235;	Indels 102; Gaps	5;

Fax: 617-495-8557
Email: dmelton@blhp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
Possible reversed clone: similarly on wrong strand
Seq. primer: -40RP from Gibco
High quality sequence stop: 445.

FEATURES
SOURCE

BASE COUNT	63 a	215 c	210 g	73 t
ORIGIN				

Query Match	Score	DB	Length
41.48;	559.4;	DB 14;	Length 561;

Matches	560;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
---------	------	--------------	----	------------	----	--------	----	------	----

OY	610	TCCCTTCGCTACCTCCGACCCATCATGATTCGAGTCTACGTGACGTGCGCATTCACCAAGATGCGC	669
Db	561	TCCTCTTCGCGCTCCCTGCTCATCATGATTCGTGTACGTGCGCATTCACCAAGATGCGC	502
OY	670	AAGCGTGCACCCGCGGTGCACCCAGCCGCGGGGTCCGAGCCGTGCGCGCGCCGCG	729
Db	501	AAGCGTGCACCCGCGGTGCACCCAGCCGCGGGGTCCGAGCCGTGCGCGCGCCGCG	442
OY	730	GGGGGACCGAGGCGGACCGCCAAAGGTTCTGGGCCCCGAGCGAGCGCGGGGCC	789
Db	441	GGGGGACCGAGGCGGACCGCCAAAGGTTCTGGGCCCCGAGCGAGCGCGGGGCC	382
OY	790	GCAGAGGCGCGAACGCTGTGCCACCCAGCTCAACGGCGGCGCTGTGCGAGCGCCGCGCGGCC	849
Db	381	GCAGAGGCGCGAACGCTGTGCCACCCAGCTCAACGGCGGCGCTGTGCGAGCGCCGCGCGGCC	322
OY	850	GGGCGCGCGGACACGACCGCTGGAACTCTGAGAGAGAGCTCTCTTCTTCGACCGCCGAG	909
Db	321	GGGCGCGCGGACACGACCGCTGGAACTCTGAGAGAGAGCTCTCTTCTTCGACCGCCGAG	262
OY	910	CGGCTCTCAAGGCGCCCGCAGACCCGAGCGCGGTCCCGCGGGGCGAAAGCGCAAGGCCCGGAGCG	969
Db	261	CGGCTCTCAAGGCGCCCGCAGACCCGAGCGCGGTCCCGCGGGGCGAAAGCGCAAGGCCCGGAGCG	202
OY	970	AGCCAGGTAGACCGGGGCGACAGCTGCCGGCGCGGGCGCGGGGCGAGCGGGGATCGGG	1023
Db	201	AGCCAGGTAGACCGGGGCGACAGCTGCCGGCGCGGGCGCGGGGCGAGCGGGGATCGGG	142
OY	1030	ACCGCGGCTGCAAGGCGCGGGGGAGGAGCGCTCGGGGGCTGCCAAAGCGTCGCGTGGGGCG	1089
Db	141	ACCGCGGCTGCAAGGCGCGGGGGAGGAGCGCTCGGGGGCTGCCAAAGCGTCGCGTGGGGCG	82
OY	1090	GGGCGGACAGACCGCGAGAGGCGTTTCACGTTCTGATCGCGCGGTGCTCATCGAGATCTTC	1149

Db 81 GGGGGGAGAGACCCGGAGAGGCGCTTCACGTTGCTGCTGGCCGTTGTCATTCGGAGTGTTC 22

Qy 1150 GTGGTGTGCTGCTGTTCGCCCTTC 1170

Db 21 GTGGTGTGCTGCTGTTCGCCCTTC 1

RESULT 2

BM967243/c				
LOCUS	492 bp	mRNA	1 linear	EST 29-APR-2002
BM967243				

DEFINITION 1332c09.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens CDNA clone IMAGE:6136336 5' similar to SW:A2A2_HUMAN P08913 ALPHA-2A ADRENERGIC RECEPTOR ;, mRNA sequence.

ACCESSION	BM96/243
VERSION	BM967243.1
KEYWORDS	GI:19561038
	EST

SOURCE

ORGANISM

REFERENCE
1. (bases 1 to 492)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHOR:

TITLE Endocrine Pancreas Consortium

JOURNAL Unpublished (2000)
COMMENT Other_ESTS: 1j32c09.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557

FEATURES

Sources

BASE COUNT	44 a	202 c	182 g	64 t
ORIGIN				

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 12:34:42 ; Search time 2684.44 Seconds
(without alignments)
8144.696 Million cell updates/sec

Title: US-09-636-259B-2

Perfect score: 1350

Sequence: 1 atgggcctccctgcagccgcga.....gggacaggaagcgagccgctg 1350

Scoring table: IDENTITY_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_ylt:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_tod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	559.4	41.4	561	14	BM967248
2	488.8	36.2	492	14	BM967243
3	479	35.5	691	10	BB643669
4	451.4	33.4	453	14	BQ129312
5	410.6	30.4	893	13	BI459381
6	395	29.3	740	13	BI838282

7	364.8	27.0	1077	9	AL544609	AL544609
8	321	23.8	855	17	CGAA2AAR	AL605540 Chicken a
9	319.4	23.7	358	13	BM352981	BM352981 ig69h02.y
10	317.6	23.5	867	9	AL530418	AL530418
11	317.4	23.5	988	14	BQ887729	BQ887729 AGENCOURT
12	272.6	20.2	297	14	BQ302172	BQ302172 QVO-BIT026
13	255.2	18.9	935	14	BQ923710	BQ923710 AGENCOURT
14	226.4	16.8	935	14	BQ923710	BQ923710 AGENCOURT
15	214.6	15.9	966	17	CNS028V2	AL236849 Tetradon
16	199.8	14.8	1135	9	AL544577	AL205895 Tetradon
17	197	14.6	805	17	CNS03CEL	AL345177 AL544577
18	194.2	14.4	350	10	BE648878	AL237702 Tetradon
19	187.4	13.9	777	17	LEPA2AAR	BE648878 UI-M-BH2.
20	185.6	13.7	801	17	GGAA2CAR	AL606561 Lamprey a
21	179.4	13.3	1010	17	CNS04CNO	AL606541 Chicken a
22	177.2	13.1	702	13	B1836679	AL284651 Tetradon
23	175.8	13.0	921	17	CCLA2BAR	B1836679 603089610
24	175	13.0	975	17	CNS039RV	AL606565 Herring a
25	173.4	12.8	691	17	HIPAA2AAR	AL606565 Sea Horse
26	173	12.8	697	17	RESA2AAR	AL606551 Frog aliph
27	172.6	12.8	774	17	AGAA2CAR	AL606580 Toothcarp
28	172.2	12.8	882	17	HIPAA2CAR	AL606568 Sea Horse
29	171.8	12.7	2146	11	AKO18378	AKO18378 Mus muscu
30	169.6	12.6	872	17	ECAA2BAR	AL606560 Horse alp
31	166.8	12.4	890	17	CNS02WK9	AL217170 Tetradon
32	166.2	12.3	825	17	ARUA2BAR	AL606576 Sturgeon
33	164.8	12.2	693	17	ARUA2BAR	AL606574 Sturgeon
34	164	12.1	535	13	BM647571	BM647571 170006873
35	163.4	12.1	723	17	AGAA2AAR	AL606581 Toothcarp
36	161.4	12.0	829	9	AL549866	AL549866
37	160.6	11.9	705	17	HGRA2AAR	AL606570 Shark alp
38	160	11.9	753	17	SCAA2CAR	AL606564 Ostrich a
39	159.4	11.8	788	17	DREA2CAR	AL606584 Zebrafish
40	158.6	11.7	699	17	LOSA2AAR	AL606553 Gar alpha
41	154.4	11.4	981	17	HIPAA2BAR	AL606569 Sea Horse
42	151.4	11.2	872	9	AL573897	AL573897
43	151	11.2	860	17	CNS03HKO	AL244403 Tetradon
44	150.4	11.1	780	17	CCLA2CAR	AL606557 Herring a
45	148	11.0	984	9	AL550664	AL550664

ALIGNMENTS

RESULT 1
LOCUS BM967248/c 561 bp mRNA linear EST 29-APR-2002
DEFINITION i132d04.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
CDNA clone IMAGE:5136374 5' similar to SW:A2AA_HUMAN P08913
ALPHA-2A ADRENERGIC RECEPTOR ; mRNA sequence.

ACCESSION BM967248
VERSION BM967248.1 GI:19561047

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 561)

AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wyllie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Rittler,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagaratshvili,R., Williams,T., Jackson,Y., and Bowers,Y.

ENDOCRINE PANCREAS CONSORTIUM

Other ESTs: i132d04.x1

Unpublished (2000)

COMMENT

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812

```

Db 909 CTTCGCGTATCACCGAGGAGGCGGGCTACGCTGTCTTCCTCCGTGTCCTTTCTA 968
QY 618 CGCTCCCTGGCTATCATGATCTGTAGTGTGCGCATCTACCATGCGC-----CAA 671
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 969 CTTGCCCATGGCGGTCTATCTGTGTATGTACTGCGCGGTGTACTGTGTCGCGGCAAC 1028
QY 672 GCGTGCACCCGCGGTGCCACCCAGCCGCGGGGTCCGGACGCCGTGCGCCGCGCGCGGG 731
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1029 CAGCGGAGGCTGAGGAGGCGGTCAAGCGCGAGCGAGGCAAGGCTCCGAGGTGGTGT 1088
QY 732 GGGCACCAGCGGCAAGGCTCTGGGCCCCGAGCGCAGCGCGGGCCCCGGGGGGCGC 791
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1089 GCGCATCTACTGTGCGGCGCGGCGCACGCGGCGCCGAGGGGCGCACGGCATGCGCAGCGC 1148
QY 792 AGAGGCGGAACCGCTGCCACCCAGCTCAACGGGCGCCCCCTGGCGAGCGCGCGC 844
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1149 CAGGGCCACACCTTCGCGAGCTGCTCTCCGTGCGGCTGTCTCAAGTTTCTCC 1201

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Search completed: February 13, 2003, 07:47:40
 Job time : 94.1176 secs

OY	18	GGAGCGGGGCAACGGAGCTGGAAACGGGAAOCGAAGGGCGCGGGGGGGGGCGCGCCCGGGGCGAC	77
Db	387	GGAGCGGGGGAGACCGGGGGCGGGCGGGCGACGTGAATGSCACGCGCGCTCGGGGGACT	446
OY	78	CCCTTACTCCCTGCAAGGTGACGCTGACGCGTGTGTGCTTGGCTGGCCGGCTGCTCATGTGCT	137
Db	447	GGTGTGAGCGGCGAGGGGCGTGGGGCGTGGGGGTCTTCTCTGGCAGCC--TTATCTTTAT	503
OY	138	CACCGTGTGGCAACGTGCTCGTCACTATGACCGGTGTTCAGCAGCCCGCGGCTCAAGGC	197
Db	504	GGCCCTGGCAGGTAACTGCTTTCATCTTCATGTCGAGTGGCCCTGGCAACCGCACCTCGACAG	563
OY	198	GGCCCCAAAACCTCTTCCGGGTGTCTGGGCGCTGGGCGGACATCGTGTGGCCACGCTGCT	257
Db	504	CGTCAACCACTATTTTCATCTGTAACCTGGGCGGTGGCGACCTCTCTGTAGCGCCACCT	623
OY	258	CATCCCTTCTCGCTGGGCAACGAGTCATGGGCTACTGTACTGTGGGAGAGGCTTGATG	317
Db	624	ACTGCCCTTCTGGCGCAACATGAGAGGTTCGTGGGTTCTGTGGGCTTTGGCGGGCGCTTGG	683
OY	318	CGAATCTTACCTGGCGCTCGACGTGCTTCTTCTGACGTGCTCCATGTGTGACACTGTGGCG	377
Db	684	CGAGCTAATGGGCGCCCGCTGGACGTGCTGTCTCACGCGCTCCATCTCAGCCTTGAC	743
OY	378	CATCAGCTTGAGCGCTACTGATGTTCATCACACAGGCGCATGATTAACCTGAAGGGCAC	437
Db	744	CATCTCGGTGACCGGTATACGTGGGGCGTGGCCCACTACTGAATACCCAGCCATCATGAC	803
OY	438	GCCGCGCGGCATCAAGGCCATCATCATCACCGTGTGGGTATCTCGGCGGTATCTCTT	497
Db	804	CGAGCGAAGCGCGCGCGCATCTCGGCGCTGTGTGGTGTGTAGCCCTGTGTGTGTCGT	863
OY	498	CCCGCCGTCTATCTTCATCGAAGAAGAGGGCGGGCGGGCGGCCCGCACCGCGGAGCC	557
Db	864	AGGGCGCT-----GCTGGGCTGTGAAGAGAACCCGTCGCCCTCGAAGAGGG	908
OY	558	GGCGTGGAGATCAACAGCACAGAAGTGTGTGTCATCTGTGTGTGTATGGGTCTCTT	617
Db	909	CTTCTGGGTATCACGAGGAGGGGGGTACGTGTCTTCTCTCGGTGTGCTCTTCTTA	968
OY	618	CGCTTCCTGCTCATTCATGTATCTGTGTCTTACGTGGCGCATTCACAGATGC-----CAA	671
Db	969	CTCTGCCCATGGCGGTCTATCTGTGTGTATGTACTCCGCGTGTACGTGTGTGCGCGACAC	1028
OY	672	GGCTGGACCGCGGTGGCCACCGACCGCGGGGGTTCGGAGCGGCGGTGGCGCGCGCGGG	731
Db	1029	CACGCGAGCTCGAGGCAGGCGCTCAAGCCCGAGCCAGGAGGAAAGGCTCTCGAAGTGTGCT	1088
OY	732	GGGCGACGAGCGAGGCGCCAAAGGTCTGTGGGCGCCGACGACGCGGCGCGCGGGGGGCG	791
Db	1089	GGCGATCACCTGTGGCGGGCGCGCACAGGGGCGCGACGGGGGCGACGCGATCGGAGGCG	1148
OY	792	AGAGGCGGAACGCTGTGCCAACCCAGCTCAAGGCGCGCCCTGGCGAGCCCGCGC	844
Db	1149	CAGGGCGCAACCTTCCGACGCTGTCTTCCGTGGCGCGCTCATGATTTCTGCC	1201

RESULT 15
 US-08-468-939-1
 ; Sequence 1, Application US/08468939
 ; Patent No. 5714381
 ; GENERAL INFORMATION:
 ; APPLICANT: Jonathan A. Bard et al.
 ; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
 ; TITLE OF INVENTION: Receptors and Uses Thereof
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: COOPER & DUNHAM LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036

```

1 COMPUTER READABLE FORM:
2 MEDIUM TYPE: Floppy disk
3 COMPUTER: IBM PC compatible
4 OPERATING SYSTEM: PC-DOS/MS-DOS
5 SOFTWARE: PatentIn Release #1.24
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: US/08/468,939
8 FILING DATE:
9 CLASSIFICATION: 435
10 ATTORNEY/AGENT INFORMATION:
11 NAME: White, John P.
12 REGISTRATION NUMBER: 28,678
13 REFERENCE/DOCKET NUMBER: 41337-1B
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: (212) 278-0400
16 TELEFAX: (212) 391-0526
17 INFORMATION FOR SEQ ID NO: 1:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 2140 base pairs
20 TYPE: nucleic acid
21 STRANDEDNESS: single
22 TOPOLOGY: unknown
23 MOLECULE TYPE: DNA (genomic)
24 HYPOTHEICAL: N
25 ANTI-SENSE: N
26 FEATURE:
27 NAME/KEY: CDS
28 LOCATION: 178..1893
29 OTHER INFORMATION:
30
31 US-08-468-939-1

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Query Match	11.48;	Score 153.4;	DB 1;	Length 2140;
Best Local Similarity	52.08;	Pred. No. 9.8e-20;		
Matches 433;	Conservative	0;	Mismatches 376;	Indels 24;
				Gaps 3;

QY	18	GGAGCGGGGCAACGAGCTGGAAAGGAGCCGAGAGCGCGGGGGGGGGCCGGGGCCAC	77
Db	387	GGAGCGGGGAGCGCGGGCGCGGGCGCGAGCTGAATGCAACGGCCGCTGGGGACT	444
QY	78	CCCTTACTCCCTGCAGGTGACGTGACGTGGTGGCTGGCGGCGCTCTCATGCTGCT	13
Db	447	GGTGGTGAACCGCGAGGGGCGTGGGCGTGGGCGCTTCTCTGGAGCG---TTCATCTTAT	50
QY	138	CACCGGTTCGGCAACGTGCTGTCATCAATCGCCGTTCACAGAGCGCGGCGCTCAAGC	19
Db	504	GGCCGGGCAAGGAACTGCTTGTCATCTCTCAAGTGGCTGCAACGCGCACCTGCAAGC	56
QY	198	GGCCCAAAACCTTTCCTGATGTCTCTTGAGCTCGGCGCGCAATCCTGTGGCCAGCTGT	25
Db	564	CGTACCAACTATTTCATCTGTGAACGTGGCGGTGGCGACCTGTCTGTGAGCGCAACGT	62
QY	258	CATCCCTTCTTCGGCTGGCCCAACGAGTCAATGAGGTACTGGTACTTGGCAAGCTTGGTG	31
Db	624	ACTGCGCTTCTGGCCACCATGGAAGTGTGTGGGCTTCTTGCGCTTGGCGCGGCTTTTG	68
QY	318	CGAGATCTACTGAGGCGCTCGAGAGTGCCTTCTGACGTCTTCATGCTGCACCTGTGGC	37
Db	684	CAGAGTATGGGCGCGCGTGAACGTGTGTGTGACGCGCTTCATCTTCAAGCTTGGAC	74
QY	378	CATCAAGCTTGAGCGCTACTGCTCATCAACAGAGCCATCGATCAACCTGAAAGCGAC	43
Db	744	CATCTCCGTGGAGCCGGTACGTGGGCGTGGCGCACTCACTCAAGTACCAGCATCATGAC	80
QY	438	GGCGGCGGCATCAAGGCGCATCATCAATACCGTGGGTCATCTGGCGGCTCATCTCTT	49
Db	804	CGAGCGCAAGCGCGCGCATCTCGGCCCTGCTCTGGGTGTGAAGCCCTGTGTGTGCT	86
QY	498	CCGCGCGCTCATCTCATCTCGAAGAAAGAGGCGCGCGGGGCGCGCGCAACCGCGAAGC	55
Db	864	AAGGCGCCCT-----CGTGGGCTGAAGAGAACCCGTGCCCCCTGAGAGAGCG	90
QY	558	GGCGTTCGAGATCAACGACGAAGAGTATGTCATCTGCTGTGCATCGGCTCTTCTT	61


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; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-855-6
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Query Match      12.2%; Score 164.8; DB 4; Length 1335;
Best Local Similarity 51.2%; Pred. No. 8.1e-22;
Matches 438; Conservative 0; Mismatches 412; Indels 6; Gaps 2;
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QY 3 GGGCTCCCTGCAAGCCGAGCGGGGCAACGAGCTGGAACGGGACCGCGGGGGG 62
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DB 6 GCGCGCGCGCGCGCGCGCGCTTCTCGGACCGCTGGAACGCTTGGGGCGCTGGCGGCGATGCGCGCG 65
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 63 GCGCGCGCGCGCGCGCGCTTCTCGGAGTGACGCTGAGCGCTGGCTGGCTGGCGG 122
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DB 66 GCGCGCGCGCGCGCGCGCTTCTCGGACCGCTGAGCGCGCTGGCGGCTCATGGC 125
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QY 123 CCGTCATGCTGCTACCGCTGTTGGCAAGCTGCTGATCATCGCCGTTCACGAG 182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 126 GCTGCTATGCTGCGACGAGTGCTGGCAACGGGCTGCTGATGCTGCTGGTGGCGA 185
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 183 CCGCGCGCTCAAGGCGCCCAAAACCTCTTCTGCTGCTGCTGCGCGGACATCT 242
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 186 CTGCACTCCGACCCAGAACACTTCTGCTCAACCTGCGCATCTCCGACTTCT 245
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QY 243 GGTGGCAGCTGCTGATCCCTTCTCGCTGGCAAGAGTGCATGGGCTACTGGTACT 302
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 246 CGTGGCGCGCTTCTGCTGATCCACTGATATGCTACCTGCTGACAGGCGCTGACCTT 305
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 303 CGGCAAGCTTGGTGGGAGATCTACCTGGCGCTCGACGCTCTTCTGCAAGCTGCTCAT 362
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 306 CGGCGCGCGCGCTGCTGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 365
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QY 363 CGTGCACCTGTGGGCTGAGCGCTGAGCGCTGAGCGCTGAGCGCTGAGCGCTGAGCGCT 422
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DB 366 CTTCACATGCTGCTGATAGCTAGACCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 425
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QY 423 C--AACCTGAAGCGCAGCGCGCGCTGATCAAGGCGCATCATCATCGCTGGTGCAT 479
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 426 CGGCGCGCGAGGAGTGAACGGGGGGGCACTGGGGAAGATGCTGCTGGTGGTGGT 485
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QY 480 CTGCGCGCTGCTGCTTCTTCCGCGCTCATCTTCATCGAAGAAAGGCGGCGGCGG 539
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DB 486 GGGCTTCTGCTGCTAGGACAGCATCTGAGCTGGGAGTACCTGCGGGGAGAGCTC 545
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 540 CCGGAGCGCGCGAGCGCGCTGGAGATCAAGCAAGGAGTGAAGTGAAGTGAAGTGAAGT 599
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 546 CATCCCGAGGCGCATGCTGATGCGAGTCTTCTTACAACTGATGCTTCTCATATCAGG 605
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QY 600 GTGATCGAGCTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 659
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 606 TTTCACCTGAGATCTTAAAGCTTCTTCAAGGCTGCAAGCTTCTTAACTGATGATCTA 665
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QY 660 CCAAGATGCGCAAGCTGCAAGCGCGCTGCAAGCGCGCGGGTCCGAGCGCGCTGCG 719
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DB 666 CCGTGAACATGCAAGGAGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 725
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 720 CCGGCGCGCGGGGCGAGCGCG--AGGCGCAAGGCTGCGCGCGCGCGCGAGCGG 776
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 726 CAGAGCGCGCTTCCGAGGCGCGAGCTTCAACACCGCGCGCTGCTGCTGCTGCTGCTG 785
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 777 GGGCGCGGGGCGAGAGCGCGAAGCGCTGCGCGCGCGCGCGCTGCGCGCGCGCGCG 836
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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DB 786 GCAGAGGGGACGCGGGAGGCCATGCCCTGCACAGGATGAGGCTGAGCGCGCGCT 845
QY 837 GCCCGCGCGCGCGCGG 852
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DB 846 AGCGCGCTGAGCGCGG 861
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RESULT 8
US-09-642-514-6
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; Sequence 6, Application US/09642514
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```
; Patent No. 6437100
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Lovenberg, Timothy
```

```
; APPLICANT: Erlander, Mark
```

```
; APPLICANT: Pyati, Jayashree
```

```
; APPLICANT: Huvar, Arne
```

```
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
```

```
; TITLE OF INVENTION: SUBTYPE
```

```
; FILE REFERENCE: ORT1290
```

```
; CURRENT APPLICATION NUMBER: US/09/642,514
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```
; CURRENT FILING DATE: 2000-08-21
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; PRIOR APPLICATION NUMBER: US 09/167,354
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; PRIOR FILING DATE: 1998-10-06
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```
; NUMBER OF SEQ ID NOS: 8
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; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO: 6
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; LENGTH: 1335
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; TYPE: DNA
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; ORGANISM: Artificial Sequence
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; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: CDNA
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US-09-642-514-6
Query Match      12.2%; Score 164.8; DB 4; Length 1335;
Best Local Similarity 51.2%; Pred. No. 8.1e-22;
Matches 438; Conservative 0; Mismatches 412; Indels 6; Gaps 2;
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QY 3 GGGCTCCCTGCAAGCCGAGCGGGGCAACGAGCTGGAACGGGACCGAGCGCGGGGG 62
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DB 6 GCGCGCGCGCGCGCGCGCGCTTCTCGGACCGCTGGAACGCTTGGGGCGCTGGCGGCGATGCGCGCG 65
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 63 GCGCGCGCGCGCGCGCGCTTCTCGGAGTGACGCTGAGCGCTGGCTGGCTGGCGG 122
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 186 CTGCACTCCGACCCAGAACACTTCTGCTCAACCTGCGCATCTCCGACTTCT 245
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 243 GGTGGCAGCTGCTGATCCCTTCTCGCTGGCAAGAGTGCATGGGCTACTGGTACT 302
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 246 CGTGGCGCGCTTCTGCTGATCCACTGATATGCTACCTGCTGACGCGCTGAGACTT 305
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 303 CGGCAAGCTTGGTGGGAGATCTACCTGGCGCTGAGCGCTGCTTCTGCAAGCTGCTCAT 362
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 306 CGGCGCGCGCGCTGCAAGGCTGAGGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 365
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 363 CGTGCACCTGTGCGCGCTGAGCGCTGAGCGCTGAGCGCTGAGCGCTGAGCGCTGAGCGCT 422
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 366 CTTCACATGCTGCTGATAGCTAGACCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 425
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 423 C--AACCTGAAGCGCAGCGCGCGCATCAAGGCGCATCATCATCATCATCATCATCATCATCAT 479
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 426 CCGGCGCGCGAGGAGTGAACGGGGGGGCACTGGGGAAGATGCTGCTGCTGCTGCTGCTG 485
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 480 CTGCGCGCTATCTCTCCGCGCTCATCTCATCTCATGAGAAAGGCGCGCGCGCGG 539
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DB 486 GGGCTTCTGCTGATGAGGACAGCAAGCTGAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 545
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QY 243 GGTGGCCACGCTGTGATCCCTTTCGTGGCCAGAGGTATGGGCTACTGTACTT 302
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Db 536 GTGGGGGCGCTCTGTGATCCCTGTATGATACCTGTACAGGGCGCGGACCTT 595
QY 303 CGGCAAGCTTGGTGGAGATCTACGAGGCGTCGACGTCCTTCTTGCACGTCGCAT 362
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 596 CGGCGGGGGGCTCTGTGACGTCGTGGCTGTAGTGGACTACTCTGTGTACCTCTCTG 655
QY 363 CGTGCACCTGTGGCCATCAGCTGTGACCGCTACTGTGTATCACAAGGCCATTCAGTA 422
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 656 CTTCACATCATGTGCTCATCAGTACAGACCGCTTCTGTGGTCACCGAGCGGTCTTCATA 715
QY 423 C---AACCCTAAGCGCAGCGCGCGCGCATCAAGGCCATCATCATCAGCTGTGGTCA 479
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 716 CCGGGCCCGACAGGTGTACAGCGGGCGGCGCATGTCCGGAAGATCTGTGTGTGGTGTCT 775
QY 480 CTGGGCGGTATCTCTTCCGCGGCTCATCTCCATCGAAGAAAGGCGGCGGCGG 539
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 776 GGGCTTCTCTGTGTACGGAGACAGCATCTGAGCTGGAGTACCTGTCCGGGGGACGCTC 835
QY 540 CCGCAGCGCGCGAGCGCGGCTGCGAGATCAACGACAGAAAGTGTACGTATCTCTC 599
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 836 CATCCCGAGGGGCGACTGATGCCGAGTCTTCTACACTGTGTACTCTCTCATCAGCG 895
QY 600 GTGCATGCGCTCTTCTGCTGCTGCTGCTCATCATGATCTGTGTAGTGGCATCTTA 659
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 896 TTCCACCTCTGAGTCTTTCACGCTCTCTCTACGCTGCTCTTTAACTTCAGCATCTA 955
QY 660 CCAAGATCGCAAGGTCGACCGCGCTGCCACCGCGGGGTCCGCGACGCGCTGCG 719
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Db 956 CTTGAACATCCAGAGGCGCACCGCGCTCGGGCTGTGATGGGGCTCGAAGAGCAGCGCGCC 1015
QY 720 CCGCGCCCGCGGGGGGACCCAGCGC---AGGCCCAAGGGTCTGGGCGCCGAGGCGCG 776
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1016 CGACCCCGCTCCGAGGCGCCAGCTTCACACCCCGACCGCTGTGCTGGGGCTGTGCG 1075
QY 777 GGGCGCGGGGGGCGCAGAGGCGCAACCGCTGCCACCGCAGCTCAAGCGCGCCCTGGCGA 836
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1076 GCAGAAAGGGGACGCGGAGGCGCATGCCGTGTACAGAGTATGGGGTGTAGAGCGCCGT 1135
QY 837 GCCCGCGCGCGCGCGG 852
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Db 1136 AGGCGCTGAGGCGCGG 1151
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
US-09-167-354-6
; Sequence 6, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Iovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-167-354-6

Query Match 12.2%; Score 164.8; DB 3; Length 1335;
Best Local Similarity 51.2%; Pred. No. 8,1e-22;
Matches 438; Conservative 0; Mismatches 412; Indels 6; Gaps 2;
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QY 3 GGGCTTCCTGCAAGCCGCGAGCGCGCAACGATGAAAGGAGNCCGAGGCGCGGGGG 62
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QY 123 CCTGTCTATGCTGTACCGCTGTGCGAAGCTGTCTCATCATCGCTGTTCACGAG 182
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QY 183 CCGCGCGCTCAAGGGGCGCGCAAAAGCTGTGTGTGTGTCTGTGCGCTGGCGCGCATCT 242
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QY 363 CGTGCACCTGTGCGCATCAGCTGTGACCGGCTACTGTGTATCACAACAGCGCATCGAGTA 422
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QY 423 C---AACCCTAAGCGCAGCGCGCGCGCATCAAGGCCATCATCACCTGTGGTCA 479
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RESULT 7
US-09-642-855-6
; Sequence 6, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Iovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
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RESULT 2
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; Sequence 3, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silverl
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
; US-08-985-090-3
Query Match 12.3%; Score 166.4; DB 2; Length 1335;
Best Local Similarity 51.3%; Pred. No. 4.1e-22;
Matches 439; Conservative 0; Mismatches 411; Indels 6; Gaps 2;
QY 3 GGGCTCCCTGCGAGCGGAGCGGCGCAACGCGAGCTGAGACGGGACCGGCGCGGGG 62
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Db 426 CGGCGCGCGAGGAGGTGACAGCGGCGGCGAGTGGCGAAGATGCTGCTGTGGGTGCT 485
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QY 660 CCAAGTGCACAGCTGTCACCGCGGTGCGACACCGCGCGGCGCGCGCGCGCTGCG 719
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Db 666 CTGAACATCCAGAGGCGGACCGCGCTCGGCTGTGATGGGGCTGAGAGAGCAGCGCGCC 725
QY 720 CGGCGCGCGGCGGAGCGAGCGC---AGGCCAAAGGTCTGCGCGCGCGAGCGAGCGC 776
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Db 726 CGAGCCCTCTCCGAGGCGCGCTTCAACACCCCAACGCGCGCTGCTGCGGCGCTGCTG 785
QY 777 GGGCGCGGCGGCGGAGAGCGCAACGCTGCGCACCGACGATCAAGCGCGCGCGCTGCGCA 836
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Db 786 GCAGAAAGGCGCACGGGAGCGCATGCGGCTGCAACAGTATGGGTGCTGAGGCGCGCGCT 845

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GenCore version 5.1.3
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Scoring table: IDENTITY_NUC
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Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	166.4	12.3	1335	2	US-08-985-090-3
3	166.4	12.3	1335	3	US-09-165-543-3
4	166.4	12.3	2689	2	US-08-985-090-1
5	166.4	12.3	2689	3	US-09-165-543-1
6	164.8	12.2	1335	3	US-09-167-354-6
7	164.8	12.2	1335	4	US-09-642-855-6
8	164.8	12.2	1335	4	US-09-642-514-6
9	164.8	12.2	2699	3	US-09-167-354-5
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13	153.4	11.4	2140	1	US-08-334-698-1
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17	153.4	11.4	2140	2	US-08-722-190-1
18	153.4	11.4	2140	2	US-08-244-354-1
19	153.4	11.4	2140	3	US-09-206-899-1
20	153.4	11.4	2140	4	US-09-444-783-1
21	153.4	11.4	2140	4	US-09-688-415-1
22	153.4	11.4	2140	5	PCRT-US95-04203-1
23	152.2	11.3	1621	1	US-08-722-001-13
24	151.8	11.2	1776	1	US-08-722-001-29
25	150.4	11.1	1956	1	US-08-313-553-6
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27	150	11.1	3335	1	US-08-194-338-1

28	147.2	10.9	1645	2	US-08-461-812-1	Sequence 1, Appl1
29	142	10.5	1134	1	US-08-087-772A-14	Sequence 14, Appl1
30	142	10.5	1227	1	US-07-916-901-1	Sequence 1, Appl1
31	142	10.5	3683	4	US-08-450-962-1	Sequence 1, Appl1
32	140.8	10.4	1581	3	US-08-313-553-8	Sequence 8, Appl1
33	140.8	10.4	1581	3	US-08-767-993-8	Sequence 8, Appl1
34	140.4	10.4	1227	1	US-08-351-473B-7	Sequence 7, Appl1
35	139.8	10.4	1338	3	US-09-165-543-6	Sequence 6, Appl1
36	139.8	10.4	1690	2	US-08-461-812-3	Sequence 3, Appl1
37	138.8	10.4	3244	3	US-09-165-543-4	Sequence 4, Appl1
38	138.4	10.3	1610	1	US-08-056-051-5	Sequence 5, Appl1
39	139.4	10.3	1610	1	US-07-928-611-21	Sequence 21, Appl1
40	139.4	10.3	1610	2	US-08-487-811A-21	Sequence 21, Appl1
41	139.4	10.3	1610	4	US-09-060-694-21	Sequence 21, Appl1
42	139.4	10.3	1610	4	US-09-378-074-21	Sequence 21, Appl1
43	138.4	10.3	1610	5	PCRT-US93-07370-21	Sequence 21, Appl1
44	138.2	10.2	1601	1	US-08-722-001-7	Sequence 7, Appl1
45	138.2	10.2	1997	1	US-08-722-001-27	Sequence 27, Appl1

ALIGNMENTS

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RESULT 1
US-07-676-174A-1
; Sequence 1, Application US/07676174A
; Patent No. 5344776
; GENERAL INFORMATION:
; APPLICANT: Ventor, J. Craig
; TITLE OF INVENTION: Octopamine receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Eleventh Floor, 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/676,174A
; FILING DATE: 19910328
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/5683/79117/KIK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)861-3000
; TELEFAX: (202)822-8944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3335 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 319..2121
; US-07-676-174A-1
;
Query Match 12.8%; Score 173; DB 1; Length 3335;
Best Local Similarity 56.2%; Pred. No. 3e-23;
Matches 351; Conservative 0; Mismatches 265; Indels 9; Gaps 1;
QY 128 TATGCTGCTACCGCTGTCGCAACGTCCTGTCATATCGCCCTGTTTCACGAGCCGCG 187
DB 674 TATGCTGCTACCGCTGTCGCAACGTCCTGTCATATCGCCCTGTTTCACGAGCCG 733
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Db 255 CGAGGTGTACTGGGCTCGACGTCCTTCTGACAGCTGCTCCATCGTGCACCTGTTGGC 314
QY 378 CATGAGCTTGAGCCGCTACTGTTGCTCATACACAGAGCCCATGAGTACAACTGAAAGGCAC 437
Db 315 CATGAGCTTGAGCCGCTACTGTTGCTCATACGAGCCGCTGAGTACAACTGAAAGGCAC 374
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QY 498 CCGCGCGCTATCTCCATCAAGAAAGAGGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCG 557
Db 435 GCGCGCGCTATCT-----ACAAGGCGGACGAGGCGCGCGCGCGCGCGCGCGCGCGCG 485
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Db 486 CCAATGCAAGCTCAACAGAGAGGCGCTGTACATCTGGGCTCCAGAGATGGATCTTCTT 545
QY 618 GCGTCCCTGCTATATGATCTCTGGCTCTACGTCGATCTACCAAGTCCAGAGCTG 677
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QY 761 GCGCGCGCGAGCGGCGCGG-----GCGCGAGAGCGCGCAACCGTGGCCAC 812
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RESULT 2
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; Sequence 1, Application US/09825923
; Patent No. US2001001638A1
; GENERAL INFORMATION:
; APPLICANT: Snapir, Amir
; APPLICANT: Heilonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Matti
; APPLICANT: Pesonen, Markku
; APPLICANT: Scheinin, Mika
; APPLICANT: Salonen, Jukka T
; APPLICANT: Tuominen, Tomi-Pekka
; APPLICANT: Lakka, Timo A
; APPLICANT: Nyys"nen, Kristina
; APPLICANT: Salonen, Riitta
; APPLICANT: Kauphanen, Jussi
; APPLICANT: Valkonen, Veli-Pekka
; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
; TITLE OF INVENTION: protein, and uses thereof
; FILE REFERENCE: Alpha-2B-AR variant
; CURRENT APPLICATION NUMBER: US/09/825,923
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/422,985
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1341)
; OTHER INFORMATION: Coding sequence for variant human
; OTHER INFORMATION: alpha-2B-adrenoceptor protein
US-09-825-923-1

Query Match 33.0%; Score 446; DB 10; Length 1344;
Best Local Similarity 62.9%; Pred. No. 2,4e-78;
Matches 827; Conservative 0; Mismatches 415; Indels 72; Gaps 6;

QY 78 CCCTTACTCCCTGCAAGGTGAGCTGACGCTGTGTGCTGCTGCGGCTGCTCATGCTGCT 137
Db 15 CCGCTACTCCGTCGACGAGCGCGCCATAGCGGCGCCATCACTTCTCATTTCTTCTT 74
QY 138 CACCGTGTGGCAACGTCCTGTCATCATCGCGTGTTCAGAGCGCGCGCTCAAGGC 197
Db 75 TACCATCTTCGGCAAGCGCTGTCGTATCTGCTGCTGTGTGACGAGCGGCTGCTGCGCG 134
QY 198 GCGCCAAACCTCTTCTGCTGTGCTGCTGCGCGCGACATCTGCTGCTGCGCGCTGCT 257
Db 135 CCGCTAGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 194
QY 258 CATCCCTTCTGCGTGGCGCAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 317
Db 195 CATCCCTTCTGCTGCGCGCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 254
QY 318 CGAGATCTAAGCTGGGCTCGACGTCCTTCTGACAGCTGCTCCATCGTGCACCTGTTGGC 377
Db 255 CGAGGTGTACTGGGCTCGACGTCCTTCTGACAGCTGCTCCATCGTGCACCTGTTGGC 314
QY 378 CATGAGCTTGAGCCGCTACTGTTGCTCATACACAGAGCCCATGAGTACAACTGAAAGGCAC 437
Db 315 CATGAGCTTGAGCCGCTACTGTTGCTCATACGAGCCGCTGAGTACAACTGAAAGGCAC 374
QY 438 GCGCGCGCGCATCAAGGCGCATCATCACCCTGTTGGGTATCTCGGCGCTCATCTTCCTT 497
Db 375 CCGCGCGCGCATCAAGGCGCATCTCTCTGTTGGCTTATCGCGCGCTCATCTTCGCT 434
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498 CCCGCCCTCATCTCCATCGAGAGAGAGCGCGCGCGCCCGCCAGCCGCGCCAGCC 557
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499 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
435 GCCGCCCTCATCT-----ACAAAGGCGGACCAAGGCGCCCGCCAGCGCGCGCGCC 485
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
558 GCGCTGCGAGATCAACGACGACGACAAATGATGATCTCTCTCTCTCTCTCTCTCT 617
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
486 CCAGTGCAGGTCACGAGAGAGCGCTGGTACATCTGCGCTCCACAGATCGATCTTCTT 545
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
618 CCGCTCCCTGCTCATGATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 677
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546 TCGCTCTTCCCTCATGATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 605
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678 CACCCGCGTGCACCA-----GCCGCCGGGCTCCGAGCGCCGCTG 718
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606 CAAACGAGAGAGTCCAGAGGCGCAAGGAGGCGCTGGGAGGCTGAGTCCAGACAGCCCG 665
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719 CCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 760
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
666 ACCCGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 725
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
761 GCCCGGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 812
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726 TCCGAGAGAGTCAACGAGACACTGCAATGCACTGGGAGAGAGAGAGAGAGAGAGAG 785
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
813 CCAAGTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 872
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786 TGAAGATCTGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 845
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873 GGAAGTGGAGAGAGTCTGCTTCCGACAGCGCGAGAGGCGCGCGCGCGCGCGCGCGAG 932
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846 GAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 905
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933 CGAGCGCGGCTCCCGGCGCAAGAGAGCGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 992
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906 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 965
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993 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1052
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966 CCGCGTGAAGAGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1025
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1053 GAGCGCGCGTCCCGGCGCAAGAGAGCGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 1103
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1026 GCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1085
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1104 CGAGAGAGCGCTTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1163
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1086 GAGAGAGAGCGCTTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1145
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1164 CCGCTTCTTCTTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1214
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1146 CCGCTTCTTCTTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1205
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1215 CAGCGCTTCTTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1274
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1206 TCGCTTCTTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1265
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1275 CTAACACATCTTCAACGAGATTTCCGCGCGCGCTTCAAGAGATCTCTGCTG 1328
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1266 CTACACCATCTTCAACGAGAGATTTCCGCGCGCTTCCGAGAGATCTCTGCTG 1319
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RESULT 3
US-10-077-870-3
; Sequence 3, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077, 870
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; PRIOR FILING DATE: 2001-02-20
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; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1350)
; OTHER INFORMATION: Coding sequence for human alpha-2b-adrenoceptor protein
US-10-077-870-3

Query Match      32.9%; Score 444.6; DB 9; Length 1353;
Best Local Similarity 63.3%; Pred. No. 4,5e-78;
Matches 838; Conservative 0; Mismatches 404; Indels 81; Gaps 7;

QY 78 CCTTACTCCCTGAGAGTACGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 137
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 15 CCGCTACTCCGTCGAGCGCACAGCGCGCATAGCGCGCATACCTTCTCATTTCTTCT 74
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 138 CAGCGTGTGGGCAAGTGTGCTGATCATGCGCGGTTCACGAGCGCGCGCTCAAGGC 197
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DB 75 TACCATCTTGAGCAACCTTGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 134
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 198 GCCCAAAACCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 257
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 135 CCGTCAAGACCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 194
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 258 CATCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 317
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 195 CATCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 254
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 318 CGAGATCTTACCTGCGCTGACAGCTGCTCTTCTGACAGCTGCTGCTGCTGCTGCTGCTG 377
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 255 CGAGGTCTTACCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 314
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 378 CATACGCTTGAAGCGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 437
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 315 CATACGCTTGAAGCGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 374
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QY 438 GCGCGCGCGATCAAGGCGCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 497
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 375 CCGCGCGCGATCAAGGCGCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 434
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QY 498 CCGCGCGCGATCAAGGCGCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 557
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DB 435 GCGCGCGCGATCAAGGCGCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 485
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QY 558 GCGCTGCGAGATCAAGGCGCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 617
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 486 CCAATGCAAGCTCAAGGCGCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 545
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 618 CCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 677
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 546 TCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 605
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QY 678 CAGCGCGTGCACCA-----GCCGCCGGGCTCCGAGCGCCGCTGAGCGCGCTG 718
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 606 CAAACGAGAGAGTCCAGAGGCGCAAGGAGGCGCTGGGAGAGGTGATCCAGACAGCCCG 665
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 719 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 760
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DB 666 ACCCGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 725
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QY 761 GCCCGGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 813
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DB 726 TCGCAGAGAGTCAACGAGATCTGAGTCCACTTGGGAGAGAGAGAGAGAGAGAGAGAG 785
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QY 814 CAGCTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 873
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 786 TGAAGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 845
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QY 874 GACCTGAGAGAGAGTCTGCTTCCGACACGCGGAGCGCGCTCCAGAGGCGCGCAGAGCC 933
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Db      846 GGGCGAAGAGAGGAGTGTGTTGGGGCATCTCCAGAGAGATGAAGCTGAAGAGAGAGAGA 905
QY      934 GAGCGCGGTCCCGGGGCAAGAGCAAGCCCGAGCCAGCCAGGTGAAGCCGGCGAGACG 993
Db      906 GGAGAGAGAGAGAGAGAGAGTGTGAACCCAGGAGTGCCATGTCTCCGGGCTCAGC 965
QY      994 CTGCGCGGCGCGGGCGGGGCGAGCGGGGATCGGG-----ACGCCGGCT 1038
Db      966 TTGACGCCCCCGCTGCAGCAGCCACAGGGCTCCCCGGGTCTGGCCACCTACGTGGCCA 1025
QY      1039 GCAGGCGCGGGGAGAGAGCGGCTCG-----GGCTGCCAAGGCGTCCGGCTGGCGGGGCG 1094
Db      1026 GGTGCTCTGGGCAAGGGGCGTGGGCGCTATAGAGTGGGAGAGTGGGCTGACAGGGCGCA 1085
QY      1095 GCAGAACCGGCAAGAGAGGCTTACAGTTCGTCTGGCGGTGCTATCGAGATGTTCTGGGT 1154
Db      1086 GCTGACCGGGAGAGAGCGCTTACCTTCGTCTGTGTCTATTTGGCTTTTGTGCT 1145
QY      1155 GTGCGGTTCCTCTCTCTACCTTACAGCTCAGCGCTCGCGG-----TGCTC 1205
Db      1146 CTGCTGGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1205
QY      1206 CGTGCGACGACGCTCTTCAAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1265
Db      1206 GGTGCGCATGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1265
QY      1266 CCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1325
Db      1266 CCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1325
QY      1326 TCG 1328
Db      1326 CCG 1328

RESULT 4
US-09-825-923-3
; Sequence 3, Application US/09825923
; Patent No. US20010016338A1
; GENERAL INFORMATION:
; APPLICANT: Snapir, Amir
; APPLICANT: Heinonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Matti
; APPLICANT: Koulu, Markku
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Scheinin, Mika
; APPLICANT: Salonen, Jukka T
; APPLICANT: Tuomainen, Tomi-Pekka
; APPLICANT: Laakka, Timo A
; APPLICANT: Nyysanen, Kristina
; APPLICANT: Salonen, Riitta
; APPLICANT: Kauhanen, Jussi
; APPLICANT: Valkonen, Veli-Pekka
; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
; FILE REFERENCE: Alpha-2B-AR variant
; CURRENT APPLICATION NUMBER: US/09/825,923
; PRIORITY FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/422,985
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1350)
; OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
; OTHER INFORMATION: protein
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US-09-825-923-3
Query Match      32.9%: Score 444.6; DB 10; Length 1353;
Best Local Similarity 63.3%: Pred No. 4,5e-78;
Matches 838; Conservative 0; Mismatches 400; Indels 81; Gaps 7;
QY      78 CCGTTACTCCCTGACAGTACGCTGAGCTGTGTGCTTGGCGGCTGTCTATCTGCT 137
Db      15 CCGCTACTCGGAGAGCCAGAGCCGATAGCGGGGCGCATACCTTCTCTCTCTCTCT 74
QY      138 CACCGTGTGCGCAAGCTCTGTATCATTCGCGGTGTACAGAGCCGGCGCTCAAGC 197
Db      75 TACCATCTTCGGCAAGCGCTGTGTATCTGTGCTGTGTGACACCGCTCGCTCGCGC 134
QY      198 GCGCCAAACCTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 257
Db      135 CCGTCAAGAACCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 194
QY      258 CATCCCTTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 317
Db      195 CATCCCTTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 254
QY      318 CGAGATCTACGTGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 377
Db      255 CGAGGTGTACGTGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 314
QY      378 CATCAGCTGTGACCGCTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 437
Db      315 CATCAGCTGTGACCGCTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 374
QY      438 GCGCGCGCGCATCAAGGCGATCATCATACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 497
Db      375 CCGCGCGCGCATCAAGGCGATCATCATACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 434
QY      498 CCGCGCGCGCATCAAGGCGATCATCATACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 557
Db      435 GCGCGCGCGCATCAAGGCGATCATCATACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 485
QY      558 GCGCTGTGAGATCAAGGCGATCATCATACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 617
Db      486 CAGTCAAGGCGATCAAGGCGATCATCATACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 545
QY      618 CGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 677
Db      546 TGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 605
QY      678 CACCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 718
Db      606 CACCGCGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 665
QY      719 CCGCGCGCGCGCGGGG-----CACGAGCGCAAGCGCCAAAGGCTGTGG 760
Db      666 ACCCGACCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 725
QY      761 GCGCGAGGCGAGCGGGGCGCGGG-----GGGCGAGAGGCGGAACCGTGTGCCAC 813
Db      726 TGCAGAGAGGTCAAGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 785
QY      814 CAGCTCAAGGCGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 873
Db      786 TGAAGTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 845
QY      874 GACCTGTGAGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 933
Db      846 GGGCGAAGAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 905
QY      934 GAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 993
Db      906 GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 965
QY      994 CTGCGCGGCGCGGGGCGAGCGGGGATCGGG-----ACGCCGGCT 1038
Db      966 TTGACGCCCCCGCTGCAGCAGCCACAGGGCTCCGGGTGTGTGTGTGTGTGTGTGTGTGT 1025
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Qy	1039	GCACGGCGGGGAGAGCGCGTGG-----GGCTGCCAAGCGCGTGGCGCGGGCG	1094
Db	1026	GGTCTCTCTTGGGAGGGGCGCTGGGTCTATAGTGTGGGCGAGTGTGGCTCCAGCGGGCGCA	1085
Qy	1095	GCACACCGGAGAGAGCGCTTACGTTTCGTGGTGGCGCGTGGCATCGGAGTTCGTGGT	1154
Db	1086	GCTACCCGGAGAGAGCGCTTACCTTCGTCGTGGTGGTGGCATGGCGTTTTTGTGCT	1145
Qy	1155	GTGCTGGTTCCTTCTTCTTCTTCACTACACAGCTCAAGCGCGCGGG-----TGCTC	1205
Db	1146	CTGCTGGTTCCCTTCTTCTTCAAGCTACAGCCTGGGCGCGCATCTGCCGAAGCACTGGCA	1205
Qy	1206	GTGCGACGACGACGCTTCAAAATCTTCTTGTGGTTCGGCTACTCAACAGCTCGTTGA	1265
Db	1206	GGTCCCCCATGGCGCTTCCAGTTCTTCTTGTGGATGGCTACTCAACAGCTCACTGA	1265
Qy	1266	CCCGGTATCTACACCATCTTCAACACGATTTCCGGCGCGCTTCAAGAAAGATCTCTG	1325
Db	1266	CCCTGTTATCTACACCATCTTCAACACGAGACTTCGCGCTTCGAGAGATCTCTG	1325
Qy	1326	TCG 1328	
Db	1326	CCG 1328	

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RESULT 5
US-09-954-531-995
; Sequence 995; Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
APPLICANT: Weaver, Zoe
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
FILE REFERENCE: 689290-77
CURRENT APPLICATION NUMBER: US/09/954,531
CURRENT FILING DATE: 2002-05-02
PRIORITY APPLICATION NUMBER: US/60/233,133
PRIORITY FILING DATE: 2000-09-18
PRIORITY APPLICATION NUMBER: US/60/234,009
PRIORITY FILING DATE: 2000-09-20
PRIORITY APPLICATION NUMBER: US/60/234,034
PRIORITY FILING DATE: 2000-09-20
PRIORITY APPLICATION NUMBER: US/60/234,509
PRIORITY FILING DATE: 2000-09-22
PRIORITY APPLICATION NUMBER: US/60/234,567
PRIORITY FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 1392
SOFTWARE: PatentIn version 3.0
SEQ ID NO 995
LENGTH: 2625
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-531-995

Query Match      12.7%; Score 171.8; DB 9; Length 2625;
Best Local Similarity 48.8%; Pred. No. 4.3e-25;
Matches 594; Conservative 0; Mismatches 602; Indels 21; Gaps 4;

OY    115 CTGGCCGCCCTGCTCATGCTCTCACCAGTGTTCGGCAACGTCGTCATCATATGCGCGTG 174
      ||| | ||||| ||| ||| ||||| ||||| ||| ||| ||| ||| ||| ||| ||| |||
Db     283 CTGCTCACCCCTGCATCATGCTGTCATCTTCGGAACGTCGTCATGATGCGCTG 342
      ||| | ||||| ||| ||| ||||| ||||| ||| ||| ||| ||| ||| ||| ||| |||

OY    175 TTCACGAGCCCCGCGTCATCAGCGCCCAAAACCTCTTCGCGGTGCTTCGGCCCTCGGCC 234
      ||| | ||||| ||| ||| ||||| ||||| ||| ||| ||| ||| ||| ||| ||| |||
Db     343 TCCCGCGAGAAGGCGCGTCAGAACCAACCACTACTGATGTCAGCGCTCGCAGTGGCC 402
      ||| | ||||| ||| ||| ||||| ||||| ||| ||| ||| ||| ||| ||| ||| |||

OY    235 GACATCTCTGATGGCCAGCGTCGTCATCCCTTTCTCGCGTCGGCCAAGAGTCATGGCGTAC 294
      ||| ||||| ||| ||| ||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db     403 GACCTCGTCGTCGACACAGCTGTCATGGCCCTGGGGTTGTCACCTGGAAGGTGTAAGTGA 462
      ||| ||||| ||| ||| ||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY    295 TGCTACTTCGGCAAGGCTTGCTGTCGAGATCTACCTGGCGCTCGACGTCGCTCTTGCGACG 354
      ||| ||||| ||| ||| ||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Dd	463	TGGAAATTCAAGCAGAGATTCACTGTGACATCTTGATCTACTCTGGACGTCATGATGTGCAGC	522
Qy	355	TCGTGCATCGGTGCACACTGTGTGCACATCAGCCTTGAGCCGCTACTGGTCCATGCACACAGCC	414
Dd	523	GCAGACACTCCTGAACCTGTGTGGCATTACAGATCGACAGGTACACAGCTGTGTGGCCATCGCC	582
Qy	415	ATCGAGTCAACCTGGAAGGCGACCGCGCGCGGATCAAGGCCATCATCATCACTACCGTGTGG	474
Dd	583	ATGTGTATCAATATACGGCCTACAGCTCCAAAGCGCGGGGTCAACCGTATGATCTCCATCTCTC	642
Qy	475	GTCACTCTGGCGGCTCATCTCTCTCCGCGCGCTCATCTTCATCGAAGAAGAAGGCGGGCGC	534
Dd	643	TGGGTCTGTCTCTTACACATCTCTCTGCGCCACTCTCTTTGGAGCTCAATATACGACAGACAG	702
Qy	535	GCGCGCCCGCAGCGCGCCGAGCGCGCTGTGAGATCAACGACAGAGAAGTGTGATCTCATC	594
Dd	703	AACGATGTGCATCATTTGGCCAAACCCGGCGCTTGTGTGTACTC-----TCTTCATCTC	750
Qy	595	TGTGTGTGCATCTGGCTCTCTCTTCTGCTCCCTGTGCTCATATCATCTGTGTACTGTGGC	654
Dd	751	GTCTCTCTTACGTGTGCGCTTCATTTGTACCTCTGTCTGTCTTACATCAAGATCTTACATTTGTC	810
Qy	655	ATCTACACGATCGGCACAGCTGTGCGACCGCGGCTGCCACCCAGCGCGCGGGGTTCGGAGCC	714
Dd	811	CTCGCAGAGCGCCGCAAGCGCAGTCTAACACCAAAACGAGACGCGAGCTTTCAGGGCCAC	870
Qy	715	GTCTCGCGCGCGCGCGGGGGACCGCAGACGCGAGGCGCCAAAGGTGTGTGGCCCCGAGCGCAGC	774
Dd	871	CTGAGGGGTCTCCACTTAAAGGGGCAACTGTACTACACCCCCGAGACATGAATACTGTGACCTGT	930
Qy	775	GCGGGCCCGGGGGGGCGCAGAGGGCGGAACCGCTGTGCCACCCAGCTCAAGAGGGCGCCCTGTGC	834
Dd	931	ATCATGAAGTCTAATGGGAGTTTCCAGTGTACAGAGCGGAGAGTGGAGGCTGTGCCGGCGA	990
Qy	835	GAGCCCGCGCGCGCGCGGGCGCGCGCAGACCGACGCGCTGGACTGTGAGAGAGAGCTGTCT	894
Dd	991	GCCAGAGAGCTGTGAGATGTGTCTCTCAGCACCAGCCACCCGAGAGAGCCGGGTAC	1050
Qy	895	TCCGACCCAGCGCGAGCGGCTCCAGGGGCCCGCAGACCCGAGCGGGGTCTCCCGGGGGCAAA	954
Dd	1051	AGCCCCATCCACCCACCCACACACACAGCTGTACTCTCCCGACCGCTCCACACAGCTGTCTC	1110
Qy	955	GGCAGAGCGCGAGCGAGCCAGAGTGAAGCCGGCGGAGACA-----GCTGTGCGGGCGGGGCGC	1010
Dd	1111	CACAGCACTCCTGTACACCCCGCCCAACCAAGAAAGAAATAGGGCAATGCCAAAGACCACCC	1170
Qy	1011	GGGGGCGAGCGGGGATCGGGAGCGCGGCGTGCAGGGGCCGGGGGAGAGCGCGTCTGGGGGCTGC	1070
Dd	1171	AAGATTTGCCAAGATCTTTGTGATTCAGAGACCATGCCAATGGCAAAACCGGGACCTCTCTC	1230
Qy	1071	CAAGGC--GTGCGCTGTGGCGCGGGCGGGCGAGAAACCGGAGAAACCGCTTTCACATGTGTGTG	1128
Dd	1231	AAGACCATGAGCCTTAAGAAAGCTCTCCACGACAAAGAGAAAGAAACCACTCATAGTGTCTC	1290
Qy	1129	GCGGTGTGCATCGAGAGTGTCTGT	1187
Dd	1291	GCAATTTGTCTCGCGCGTTCATCATCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1350
Qy	1188	--CACGGCGGT	1245
Dd	1351	AACATACACTGTGTACTGTCAACATCCGCGCTGTCTGTACAGCGCCTTACAGTGTGTGTGGC	1410
Qy	1246	TATGTGCAACAGCTGTGTGAACCGCGGTGCATCTACACATTTCAACACAGATTTGTGTGTGTGT	1305
Dd	1411	TATGTGCAACAGCGCGCGTGAACCCCATCATCATCTACACACCTTCAACATTTGATGTGTGTGTGT	1470
Qy	1306	GCGTTCAAGAGATCTCT 1322	
Dd	1471	GCGTTCTGGAAGATCTCT 1487	

RESULT 6
US-09-349-755-3

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; Sequence 3, Application US/09349755
; Patent No. US20020166131A1
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/349,755
; FILING DATE: 08-Jul-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,780
; FILING DATE: <Unknown>
; APPLICATION TYPE: US 08/985,090
; FILING DATE: 04-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: NMT-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-349-755-3

Query Match      12.3%; Score 166.4; DB 9; Length 1335;
Best Local Similarity 51.3%; Pred. No. 4.4e-24;
Matches 439; Conservative 0; Mismatches 411; Indels 6; Gaps 2;

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Db 306 CGGCGGGGCGCTCTGCAAGCTGTGGCTGTAGTGACTACCTGCTGTGACCTCTCTGCG 365
QY 363 CGTGCACCTGTGCGGCATCAGCTGTGAGCGGTACTGTGCTCATACAGCGCATGAGTA 422
Db 366 CTTCAACATCTGTCTCATAGCTACAGCGCTTCTGTGCGTCAACGAGGCTCTATA 425
QY 423 C---AACCTGAAGCGCACCGCGCGCGCATCAAGCGCATCATCAACCGTGGTCAAT 479
Db 426 CCGGGCCAGAGAGGTGACACAGCGCGCGCGAGTGGGAGAAATGCTGCTGTGGGTGCT 485
QY 480 CTCGGCGCTCATCTCTCTTCCCGCGCTCATCTCCATCGAAGAAAGGCGGCGCGCG 539
Db 486 GCGCTTCTGTGTGTAGCGAGCGCATCTAGCTGGGAGTACCTGTGCGGCGCACCTC 545
QY 540 CCGGAGCGCGCGCGCGCGCGCTGAGATCAAGACAGACAGAGTGTACGATCTGTGTC 599
Db 546 CATCCCGAGAGGCGCACCTCTATGCGGAGTCTTCTACAGACGTACTTCTCATACAGGC 605
QY 600 GTGATCGGCTCTCTCTTCTGCTCCCTGCTCATCATATGATCTGTGCTTACGTGCGCATCTA 659
Db 606 TTCCACCTTGAGGTTCTTTACGCGCTTCTCAGCGTCACTTCTTAACTCAGACATCTTA 665
QY 660 CCAGATCGCCAAAGGTGTGCGACCGCGTGCACACCGAGCGCGGCGTCCGAGCGCGTCCG 719
Db 666 CCGTGAACATCCAGAGGCGCACCGCTCTCGGCTGTGAGTGGGCTCAGAGCGAGCGCGCC 725
QY 720 CGCGCGCGCGGGGGGCGACAGCGCG---AGGCGCAAGGGTCTGGGCGCGCGCGAGCGCAGCGC 776
Db 726 CGAGCGCGCTCCCGAGGCGCGACCGCTTCACACCGCGCTGCTGCTGCTGCTGCTGCTG 785
QY 777 GGGCGCGGGGGGCGCAGAGCGCGCAACCGCTGTCCCAACCGCTCAACGCGCGCGCTGCGCA 836
Db 786 GCAGAGAGGGGCGCAGGGGCGCGCATCGCTGCACAGATATGGGTGGTGAAGCGCGCGCT 845
QY 837 GCGCGCGCGCGCGCGCGG 852
Db 846 AGCGCTGAGCGCGG 861

RESULT 7
US-09-166-334-3
; Sequence 3, Application US/09166334
; Patent No. US20020168708A1
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,334
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,780
; FILING DATE:
; APPLICATION TYPE: US 08/985,090
; FILING DATE: 04-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: NMT-032CP
; TELECOMMUNICATION INFORMATION:

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? TELEPHONE: (617)227-7400
 ? TELEFAX: (617)742-4214
 ? INFORMATION FOR SEQ ID NO: 3:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 1335 base pairs
 ? TYPE: nucleic acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: cDNA
 ? FEATURE:
 ? NAME/KEY: CDS
 ? LOCATION: 1..1335
 ? US-09-166-334-3

Query Match 12.3% Score 166.4; DB 9; Length 1335;
 Best Local Similarity 51.3%; Pred. No. 4,4e-24;
 Matches 439; Conservative 0; Mismatches 411; Indels 6; Gaps 2;

QY 3 GGGCTCCCTGCAAGCCGCGGCGGCAAGCGAGCTGGAACGGGAGCCGCGGGGG 62
 DB 6 GCGCGGCGCGCGCGGAGCGGCGGTGAAGCTTCGGGGGGCTGGCGGGGAGCGCGGCG 65
 QY 63 GCGCGCGCGCGCGCGCTTACTCCCTGCAAGTGAAGCTGACGCTGAGCTGGCTGGCGCGG 122
 DB 66 GCGCGCGCGCGCGCGCTTCTCGGCAAGCTGACCGCGGCTGGCGCGCTCATGGC 125
 QY 123 CCGTGTATGCTGCTGCAAGCGGTGTCGCAAGTGTGCTCATCATCGCGCTGTACAGAG 182
 DB 126 GCTGCTATGCTGCGCAAGCTGTGGCAAGCGGCTGCTGATGCTGCGCTTGTGGCGGA 185
 QY 183 CCGCGCGCTCAAGGCGCGCGCAAAACCTTCTGTGTCTGTGCTGCGCGCGAGATCT 242
 DB 186 CTGAGCTCTCGGACCGCAAGAACATTTCTTCTGCTCAACCTGCGCATCTCGAGCTTCT 245
 QY 243 GGTGGCGAGCTGCTGATCCCTTTCTGCTGCGCAAGAGTCAATGGCTACTGTACTT 302
 DB 246 GCTGGCGCTTCTGCTGATCCCACTGTATGTACCTTACGCTGCAAGCGCGCTGACCTT 305
 QY 303 CCGCAAGGCTTGGTGGAGATCTACCTGGCGCTCGACGCTCTTCTGCAAGCTGCTCA 362
 DB 306 CCGCGCGCGCGCTTGTCAACCTGTGGTGTGAGTGAAGTCACTGCTGTGCACTCTCTGC 365
 QY 363 CGTGACCTGTGGCGCAAGCTTGAAGCTGCTGCTGCTCAACAGAGCCATCGAGTA 422
 DB 366 CTTCACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 425
 QY 423 C---AACCTGAAGCGCAAGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 479
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 QY 480 CTGCGCGCTGATCTCTTCCGCGCTCATCTCAATCGAAGAGAGGCGCGCGCGCG 539
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 QY 600 GTGATCGAGCTCTTCTGCTCCGCTCATGATGATCGGTGCTGCTGCTGCTGCTGCT 659
 DB 606 TTTCACCTCTGAGATCTTTTACGCTCTTCTCTCAAGCTCACTTTTAACTTACGATCT 665
 QY 660 CCAAGATCGCAAGAGCTGCAAGCGCGGTGCGACCGCGCGGGTCCGAGCGCGTGC 719
 DB 666 CCGAATCATTCAGAGGCGGAGCGCGCTCGGCTGAGTGGGGCTCGAGAGGAGCGCGGCC 725
 QY 720 CCGCGCGCGCGGGGAGCGAGCGC---AGCGCCAAAGGCTGTGGCGCGCGAGCGCGC 776
 DB 726 CAGAGCCCTTCCCGAGAGCGCAAGCTTCAACACCGCACCGCTGTGTGGGCTGTG 785
 QY 777 GGGCGCGCGGGGCGAGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 836
 DB 786 GCAAGAGGGGAGCGGGGAGGCGATGCGCTGCTGCAAGGTATGGGGTGGGTGAGGGCGCT 845

QY 837 GCCCGCGCGCGCGG 852
 DB 846 AGCGCTGAGCGCGG 861

RESULT 8
 US-09-350-206-3
 ; Sequence 3, Application US/09350206
 ; Patent No. US2002099199A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
 ; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
 ; NUMBER OF SEQUENCES: 39
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; STREET: 28 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/350,206
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/042,780
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Elizabeth A. Hanley
 ; REGISTRATION NUMBER: 33,505
 ; REFERENCE/DOCKET NUMBER: MNI-032CP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)742-4214
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1335 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..1335
 ; US-09-350-206-3

Query Match 12.3% Score 166.4; DB 10; Length 1335;
 Best Local Similarity 51.3%; Pred. No. 4,4e-24;
 Matches 439; Conservative 0; Mismatches 411; Indels 6; Gaps 2;

QY 3 GGGCTCCCTGCAAGCGCGGCGGCAAGCGAGCTGGAAGGAGCGAGGCGCGGGGG 62
 DB 6 GCGCGCGCGCGCGAGCGGCGCTGAAGCGCTTGGGGGCGCTGGCGAGCGGCGGCG 65
 QY 63 GCGCGCGCGCGCGAGCGCTTACTCCCTGCAAGTGAAGCTGACGCTGAGCTGTGCTGGCGG 122
 DB 66 GCGCGCGCGCGCGCGCTTCTCGGCAAGCTGAGCGCGGCTGGCGCGGCTCATGGC 125
 QY 123 CCGTGTATGCTGCTCAAGCGGTTCGGCAAGTGTCTGTATATTCGCGCTGTTCAGAG 182
 DB 126 GCTGCTATGCTGCGCAAGGCTGTGGGCAAGCGCTGTATGCTGCTGCTGCTGCGCGGA 185
 QY 183 CCGCGCGCTCAAGGCGCGCGCAAAACCTTCTGCTGCTGCTGCTGCTGCGCGCAATCT 242
 DB 186 CTGAGCTCTCGGACCGCAAGAACATTTCTTCTGCTCAACCTGCGCATCTCGACTTCT 245
 QY 243 GGTGGCACGCTGCTATCCCTTTCTGCTGCGCAAGAGGTCAATGGGCTACTGTACTT 302

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OY 363 CGTGACCTGTGTGCGCATCAGCTGTGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 422
Db 366 CTTCACATCTGT 425
OY 423 C---AACCTGAAGCGCACGCGCGCGCGCATCAAGCCATCATCATCATCATCATCAT 479
Db 426 CGGCG 485
OY 480 CTGCG 539
Db 486 GCGCTTCTGT 545
OY 540 CCG 599
Db 546 CATCCCG 605
OY 600 GTGATGCGCTGTCTTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 659
Db 606 TTCCACCTGTGAGTCTTCTTACCGCTTCTTACGCTCCTTCTTAACTCAGCATCTA 665
OY 660 CCAAGTCCGCAAGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 719
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OY 720 CG 776
Db 726 CGAGCG 785
OY 777 GGGCG 836
Db 786 GCAGAGAGGGGCG 845
OY 837 GCG 852
Db 846 AGCG 861

RESULT 9
US-09-349-755-1
Sequence 1, Application US/09349755
Patent No. US20020166131A1
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/349,755
FILING DATE: 08-Jul-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/042,780
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/985,090
FILING DATE: 04-DEC-1997

ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2689 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 291..1625
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-349-755-1
Query Match 12.3%; Score 166.4; DB 9; Length 2689;
Best Local Similarity 51.3%; Pred. No. 4.8e-24;
Matches 439; Conservative 0; Mismatches 411; Indels 6; Gaps 2;
OY 3 GGGCTCCCTGACAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 62
Db 296 GCG 355
OY 63 CGGCG 122
Db 356 GGGCG 415
OY 123 CTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 182
Db 416 GCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 475
OY 183 CG 242
Db 476 CTCGAGCTCCG 535
OY 243 GGTGGCGAGCTGTGATCCCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 302
Db 536 CGTGGCGCGCTTGTGATCCCTGATGATGATGATGATGATGATGATGATGATGAT 595
OY 303 CGGCAAGCTTGTGCGGATCTACCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 362
Db 596 CGGCG 655
OY 363 CGTGACCTGTGTGCGCATCAGCTGTGAGCGCGCTGTGTGTGTGTGTGTGTGTGT 422
Db 656 CTTCACATCTGTCTCATCAGCTGTGAGCGCGCTGTGTGTGTGTGTGTGTGTGT 715
OY 423 C---AACCTGAAGCGCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 479
Db 716 CGGCG 775
OY 480 CTGCG 539
Db 776 GCGCTTCTGT 835
OY 540 CCG 599
Db 836 CATCCCG 895
OY 600 GTGATGCGCTGTCTTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 659
Db 896 TTCCACCTGTGAGTCTTCTTACCGCTTCTTACCGCTTCTTAACTCAGCATCTA 955
OY 660 CCAAGTCCGCAAGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 719
Db 956 CTGGAACATCCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1015
OY 720 CGGCG 776

APPLICATION NUMBER: US/09/350,206
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNT-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2689 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 291..1625
US-09-350-206-1

Query Match 12.3%; Score 166.4; DB 10; Length 2689;
Best Local Similarity 51.3%; Pred. No. 4,8e-24;
Matches 433; Conservative 0; Mismatches 411; Indels 6; Gaps 2;

QY 3 GGGCTCCTCGAGCGGAGCGGGCAACGCGAGCTGAGACGGAGCGGAGCGGCGGCGG 62
DB 296 GCGGCGCGCGCGCGCGCGCGCGCTGAGAGCTGCGGGGCGCTGGCGGCGAGCGCGCG 355
QY 63 CGGGCGCGCGCGCGCGCGCGCGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 122
DB 356 GCGGCGCGCGCGCGCGCGCGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 415
QY 123 CTTGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 182
DB 416 GCTGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 475
QY 183 CCGCGCGCTCAAGCGCGCGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTG 242
DB 476 CTCGAGCGCTCGAGCGCGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTG 535
QY 243 GGTGGCCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 302
DB 536 CGTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 595
QY 303 CGGCGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 362
DB 596 CGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 655
QY 363 CGTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 422
DB 656 CTTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 715
QY 423 C---AACCTGAAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 479
DB 716 CCGGGCGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 775
QY 480 CTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 539
DB 776 GGCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 835
QY 540 CCGCGAGCG 599
DB 836 CATCCCGAGGCGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 855
QY 600 GTGCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 659
DB 896 TTCCACCGCTGAGCTTCTTACCGCTTCTGAGCGCTGAGCGCTTCTTACCGCTGAG 955

QY 660 CCAGATCGCCAGCGCTGCGACCGCGCGCTGCGACCGAGCGCGCGCGCGCGCGCGCTGCG 719
DB 956 CCTGAACATCGACGAGCGCGCGCGCGCTGCGAGCGCGCGCGCGCGCGCGCGCGCG 1015
QY 720 CG 776
DB 1016 CGAGCG 1075
QY 777 GGGCG 836
DB 1076 GGAGAGGCG 1135
QY 837 GCCCG 852
DB 1136 AGCGCGTGAAGCG 1151

RESULT 12
US-10-185-991-1
Sequence 1, Application US/10185991
Publication No. US20030022900A1
GENERAL INFORMATION:
APPLICANT: Charles Gluchowski, et al.
TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN PROSTATIC HYPERPLASIA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/185,991
FILING DATE: 28-Jun-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/444,783
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-AA-PCT-US/JPW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 178..1893
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-185-991-1

Query Match 11.4%; Score 153.4; DB 9; Length 2140;
Best Local Similarity 52.0%; Pred. No. 1.5e-21;
Matches 433; Conservative 0; Mismatches 376; Indels 24; Gaps 3;

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QY 18 GAGCGCGGCAACGCGAGCTGGAGACGAGCGCGCGGGGGGCGCGCGCGCGCGCGC 77
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Db 387 GAGCGCGGGGAGCGCGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 446
QY 78 CCCTTACTCCCTGAGAGTACGCTGACGCTGTGTGCTGCGCGCGCGCGCGCGCGCT 137
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Db 447 GGTGTGAGACGCGCGAGGCGGTGGGCGGTGGCGCTCTTCCCGCAGAGC--TTGATCCTTAT 503
QY 138 CACCGGTCTGGCAACGCTGCTGATCATGCGCGGTTCACAGACCGCGCGCGCTCAAGGC 197
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Db 504 GCGCGGTGAGAGTACCTCTGTCTCTCTGAGGCGCTGCAACCGCGCGCGCTCAAGC 563
QY 198 GCGCGCAAAACCTTCTGCTGTCTGTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCT 257
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Db 564 CGTACACCACTATTTCATGTGTAACCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 623
QY 258 CATCCCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 317
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Db 624 ACTGCGCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 683
QY 318 CGAGATCTACCTGCGCGCTGAGCTGCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 377
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Db 684 CGAGCGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 743
QY 378 CATCAAGCTGAGCGCGCTGAGTCCATCACAGCGCGCGCGCGCGCGCGCGCGCGCGCG 437
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Db 744 CATCTCCGTGAGACCGGTGAGTGGCGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 803
QY 438 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 497
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Db 804 CGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 863
QY 498 CCGCGCGCTCATCTCCATCGAGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 557
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Db 864 AGCGCGCGCT-----GCTGGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCG 908
QY 558 GCGCGCGCGAGATCAACGAGACGAGAGAGTGTGCTCATCTGCTGCTGCTGCTGCT 617
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Db 909 CTCTGCGGTATCACCGGAGAGCGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCT 968
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Db 969 CCGTGGCGATGGGCGGTATCTGTGTATCTGCGCGCGGTGAGTGTGCGCGCGCGAGC 1028
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Db 1029 CAGCGCGAGCGCTGAGGAGCGGTCAAGCGGAGGAGGAGGAGGAGGAGGAGGAGG 1088
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Db 1089 GCGCATCTCACTGTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1148
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RESULT 13
US-10-005-010-1

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; Sequence 1, Application US/10005010
; Patent No. US2002011519A1
; GENERAL INFORMATION:
; APPLICANT: Weishank et al, Richard L.
; TITLE OF INVENTION: Method of Obtaining A Composition Comprising A 5-HT1D
; FILE REFERENCE: 36536-BA
; CURRENT APPLICATION NUMBER: US/10/005,010
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/371,705
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1

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; LENGTH: 1645
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (284)..(1414)
US-10-005-010-1
Query Match      10.9%; Score 147.2; DB 12; Length 1645;
Best Local Similarity 52.9%; Pred. No. 2,4e-20;
Matches 348; Conservative 0; Mismatches 298; Indels 12; Gaps 1;

QY 67 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 126
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Db 365 GCTTGGATCCAGAGACCTCCAGCGCGCTCAAGATTCCTTGGCGGTGCTTTCGCT 424
QY 127 CTATGCTGTCAACCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 186
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Db 425 ATCACTAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 484
QY 187 GCGCTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 246
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Db 485 AAGCTCCACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 544
QY 247 GCCAGCGCTGCTATCCCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 306
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Db 545 TCCATCTTGGATGATGCCCATATGCGATGCGCTTATACATCCACACCGCTGGAATTTGGC 604
QY 307 AAGCGTTGGTGCAGATCTACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 366
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Db 605 CAATCTTGTGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 664
QY 367 CACTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 426
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Db 665 CATCTGTGTGATGCTGCTGCGAGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCG 724
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Db 785 TGCATCTTCATCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 804
QY 547 CCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 606
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Db 833 GAGATGTGCGAGCTGTGTGGAACCTCTCAATCTCTCAACATCTACCTCACCTGT 892
QY 607 GCGTCTTCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 666
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Db 893 GGGCGCTTTTCAATCTTCCCTGGGTGTGTCTATCATCTCTTAATGCGCGGATCTACCGGCT 952
QY 667 GCCAGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 724
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Db 953 GCGCGGAGACCGCATCTGATTCACCGCTCACTATGGAAGGCGCTTACACAGCGCGCC 1010

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RESULT 14
US-09-864-761-3769/c

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; Sequence 3769, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemilica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 05/60/180,312
; PRIOR FILING DATE: 2000-02-04

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; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 3769
; LENGTH: 1973
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL049576.15
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2
US-09-864-761-3769

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Query Match          10.9%; Score 147.2; DB 10; Length 1973;
Best Local Similarity 52.9%; Pred. No. 2.5e-20;
Matches 348; Conservative 0; Mismatches 298; Indels 12; Gaps 1;

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QY 67 GCCCGGCCACCCCTTACTCCGTCGACGAGTACGCTGACGCTGCTGCGCCGCGGCGCTG 126
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DB 1234 GCTTGGATCCAGAGACCCCTCCAGGCGCTCAAGATCTCCCTTCCGTGCTTTCCGCTC 1175
QY 127 CTCATGCTGCTCAACGCTTTCGCGACGTCGTCATCATCCGCTGTTTCACAGACCGC 186
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DB 1174 ATCACTGCGCACAGCTCTCCAAATGCTTGTACTCCACCACTTACTACACAG 1115
QY 187 GCGCTCAAGGCGCCCAAAACCTTCTCTGTCTGTGCTTGTGCGCCGACATCCGCTG 246
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DB 1114 AAGCTCCACACCCCTGCACTACTGATGCTCCCTGCGCACACCGACCTCTTGGTT 1055
QY 247 GCCAGCGTGCATCCCTTCTGCTGCGCAAGAGTCAAGGCTACTGACTTCCGCG 306
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DB 1054 TCCATCTTGGTAATGCCCATGACATGCTATACATCAACCAACACCTGGAACCTTGGC 995
QY 307 AAGGCTTGTGCGAGATCTACTGCGCTGACGCTGCTTCTTTCACAGTGTCCATCGT 366
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DB 994 CAATCTTGTGTGACATCTGCGTGTCTCTGACATCAACGCTGACAGCCTCCATCCTG 935
QY 367 CACCTGCGGCATACGCTTGAGCCGCTACTGCTTCATCAACAGGCCATCGAGTACAC 426
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DB 934 CATCTGTGTGCTATTGCTTGACAGGTACTGGGCATTCACAGATGCTCGAATACAGT 875
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DB 874 AAAGCGAGAGCGGCTGCGCACGCGCCACCATGATGCTCCATTTGCTGGCATCTCCATC 815
QY 487 GTCATCTCCTTCCCGCGCTCATCTCCATGAGAAAGAGGCGCGCGCGCGCCCGCAG 546
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DB 814 TGCACTTCATCCCGCTCCGCTTCTTGTGGCGGACAGCCAAAGC-----CGAAGAG 767
QY 547 CCGGCGGACCGCGCTGAGATCAACGACAGAAAGTGAAGTCACTCTGCTGTCATC 606
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DB 706 GGGGCTTCTCAATTCCTCGTGTCTCATCTCAATCTATATGAGCCGGAATCTACGGGCT 647
QY 667 GCCAAGCGTGCACCGCGCTGACCCAGCCGCGGCGGCGGAGCGCGCTGCGCGCGC 724
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RESULT 15
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; Sequence 13, Application US/09993844
; Patent No. US20020106739A1
; GENERAL INFORMATION:
; APPLICANT: Oakley, Robert H.
; APPLICANT: Barak, Lawrence S.
; APPLICANT: Laporte, Stephanie A.
; APPLICANT: Caron, Marc G.
; TITLE OF INVENTION: Modified G-protein Coupled Receptors
; FILE REFERENCE: 033072-026
; CURRENT APPLICATION NUMBER: US/09/993,844
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/245,772
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/260,363
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1185
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence of beta3-Ar-V2R chimera
US-09-993-844-13

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Query Match          10.5%; Score 142; DB 10; Length 1185;
Best Local Similarity 52.6%; Pred. No. 2.4e-19;
Matches 341; Conservative 0; Mismatches 295; Indels 12; Gaps 1;

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QY 169 GCGGTGTACAGGCGCGCGCTCAAGGCGCCCAAAACCTTCTTCTGTGCTTGCGCC 228
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QY 229 TCGGCGGACATCTGCTGCGACAGCTGTATCTCTTCTGCTGCGCCACAGAGTATG 288
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QY 289 GCGTATGCTACTTGGGCAAGGCTGTGTGAGATCTACTGCGCGCTGACGTGCTCTTC 348
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DB 301 GCGCACTGCGCTGTGCGCGCACCTGCTGCGAGCTGTGACCTGTGTGAGAGTGTGTGT 360
QY 349 TGCAGTGTGCTATGTCGACCTGTGCGCATCAACCTGAGACCGCTACTGCTCATCA 408
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DB 361 GTGACCGCGACGATGAAACCTGTGCGCGCTGTGCGCGTGTGAGACCGCTACTGCTGTAC 420

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OY 409 CAGGCCATCGAGTACACCTGAGCGCAGCGCCGCAATCAGGCCATCATCATCACC 468
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Db 421 AACCCGCTGCGTTACGGCGCACTGGTCAACAGCGCTGCGCCGAGACATGTGCTCTG 480
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OY 469 GTGTGGTCAATCTCGCCGTCATCTCCCTCCCGCGCTCATCTCATGAGAGAAGGGC 528
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Db 481 GTGTGGTGTGTGGCGCGGGGTGTGTTGGCCATCATAGCCAGTGGTGGCGGTA 540
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OY 529 GGGGGCGCGG-----GCCCGCAGCCGCGCGAGCCGCTGCGAGATCAACGAC 576
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Db 541 GGGGCCGAGCGCGAGCGCGAGCGCTGCGCACTGCAACCGCGCTGCTGCTTCGCTCC 600
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OY 577 CAGAACTGTACGTATCTGTCGTGTCATCGAGCTCTTCTTGCTGCCCTCATCATG 636
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Db 601 AACATGCCCTACGTGCTGCTGCTCTCCGTCCTCTCTACCTTCCTCTCGTGATG 660
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OY 637 ATCTGTGTCACGTGGGCATCTACAGATCGGCAAGCGTGCACCGCGGTGCCACCAGC 696
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Db 661 CTCTGTGTCACGCGCGGCTTTCGTGTGGCTACGCGCCAGCTGCGCTTGCTGCGCGG 720
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OY 697 CGCCGGGTCGCGAGCGCTGCGCCGCGCGCGCGGGGACCGAGCGC 744
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Db 721 GAAGTGGCGCGCTTCCGCCGAGAGTCTCCGCGCGCGCGCGCTGCGGC 768
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Job time : 111.871 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 11:01:28 ; Search time 11.7706 Seconds
(without alignments)
7844.310 Million cell updates/sec

Title: US-09-636-259B-2_COPY_730_770

Perfect score: 41

Sequence: 1 99999cacccagcagcagcc.....aagggtcggcccgagcg 41

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Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Length	DB ID	Description
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2	39.4	96.1	23	AA199917 Human alpha-2AAR e
3	25	14855	22	ABA5164 Human nervous syst
4	25	61.0	24	ABA93286 Human acetyl-Coenz
5	25	61.0	24	ABA93288 Human acetyl-Coenz
6	24.2	978	23	AB10491 Drosophila melanog
7	23.6	57.6	22	AAFA4733 Novel protein kina
8	23.4	57.1	24	AB047498 Oligonucleotide fo
9	23.4	1733	24	AB047499 Oligonucleotide fo

10	23.4	57.1	7353	24	ABL32072	Human immune syste
11	23.4	57.1	7353	24	AA028362	Human chemically t
12	22.4	54.6	36	21	AAZ94312	Rat cholecystokini
13	22.4	54.6	37	21	AAZ94369	Human alpha 2A adr
14	22.4	54.6	2286	23	AA567824	DNA encoding novel
15	22.4	54.6	2286	23	AA571762	DNA encoding novel
16	22.4	54.6	2286	23	AA571900	DNA encoding novel
17	22.4	54.6	2286	23	AA578340	DNA encoding novel
18	22.4	54.6	5661	20	AA579645	Human LKB1 gene fr
19	22.4	54.6	5661	24	ABA03936	Human STRK11 gene f
20	22.4	54.6	5935	24	ABA04007	Human immune/haema
21	22.2	54.1	1396	22	AAK65896	Human immune/haema
22	22.2	54.1	1396	22	AAK65897	Human immune/haema
23	22.2	54.1	1397	22	AAK65898	Human acetylcholin
24	22.2	54.1	12113	24	AA517492	Human genomic regi
25	22.2	54.1	155074	24	ABN55735	Pseudomonas aerugi
26	22	53.7	2622	23	AA554234	Porcine BAC-PIGF2-
27	21.8	53.2	450	21	AAAB5472	Human musculoskele
28	21.8	53.2	967	22	AAH35843	Human CDNA sequenc
29	21.8	53.2	2651	22	AAH18567	Human CDNA clone (
30	21.6	52.7	890	22	AAH03553	Oligonucleotide fo
31	21.6	52.7	1733	24	AB047500	Oligonucleotide fo
32	21.6	52.7	1733	24	AB047501	Human CDNA sequenc
33	21.6	52.7	1733	24	AAH13763	Human immune syste
34	21.6	52.7	1733	24	ABL32073	Human chemically t
35	21.6	52.7	7353	24	AAV34854	Human retinal deg
36	21.4	52.2	4190	19	AAV34854	DNA encoding novel
37	21.4	52.2	10672	23	AA583705	Corn tassal-derive
38	21.2	51.7	224	24	ABL74394	Malassezia fungus
39	21.2	51.7	1008	18	AAH85901	Human colon cancer
40	21.2	51.7	1075	22	AAH33653	Human ovarian anti
41	21.2	51.7	1075	24	AB054187	Human RARL1d6 (reg
42	21.2	51.7	2254	24	AAV39359	Human DNA sequence
43	21.2	51.7	3668	24	AA594806	Drosophila melanog
44	21	51.2	844	23	ABL06697	Drosophila melanog
45	21	51.2	2173	23	ABL06696	Drosophila melanog

ALIGNMENTS

RESULT 1
AA199918
ID AA199918 standard; DNA: 1350 BP.
XX
AC AA199918;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human alpha-2AAR variant encoding DNA.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2AAR; chromosome 10; ds.
XX
KW
OS Homo sapiens.
XX
FH Key
FT CDS 1..1353 Location/Qualifiers
FT FT /*tag= a
FT FT /product= "alpha-2AAR"
FT FT replace(753,C)
FT FT /*tag= b
XX
PN WO200179561-A2.
XX
PD 25-OCT-2001.
XX
PF 17-APR-2001; 2001WO-US12575.
XX
PR 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.

```

PR 19-OCT-2000; 2000US-0692077.
XX
XX (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
XX Liggett SB, Small KM;
XX
XX WPI: 2001-611728/70.
DR P-PSDB; AAM52123.
XX
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
XX Disclosure; Page 152; 163pp; English.
XX
XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (II)
CC or a site comprising (A) (999gcg99gcg) or (B) (999gcgctgag) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfosine, idazoxan, tolazoline, phenolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2AAR variant
CC gene.
XX
XX Sequence 1350 BP; 199 A; 489 C; 442 G; 220 T; 0 other;
SQ
Query Match 100.0%; Score 41; DB 23; Length 1350;
Best Local Similarity 100.0%; Pred. No. 7.5e-05;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGGCACCAGCGAGCCCAAGGCTGTGGGCCCCGAGCG 41
DB 730 GGGGGCACCAGCGAGCCCAAGGCTGTGGGCCCCGAGCG 770

```

```

FT /Product- "alpha-2AAR"
XX
XX WO200179561-A2.
PN
XX
XX 25-OCT-2001.
PD
XX
XX 17-APR-2001; 2001WO-US12575.
PE
XX
XX 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
XX
XX (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
XX Liggett SB, Small KM;
XX
XX WPI: 2001-611728/70.
DR P-PSDB; AAM52122.
XX
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
XX Example 7; Page 151; 163pp; English.
XX
XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (II)
CC or a site comprising (A) (999gcg99gcg) or (B) (999gcgctgag) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfosine, idazoxan, tolazoline, phenolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2AAR gene
CC (GenBank Accession AF281308).
XX
XX Sequence 1350 BP; 199 A; 490 C; 441 G; 220 T; 0 other;
SQ
Query Match 96.1%; Score 39.4; DB 23; Length 1350;
Best Local Similarity 97.6%; Pred. No. 0.00026;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGGGCACCAGCGAGCCCAAGGCTGTGGGCCCCGAGCG 41
DB 730 GGGGGCACCAGCGAGCCCAAGGCTGTGGGCCCCGAGCG 770

```

```

RESULT 2
AAI99917
ID AAI99917 standard; DNA; 1350 BP.
XX
XX AAI99917;
XX
XX 18-FEB-2002 (first entry)
DE Human alpha-2AAR encoding DNA.
XX
XX Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2AAR;
KW GenBank Accession AF281308; Chromosome 10; ds.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1.1353
FT CDS
FT /*tag- a

```

```

RESULT 3
ABA15164
ID ABA15164 standard; DNA; 14855 BP.
XX
XX ABA15164;
XX
XX 23-JAN-2002 (first entry)
DE Human nervous system related polynucleotide SEQ ID NO 7495.
XX
XX Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;

```


PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251988.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-541565/60.
XX
PT Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system
PT cancers and metastases -
XX
PS Disclosure; SEQ ID NO 7495; 1701pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABA11004-ABA21534) and proteins
CC (ABBI4678-ABBI8001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 14855 BP; 3335 A; 3554 C; 4013 G; 3953 T; 0 other;
XX
Query Match 61.0%; Score 25; DB 22; Length 14855;
Best Local Similarity 75.6%; Pred. No. 16;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
OY 1 GGGGGCACCAGCGCCAGCGTCTGGCCCGAGCG 41
Db 265 GCGCGCTTCAGAGTGAGGCCCGAGGCTGGCGCGCGAGCG 305
RESULT 4
ABA93286
ID ABA93286 standard; DNA; 22028 BP.
XX
AC ABA93286;
XX
DT 22-APR-2002 (first entry)
XX
DE Human acetyl-Coenzyme A acyltransferase 1 gene SEQ ID NO:1.
XX
DE Human: acetyl-Coenzyme A acyltransferase; ACNA1; chromosome 3p23-p22;
KM peroxisomal 3-oxoacyl-Coenzyme A thiolase; SNP; genotype: haplotype;
KM single nucleotide polymorphism; polymorphic variant; enzyme; gene; ds.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT variation replace(3546,A)
FT /*tag= a
FT /*standard_name= "single nucleotide polymorphism (SNP)"
FT /*tag= b
FT /*replace(3637,A)
FT /*standard_name= "single nucleotide polymorphism (SNP)"
FT /*tag= c
FT /*replace(4033,T)
FT variation

FT /*standard_name= "single nucleotide polymorphism (SNP)"
FT /*replace(4157,T)
FT /*tag= d
FT /*standard_name= "single nucleotide polymorphism (SNP)"
FT /*replace(4176,A)
FT /*tag= e
FT /*standard_name= "single nucleotide polymorphism (SNP)"
FT /*replace(4276,C)
FT /*tag= f
FT /*standard_name= "single nucleotide polymorphism (SNP)"
FT /*replace(9110,G)
FT /*tag= g
FT /*standard_name= "single nucleotide polymorphism (SNP)"
FT /*replace(9182,A)
FT /*tag= h
FT /*standard_name= "single nucleotide polymorphism (SNP)"
FT /*replace(9600,G)
FT /*tag= i
FT /*standard_name= "single nucleotide polymorphism (SNP)"
FT /*replace(11702,T)
FT /*tag= j
FT /*standard_name= "single nucleotide polymorphism (SNP)"
FT /*replace(11756,C)
FT /*tag= k
FT /*standard_name= "single nucleotide polymorphism (SNP)"
FT /*replace(13390,T)
FT /*tag= l
FT /*standard_name= "single nucleotide polymorphism (SNP)"
FT /*replace(14441,G)
FT /*tag= m
FT /*standard_name= "single nucleotide polymorphism (SNP)"
FT /*replace(14872,C)
FT /*tag= n
FT /*standard_name= "single nucleotide polymorphism (SNP)"
FT /*replace(14931,C)
FT /*tag= o
FT /*standard_name= "single nucleotide polymorphism (SNP)"
FT /*replace(15471,C)
FT /*tag= p
FT /*standard_name= "single nucleotide polymorphism (SNP)"
FT /*replace(15486,G)
FT /*tag= q
FT /*standard_name= "single nucleotide polymorphism (SNP)"
FT /*replace(18004,T)
FT /*tag= r
FT /*standard_name= "single nucleotide polymorphism (SNP)"
FT /*replace(18192,T)
FT /*tag= s
FT /*standard_name= "single nucleotide polymorphism (SNP)"
XX
PN WO200187903-A2.
XX
PD 22-NOV-2001.
XX
PF 03-MAY-2001; 2001WO-US14330.
XX
PR 18-MAY-2000; 2000US-205022P.
XX
PA (GENA-) GENAISANCE PHARM INC.
PA (DUDA/) DUDA A E.
XX
PI Chew A, Koshy B;
XX
DR WPI; 2002-164134/21.
XX
PT Isolated polynucleotide, comprising a polymorphic variant of the
PT acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A
PT thiolase) gene useful for providing haplotype information and in
PT therapy for treating related disorders -
XX
PS Claim 19; Fig 1A-I; 93pp; English.
XX
CC The present invention describes a polypeptide (I) which is a polymorphic

represents the human ACAA1 gene, where all the single nucleotide

QY 3 GGGCACCCGAGCGCAGGCCCAAGGGCTGGGCCCGAG 39
111 111 111 111 111 111 111 111 111 111
Db 126 GGGAACTTGGGGCAGCCCCAAGGGTCAGGTCACCGAG 1622

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RESULT 7
ID AAF44733 standard; cDNA; 3036 BP.
XX AAF44733;
AC AAF44733;
DE 27-MAR-2001 (first entry)
XX Novel protein kinase cDNA, SEQ ID NO: 114.
DE
XX Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
KW immunosuppressive; cardiact; renal; antiinflammatory; antiasthmatic;
KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;
KW immune disorder; cardiovascular disease; neurodegenerative disease;
KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
KW inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
XX
OS Homo sapiens.
XX WO200073469-A2.
XX 07-DEC-2000.
XX 26-MAY-2000; 2000WO-US14842.
XX 28-MAY-1999; 99US-0136503.
XX (SUGEN-) SUGEN INC.
XX Plowman GD, Martinez R, Whyte D, Sudersanam S;
PI WPI; 2001-032161/04.
XX P-PSDB; AAB65704.
DR Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT treating immune-related diseases and disorders, cardiovascular disease,
PT neurodegenerative diseases and/or cancers -
XX Example 4; Fig 2; 310pp; English.
XX The present sequence encodes a novel protein kinase. The nucleic acids
CC and the protein kinases they encode may be used in the treatment and
CC diagnosis of diseases associated with inappropriate kinase expression
CC such as immune-related diseases and disorders, cardiovascular disease,
CC neurodegenerative diseases and/or cancers. The nucleic acids and
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays. The kinase polypeptides may be used as antigens in the production
CC of antibodies of kinase expression and activity. Anti-kinase antibodies
CC and kinase antagonists may also be used to down regulate kinase
CC expression and activity. Diseases related to kinase expression and
CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC disorders, complications of organ transplantation, myocardial infarction,
CC immune disorders, cardiomyopathies, strokes, renal failure,
CC oxidative-stress related disorders, chronic inflammatory bowel disease,
CC chronic inflammatory pelvic disease, multiple sclerosis, asthma,
CC osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
CC reproductive disorders.
XX
SQ Sequence 3036 BP; 595 A; 964 C; 918 G; 559 T; 0 other;
Query Match 57.6%; Score 23.6; DB 22; Length 3036;
Best Local Similarity 86.7%; Pred. No. 46;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 11 AGCGAGGCCAAGGCTGTGGCCCGAGC 40
DB 2393 AGCGAGGCCAAGGCTGTGGCCCGAGC 2364
RESULT 8
ID ABQ47498 standard; DNA; 1733 BP.
XX

```

```

AC ABQ47498;
XX 12-JUL-2002 (first entry)
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 34089.
XX
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
XX Homo sapiens.
XX WO200218632-A2.
XX 07-MAR-2002.
XX 01-SEP-2001; 2001WO-EP10074.
XX 01-SEP-2000; 2000DE-1043826.
XX 05-SEP-2000; 2000DE-1044543.
XX (EPIC-) EPICGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K, Gnetig D;
PI WPI; 2002-371829/40.
XX Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
SQ Sequence 1733 BP; 252 A; 211 C; 585 G; 685 T; 0 other;
Query Match 57.1%; Score 23.4; DB 24; Length 1733;
Best Local Similarity 73.2%; Pred. No. 54;
Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
OY 1 GGGGCGATGACGCGTAAAGGTTTAAAGGTTTGGGTTTCGACG 41
DB 990 GGGGCGATGACGCGTAAAGGTTTAAAGGTTTGGGTTTCGACG 1030
RESULT 9
ID ABQ47499 standard; DNA; 1733 BP.
XX
XX ABQ47499;
XX 12-JUL-2002 (first entry)
XX

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KM	Human; immune system disease; cytosine methylation; antiasthmatic;
KW	antiarteriosclerotic; antihaemic; cytosolic; noctropic;
KW	neuroprotective; anti-HIV; anticoagulant; ophthalmological;
KW	antihemmatic; antiarthritis; antidiabetic; antipsoriatic;
KW	antiflamatory; cancer; eye disease; arteriosclerosis; anaemia;
KW	acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW	neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
OS	gene; ds.
XX	
XX	Homo sapiens.
XX	
PN	MO200200928-A2.
PD	
XX	03-JAN-2002.
XX	
PF	02-JUL-2001; 2001WO-EP07537.
PR	
PR	30-JUN-2000; 2000DE-1032529.
PR	01-SEP-2000; 2000DE-1043826.
PA	(EPIG-) EPIGENOMICS AG.
XX	
PI	Olek A, Piepenbrock C, Berlin K;
DR	WPI; 2002-130909/17.
XX	
PT	Nucleic acid comprising fragment of chemically modified gene, useful
PT	for diagnosis and treatment of diseases associated with abnormal
PT	cytosine methylation -
XX	
PS	Claim 1; SEQ ID NO 45; 32pp + sequence listing; German.
CC	
CC	The present invention provides a number of human immune system associated
CC	genes which are modified by the methylation of cytosines. The sequences
CC	can be used in the diagnosis and treatment of immune system disorders,
CC	including eye diseases such as retinopathy, neovascular glaucoma and
CC	macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC	leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC	rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
XX	diseases. The present sequence is a gene of the invention.
XX	
SQ	Sequence 7353 BP; 1544 A; 384 C; 1956 G; 3469 T; 0 other;
	Query Match 57.1%; Score 23.4; DB 24; Length 7353;
	Best Local Similarity 73.2%; Pred. NO. 54;
	Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0
OY	1 GGGGGCAGCGAGCGGCCCAAGGCTCGGCCCGCAGCG 41
Dd	5730 GGGGGATCGACCGTAGGTTTAAAGGTTTGGGTTTCGACG 5770
RESULT 11	
ID	AAD28362
XX	
AC	AAD28362;
XX	
DT	22-APR-2002 (first entry)
XX	
DE	Human chemically treated genomic DNA #3.
XX	
KW	Human; cytostatic; antidepressant; neuroleptic; nootropic; antiaddictive;
KW	adrenergic alpha-1C-receptor; cytosine methylation; therapy; alcoholism;
KW	behavioral disorder; neurological; psychiatric; cancer; schizophrenia;
KW	Tourette's syndrome; smoking; human immunodeficiency virus dementia;
XX	drug abuse; migraine; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200202809-A2.
PD	
XX	10-JAN-2002.

```

XX 02-JUL-2001; 2001WO-EP07540.
PF 30-JUN-2000; 2000DE-1032529.
XX 01-SEP-2000; 2000DE-1043826.
PR (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI: 2002-154759/20.
DR
XX Novel nucleic acid useful for diagnosis and therapy of behavioral
PT disorder, neurological disorder and cancer, comprises a sequence of a
PT segment of chemically pretreated DNA of adrenergic alpha-1c-receptor
PT gene -
XX
XX Claim 1; Page 32-36; 190pp; English.
XX
XX The invention relates to nucleic acids comprising a segment of chemically
CC pretreated DNA of adrenergic alpha-1c-receptor gene. The invention also
CC relates to oligonucleotides or peptide nucleic acid (PNA) oligomers
CC useful for detecting cytosine methylations. The pretreated DNA is useful
CC for the diagnosis or therapy of behavioural disorders, neurological
CC disorders and cancer, in particular major depressive disorder, Tourette's
CC syndrome, schizophrenia, psychiatric and neurological disorders, human
CC drug abuse, alcoholism, personality traits, compulsive gambling, human
CC immunodeficiency virus dementia, migraine, behaviours in schizophrenic
CC and schizophrenic patients, and suicidal behaviour in patients with
CC schizophrenia. The nucleic acid is useful for detecting the methylation
CC state of all CpG dinucleotides and/or single nucleotide polymorphisms
CC (SNPs). The present sequence is human chemically treated genomic DNA.
XX
XX Sequence 7353 BP; 1544 A; 384 C; 1956 G; 3469 T; 0 other;
SQ
XX
XX Query Match 57.1%; Score 23.4; DB 24; Length 7353;
XX Best Local Similarity 73.2%; Pred. No. 54;
XX Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
OY 1 GGGGCAACGAGCGAGCCCAAGGCTGCGCCCGAGCG 41
DB 5730 GGGGATATGACGCGTAGGTTTACGGTTGTCGAGCG 5770
RESULT 12
AAZ94312/C
ID AAZ94312 standard; DNA; 36 BP.
XX
XX AAZ94312;
AC
XX
XX 03-JUL-2000 (first entry)
DT
XX
XX Rat cholecystokinin CCKB receptor PCR primer.
DE
XX
XX G protein coupled receptor; cholecystokinin CCKB receptor;
KM rat; alpha-2A adrenergic receptor; human; screening; PCR primer;
KM ss.
XX
XX Rattus sp.
OS
XX
XX WO200012704-A2.
XX
XX
XX 09-MAR-2000.
PD
XX
XX 01-SEP-1999; 99WO-US20011.
PF
XX
XX 01-SEP-1998; 98US-0098704.
PR
XX
XX (PAUS/) PAUSCH M H.
PA (LAIM/) LAI M.
PA (SILV/) SILVERMAN S.
PA (BIRS/) BIRSAN C.
PA (BAUM/) BAUMBAUCH W.

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PA (TSEN/) TSENG E.
PA (KAJK/) KAJKOWSKI E M.
PA (OZEN/) OZENBERGER B A.
XX
XX Pausch MH, Lai M, Silverman S, Birsan C, Baumbauch W, Tseng E;
PI Kajkowski EM, Ozenberger BA;
XX
XX WPI: 2000-246753/21.
DR
XX
XX Novel host cells comprising heterologous G protein-coupled receptor
PT modified to be constitutively active, useful for high throughput
PT screening assays for e.g. drugs, insecticides or nematocides -
XX
XX Example 3; Page 25; 75pp; English.
XX
XX This is the DNA sequence of a primer that was used in the PCR
CC amplification of DNA encoding the N-terminal portion (including 22
CC amino acids proximal to the 5th transmembrane domain) of rat
CC cholecystokinin CCKB receptor, a G protein coupled receptor (GPCR).
CC The PCR product was used in the construction of an intracellular
CC loop 3 (IC3) deleted CCKB receptor mutant. Deletion of a portion
CC of IC3 of mammalian GPCRs is correlated with improved functional
CC expression in yeast cells with retention of full ability to couple
CC to the heterotrimeric G protein. The invention relates to mutant
CC GPCRs with constitutively activating mutations that permit the
CC detection of the receptors' functional activity in the absence of
CC activating ligands, host cells that contain mutations that promote
CC the functional activity of the GPCRs, host cells expressing such
CC receptors, and vectors useful for making such cells. The host cells
CC are useful in high throughput screening assays for therapeutic drugs,
CC insecticides, nematocides etc., and are especially useful for assays
CC using orphan receptors.
XX
XX Sequence 36 BP; 2 A; 15 C; 16 G; 3 T; 0 other;
SQ
XX
XX Query Match 54.6%; Score 22.4; DB 21; Length 36;
XX Best Local Similarity 95.8%; Pred. No. 1.2e+02;
XX Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 18 GCCCAAGGCTGTGGGCCCGAGCG 41
DB 36 GCCCAAGGCTGTGGGCCCGAGCG 13
RESULT 13
AAZ94369/C
ID AAZ94369 standard; DNA; 37 BP.
XX
XX AAZ94369;
AC
XX
XX 03-JUL-2000 (first entry)
DT
XX
XX Human alpha 2A adrenergic receptor PCR primer.
DE
XX
XX G protein coupled receptor; GPCR; human;
KM alpha 2A adrenergic receptor; drug screening; PCR primer; ss.
KM
XX
XX Homo sapiens.
OS
XX
XX WO200012705-A2.
XX
XX
XX 09-MAR-2000.
PD
XX
XX 01-SEP-1999; 99WO-US20013.
PF
XX
XX 01-SEP-1998; 98US-0098704.
PR
XX
XX (PAUS/) PAUSCH M H.
PA (WESS/) WESS J.
PA
XX
XX Pausch MH, Wess J;
PI
XX
XX WPI: 2000-246754/21.
DR

```


XX New G protein-coupled receptors with a mutation in an intracellular
PT domain, useful for high throughput screening assays for e.g. drugs,
PT Insecticides or nematocides
XX
PS Example 5; Page 16; 37pp; English.
XX
CC This is the DNA sequence of a primer that was used in the PCR
CC amplification of DNA encoding the N-terminal portion (including 39
CC amino acids proximal to the 5th transmembrane domain) of human
CC alpha 2A adrenergic receptor, a G protein coupled receptor (GPCR).
CC The PCR product was used in the construction of an intracellular
CC loop 3 (IC3) deleted receptor mutant. Deletion of a portion
CC of IC3 of mammalian GPCRs is correlated with improved functional
CC expression in yeast cells with retention of full ability to couple
CC to the heterotrimeric G protein. The invention provides modified
CC GPCRs having a mutation in IC3 that results in an improved functional
CC response in cell-based assays. The modification promotes growth
CC stimulation by a GPCR agonist, especially by improving coupling
CC between the receptor and a heterotrimeric G protein. Polynucleotides
CC encoding the mutated GPCR, chimeric GPCR, vectors and host cells are
CC also claimed. The modified GPCRs can be used in improved high
CC throughput screening assays (especially in yeast cells) for
CC therapeutic drugs, insecticides, nematocides etc.
XX
SQ Sequence 37 BP; 2 A; 15 C; 17 G; 3 T; 0 other;
XX
Query Match 54.6%; Score 22.4; DB 21; Length 37;
Best Local Similarity 95.8%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 18 GCCCAAGGCTGTGGCCCGAGCG 41
||||| |||||||
DB 37 GCCCAAGGCTGTGGCCCGAGCG 14
RESULT 14
AAS67824
ID AAS67824 standard; CDNA; 2286 BP.
XX
AC AAS67824;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #3628.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR P-PSDB; ABG03637.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 3628; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2286 BP; 604 A; 575 C; 617 G; 490 T; 0 other;
XX

Query Match 54.6%; Score 22.4; DB 23; Length 2286;
Best Local Similarity 72.5%; Pred. No. 1.2e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 2 GGGCACCAGCGAGCGCCCAAGGCTGTGGCCCGAGCG 41
||||| ||||| || || ||||| ||||||| |||
DB 2055 GGGCACCAGCGAGCGCCTGAACTAGGCGCCCGCCCGCGC 2094

RESULT 15

AAS71762
ID AAS71762 standard; CDNA; 2286 BP.

AC AAS71762;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #7566.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI: 2001-639362/73.

DR P-PSDB; ABG07575.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

PS Claim 1; SEQ ID No 7566; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 2286 BP; 604 A; 575 C; 617 G; 490 T; 0 other;

Query Match 54.6%; Score 22.4; DB 23; Length 2286;
Best Local Similarity 72.5%; Pred. No. 1.2e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 2 GGGGACACGAGCGAGCCCAAGGGGTGAGGCCCGCGAGCG 41
||||| |||| | | | |||| | ||||| |||
Db 2055 GGGGACGAGGAGGCTGAACTAGGCGCCGCGCGCG 2094

Search completed: February 15, 2003, 14:30:43
Job time : 25.0206 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 12:34:42 ; Search time 81.5273 Seconds

Title: US-09-636-259B-2_COPY_730_770
 Perfect score: A1

Sequence: 1 ggggcaccgagcgagcc.....aaggtctgccccgagcg 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

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Database :
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1: em.estba:*
2: em.esthum:*
3: em.estin:*
4: em.estmu:*
5: em.estcov:*
6: em.estpl:*
7: em.estro:*
8: em.htc:*
9: gb.est1:*
10: gb.est2:*
11: gb.htc:*
12: gb.est3:*
13: gb.est4:*
14: gb.est5:*
15: em.estfun:*
16: em.estom:*
17: gb.gss:*
18: em.gss_hum:*
19: em.gss_inv:*
20: em.gss_pln:*
21: em.gss_vrt:*
22: em.gss_fun:*
23: em.gss_mam:*
24: em.gss_mus:*
25: em.gss_other:*
26: em.gss_pro:*
27: em.gss_rod:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
C	1	39.4	96.1	453	14	B0129312	B0129312_1j34d05.y
C	2	39.4	96.1	492	14	BM967243	BM967243_1j32c09.y
C	3	39.4	96.1	561	14	BM967248	BM967248_1j32d04.y
4		25.2	61.5	606	9	AT935256	AT935256_wpl6a07.x
5		25	61.0	235	9	AV250353	AV250353_AV250353
C	6	25	61.0	463	14	BM800068	BM800068_A6NC000068

c	7	25	61.0	529	14	BM7043323
8	25	61.0	606	14	BM671525	
9	25	61.0	793	13	BI952735	
c	10	25	61.0	3689	11	AK014589
11	24.2	59.0	259	13	BI243119	
12	24.2	59.0	297	13	BI482295	
13	24.2	59.0	393	13	BI589545	
14	24.2	59.0	438	13	BI353946	
15	24.2	59.0	448	13	BI241551	
16	24.2	59.0	457	13	BI578058	
17	24.2	59.0	467	13	BI584252	
18	24.2	59.0	468	13	BI239413	
19	24.2	59.0	470	9	AA567681	
20	24.2	59.0	503	13	BI654092	
21	24.2	59.0	525	13	BI585510	
22	24.2	59.0	526	13	BI576424	
23	24.2	59.0	526	13	BI615125	
24	24.2	59.0	533	13	BI361680	
25	24.2	59.0	537	9	AI402612	
26	24.2	59.0	537	13	BI613704	
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28	24.2	59.0	552	9	AI259030	
29	24.2	59.0	554	9	AI404885	
30	24.2	59.0	572	13	BI590050	
31	24.2	59.0	573	13	BI27477	
32	24.2	59.0	576	13	BI606741	
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34	24.2	59.0	589	13	BI589749	
35	24.2	59.0	591	13	BI165996	
36	24.2	59.0	607	13	BI568381	
37	24.2	59.0	613	13	BI357338	
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39	24.2	59.0	614	13	BI590288	
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41	24.2	59.0	639	9	AI114144	
42	24.2	59.0	640	9	AI135240	
43	24.2	59.0	644	12	BE974921	
44	24.2	59.0	663	13	BI169590	
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					AK014589	
					Mos muscu	
					BI243119	
					RE406756	
					BI482295	
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					BI353946	
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					RH32981.5	
					BI615125	
					RE44663.5	
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					RE46007.5	
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					BI606741	
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					BI357417	
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					RE43752.5	
					BI172535	
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					AI135240	
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					BS37409.y	
					BI369569	
					RE55787.5	
					BI629282	
					RH58125.5	

Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center This clone is
available royalty-free through LNL; please contact the IMAGE
consortium (info@image.llnl.gov) for further information
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from gibco.
Location/Qualifiers
1. .453
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6136736"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
Superscript Plasmid Library Kit (Life Technologies). cDNA
made by oligo-dt priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an EcoT of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

FEATURES
source

BASE COUNT 41 a 189 c 164 g 59 t
ORIGIN

Query Match 96.1%; Score 39.4; DB 14; Length 453;
Best Local Similarity 97.6%; Pred. No. 0.0035;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGGCACCAGCGCCCAAGGCTGTGGCCCCCGAGCG 41
|||||
Db 441 GGGGGCACCAGCGCCCAAGGCTGTGGCCCCCGAGCG 401

RESULT 2
LOCUS BM967243/c 492 bp mRNA linear EST 29-APR-2002
DEFINITION l332c09.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
cDNA clone IMAGE:6136336 5' similar to SW:AZAA_HUMAN P08913
ALPHA-2A ADRENERGIC RECEPTOR ; , mRNA sequence.

ACCESSION BM967243
VERSION BM967243.1 GI:19561038
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 492)
AUTHORS Melton,D., Brown,J., Kenly,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
, M., Gibbons,M., McCann,R., Cole,R., Tsagarishvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.

TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other ESTs: l332c09.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812

Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from gibco
High quality sequence stop: 455.
Location/Qualifiers
1. .492
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6136336"
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/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
Superscript Plasmid Library Kit (Life Technologies). cDNA
made by oligo-dt priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an EcoT of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

FEATURES
source

BASE COUNT 44 a 202 c 182 g 64 t
ORIGIN

Query Match 96.1%; Score 39.4; DB 14; Length 492;
Best Local Similarity 97.6%; Pred. No. 0.0036;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGGCACCAGCGCGCCCAAGGCTGTGGCCCCCGAGCG 41
|||||
Db 441 GGGGGCACCAGCGCGCCCAAGGCTGTGGCCCCCGAGCG 401

RESULT 3
LOCUS BM967248/c 561 bp mRNA linear EST 29-APR-2002
DEFINITION l332d04.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
cDNA clone IMAGE:6136374 5' similar to SW:AZAA_HUMAN P08913
ALPHA-2A ADRENERGIC RECEPTOR ; , mRNA sequence.

ACCESSION BM967248
VERSION BM967248.1 GI:19561047
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 561)
AUTHORS Melton,D., Brown,J., Kenly,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
, M., Gibbons,M., McCann,R., Cole,R., Tsagarishvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.

TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other ESTs: l332d04.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138

Tel: 617-495-1812
Fax: 617-495-8557
Email: dmeltont@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brownjfas.harvard.edu)
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from GIBCO
High quality sequence stop: 445.
Location/Qualifiers
1. .561
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/db_xref="taxon:9606"
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/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pSPOR1; Site:1: Not 1;
Site:2: Sal 1: Starting library constructed using
SuperScript Plasmid Library Kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an EcoT of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

BASE COUNT 63 a 215 c 210 g 73 t
ORIGIN

Query Match 96.1%; Score 39.4; DB 14; Length 561;
Best Local Similarity 97.6%; Pred. No. 0.0037;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGGGGACCGAGCGAGCGCCAGGCGTCTGGGCCCCGAGCG 41
|||||
Db 441 GGGGGACCGAGCGAGCGCCAGGCGTCTGGGCCCCGAGCG 401

RESULT 4
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LOCUS
DEFINITION
A1935256 606 bp mRNA linear EST 08-MAR-2000
ACCESSION
A1935256
VERSION
A1935256.1 GI:5674126
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 606)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrrp/image/image.html

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Seq primer: -40UP from GIBCO
High quality sequence stop: 390.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:2464980"
/clone_1lb="NCI-CGAP-Lu19"
/tissue_type="squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary and
metastatic)"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pTR73D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
pooled lung tumor tissue, and was then primed with a Not I
- oligo(dT) primer. Double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pTR73 vector. Library went through one round of
normalization. Library constructed by Bento Soares and M.
Fatima Bonaldo."

BASE COUNT 113 a 219 c 197 g 77 t
ORIGIN

Query Match 61.5%; Score 25.2; DB 9; Length 606;
Best Local Similarity 78.9%; Pred. No. 1.6e+02;
Matches 30; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 3 GGGCACCGAGCGAGCGCGGCTCGGGCCCGAGC 40
||| ||| ||||| || ||| ||||| |||||
Db 146 GAGCGCCCGCGCAGGCGCCAGCGCTTGCCCCCGAGC 183

RESULT 5
AV250353 235 bp mRNA linear EST 04-NOV-1999
LOCUS
DEFINITION
AV250353 RIKEN full-length enriched, 0 day neonate head Mus
musculus cDNA clone 4833422109 3', mRNA sequence.
ACCESSION
AV250353
VERSION
AV250353.1 GI:6237812
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 235)
Kono, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
Kono, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Horii, F.,
Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai,
C., Kawai, J., Kiyuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata,
Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Suganara, Y., Suzuki, H.,
Suzuki, H., Takahashi, F., Tateo, M., Tomioka, N., Tsunoda, Y.,
Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T.,
Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Kono, H., et al. 1999)
TITLE
Unpublished (1999)
JOURNAL
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Saitama-cho, Tsukuba-shi, Ibaraki, Japan
COMMENT
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Saitama-cho, Tsukuba-shi, Ibaraki, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Sasaki, N., Izawa, M., Watahiki, M., Okazaki, Y., Tanaka, T., Yoneda, Y.,
Matsunaga, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki,
Y.

Transcriptional sequencing: A method for DNA sequencing using RNA

following tissue(s): Retina Foveal and Macular. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

BASE COUNT 83 a 173 c 161 g 111 t 1 others

BASE COUNT 138 a 173 c 189 g 104 t 2 others

Query Match 61.0%; Score 25; DB 14; Length 529;
Best Local Similarity 75.6%; Pred. No. 1.8e+02;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Query Match 61.0%; Score 25; DB 14; Length 606;
Best Local Similarity 75.6%; Pred. No. 1.9e+02;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 GGGGGACCGAGCGAGCGGTCTGGCCCGAGCG 41
|||||
Db 288 GGGGGACCGAGCGAGCGGTCTGGCCCGAGCG 248

OY 1 GGGGGACCGAGCGAGCGGTCTGGCCCGAGCG 41
|||||
Db 325 GGGGGACCGAGCGAGCGGTCTGGCCCGAGCG 365

RESULT 8
LOCUS BM671529

RESULT 9
LOCUS BI952735/C

DEFINITION UI-E-CK1-afj-j-22-0-UI-s2 UI-E-CK1 Homo sapiens cDNA clone

DEFINITION HVSMDM007J12f Hordeum vulgare green seedling EST library

ACCESSION BM671529

ACCESSION HVSMDM007J12f

VERSION BM671529.1

VERSION BI952735.1

KEYWORDS EST.

KEYWORDS EST.

SOURCE

SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

ORGANISM Hordeum vulgare.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae

REFERENCE 1 (bases 1 to 606)
Bonaldo,M.F., Lennon,G. and Soares,M.B.

REFERENCE 1 (bases 1 to 793)
Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons

TITLE Normalization and subtraction: two approaches to facilitate gene discovery

TITLE ; Triflucene; Hordeum.

JOURNAL Genome Res. 6 (9), 791-806 (1996)

JOURNAL Unpublished (2001)

COMMENT 97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: twing@clemson.edu

Tissue Procurement: Dr. Gregg Hageman
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).

Tissue Procurement: Dr. Gregg Hageman
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).

Seq primer: M13 Forward

Seq primer: AATTAACCTTCACCTAAGG

PolyA=yes.

High quality sequence start: 22
High quality sequence stop: 590.

FEATURES

source 1..606
Location/Qualifiers

FEATURES

source 1..793
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-CK1-afj-j-22-0-UI"
/clone_lib="UI-E-CK1"
/tissue_type="Retina Foveal and Macular"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-CK1 is a normalized cDNA library containing the following tissue(s): Retina Foveal and Macular. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand

cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
TAG_LIB=UI-E-CK1
TAG_TISSUE=Foveal and Macular Retina
TAG_SEQ=GTCC"

/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMDM007J12f"
/clone_lib="Hordeum vulgare green seedling EST library
HVSMDM0014 (Blumeria infected)"
/tissue_type="green seedling leaf"
/lab_host="TJC121"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Morex (mls) plants were greenhouse grown in the R wise lab at Iowa State University, Ames, IA; 7 day old green seedlings were infected with isolate 5874 of Blumeria graminis f. sp. hordei, and leaves were harvested

24, 48 and 72 hr post-inoculation and snap frozen (Mise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give plasmidscript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Fritsch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Fritsch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinholz A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)"

Query Match	61.0%;	Score 25;	DB 13;	Length 793;
Best Local Similarity	75.6%;	Pred. No. 2e+02;		
Matches 31;	Conservative	0;	Mismatches 10;	Indels 0;
				Gaps 0;
OY	1	GGGGCACCAGCGCCAGGCCCAAGGTCGTGGGCCCGACG	41	
Db	743	GGGGGTCCGCCCCCAAGCTTAAGGTTCGGGCCCGGAGTG	703	

RESULT	10
AK014589	
LOCUS	AK014589
DEFINITION	mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4632A19J12.homoolog to ALPHA-1-ANTITRYPSIN PRECURSOR (ALPHA-1 ANTITRYPSTN) (ALPHA-1- PROTEINASE INHIBITOR), full insert sequence.
AK014589	3689 bp mRNA linear HTC 19-JAN-2002
DEFINITION	Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4632A19J12.homoolog to ALPHA-1-ANTITRYPSIN PRECURSOR (ALPHA-1 ANTITRYPSTN) (ALPHA-1- PROTEINASE INHIBITOR), full insert sequence.

ACCESSION	AK014589
VERSION	AK014589.1
KEYWORDS	GI:12852536
SOURCE	HTC; CAP trapper. Mus musculus (strain:C57BL/6J) 0 day neonate skin cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:4632419J12.

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE	1
AUTHORS	Carninci, P. and Hayashiraki, Y.
TIME	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)

MEDLINE	99279253
PUBMED	10349636
REFERENCE	2
AUTHORS	Carinci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Shibata, Y., Watanabe, M., and Hasegawa, I. Y.

TOH, M., KONDO, H., UKAZAKI, I., MURAMATSU, M. and NAGASAKI, T.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
0885-0774

REFERENCE	AUTHORS	PUBMED	MEDLINE
3	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kozuka, H., Akizawa, T., Nishi, K., Katsunai, T., Tachiro, H., Itoh, M.	11042159	20499374

KOUNO, T., Akiyama, J., Nishira, R., Kikuchi, Y.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wathiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated system analysis (RISA) system-384-format

JOURNAL	sequencing pipeline with 384 multicapillary sequencer
MEDLINE	Genome Res. 10 (11), 1757-1771 (2000)
PUBMED	20530913
REFERENCE	11076861
AUTHORS	4
	Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Miyazaki, T., Nakazaki, Y., Kono, N., Adachi, T., Fukuda, S.

Atakawa, T., Hata, R., Furukawa, T., Komuro, Y., Nakagawa, T.,
 Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
 Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
 Kadoe, K., Matsuda, H., Ashburner, M., Batilov, S., Casavault, T.,
 Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
 Kuehl, P., Lewis, S., Matsuno, Y., Nikaido, I., Pesole, G.,
 Quackenbush, J., Schriml, L.M., Staudli, F., Suzuki, R., Tomita, M.,
 Wagne, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
 Badarrelli, R., Barsi, G., Blake, J., Boffelli, D., Bojunga, N.,
 Carninci, P., de Bonaldo, M.F., Brownstein, M.J., But, C.,
 Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
 Hofmann, M., Hume, D.A., Kamliya, M., Lee, N.H., Lyons, P.,
 Marchionni, L., Mashima, J., Mazzarelli, J., Momtazts, P.,
 Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
 Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,
 Toyok-Oka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilmung, L.,
 Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S.,
 and Hayashizaki, Y.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409 (6821), 685-690 (2001)

MEDLINE	21085660
PUBMED	11217851
REFERENCE	5 (bases 1 to 3689)
AUTHORS	Adachi,J., Alzawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Ishida,M., Iwata,D., Kato,N., Kawabe,M., Naito,C.

Aikawa, T., Balastracci, R., Boni, R., Brownstein, M., Carey, J.,
 Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hasegawa, T.,
 Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Horii, F.,
 Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T.,
 Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S.,
 Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K.,
 Nunakata, R., Ono, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J.,
 Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
 Schraml, L., Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T.,
 Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
 Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamane, K.,
 Yasunishi, A., Yoshida, K., Yoshino, M., Yamamoto, M., and
 Hayashizaki, Y.
 Direct Submission
 Submitted (10-JUL-2000) yoshinide Hayashizaki, The Institute of
 Genome Research, National Institute of Advanced Industrial Science and Technology, 1-1-1 Higashi, Tsukuba, Ibaraki 305-8565, Japan

Physical and Chemical Research (RIKEN), Laboratory for Genomic Sciences (GSC),
Exploration Research Group, RIKEN Genomic Sciences Center, Yokohama,
RIKEN Yokohama Institute, 1-7-22 Sukeni-cho, Tsukuba-shi, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for
further details.

cDNA library was prepared and sequenced in mouse genomic Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'-GAAGGAGACAGACATCCAAAGCCCTTTTGTGGTTTTTTCVN-3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGCAGAGATCTCGAGATTAAATTAATATCCCCCCCCCCC-3']. cDNA was cleaved with BamHI and XhoI. cDNA of size compressed between 3 and 7 kb was selected before cloning. Vector: a modified plasmidscript KS(+) after bulk excision from lambda FLC I. Cloning sites, 5' end: SalI, 3' end: BamHI. Host: DH10B.

```
FEATURES
source      location/Qualifiers
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/strain="C57BL/6J"
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	/sex="male and female"	
	/dev_stage="0-24 hours mixed stage embryonic"	
	/lab_host="DHS-alpha Tona"	
	/note="Organ: embryo; Vector: pFLC1; Site_1: XhoI; Site_2: BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."	

BASE COUNT	85 a	52 c	60 g	62 t
ORIGIN				

Query Match	59.0%;	Score 24.2;	DB 13;	Length 259;
Best Local Similarity	78.4%;	Pred. No. 3e+02;		
Matches	29;	Conservative	0;	Indels 8; Gaps 0;

Oy	3	GGGACCGAGCCGAGGCCAAGGCTGGTGGCCCCGAG	39
Db	153	GGGACCTGTGGCAGCCCAAGGTCAGTGCACCGAG	189

RESULT 12				
LOCUS	BI482295	297 bp	mRNA	linear EST 27-AUG-2001
DEFINITION	BE694967.5prime RE Drosophila melanogaster normalized Embryo pFLC-1			
	Drosophila melanogaster cDNA clone BE64967 5 similar to CG6084:			
	Pban0006084 GO:[enzyme (GO:0003824)] located on: 3L 68C9-68C9;:			
	05/21/2001, mRNA sequence.			
ACCESSION	BI482295			
VERSION	BI482295.1	GI:15317308		
KEYWORDS	EST			
SOURCE	fruit fly,			
ORGANISM	Drosophila melanogaster			
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
	Ephydroidea; Drosophilidae; Drosophila.			
	1 (bases 1 to 297)			
	Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Carlson			
	,J., Chame,M., Chavez,C., Dorsett,V., Fartan,D., Frise,E., George			
	,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Lao,G., Misra,S.,			
	Mungall,C.J., Nuno,J., Paclel,J., Paragas,V., Park,S.,			
	Phuanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celinker,S. and Rubin			
	,G.M.			
TITLE	BDGP/HMT RE Drosophila ESF Project			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Stapleton, M.			
	BDGP			
	Lawrence Berkeley National Lab			
	One Cyclotron Rd, Berkeley, CA 94720, USA			
	Fax: 510 486 6798			
	Email: http://www.fruitfly.org/est_est@fruitfly.berkeley.edu			
	hit genomic AE003544: arm:3L [11370031,11651899]			
	estimated cyto:68C3-68C15: 05/21/2001			
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	High quality sequence stop: 260.			
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	/clone="R64967"			
	/clone_id="RE Drosophila melanogaster normalized Embryo			
	pFLC-1"			
	/sex="male and female"			
	/dev_stage="0-24 hours mixed stage embryonic"			
	/lab_host="DHS-alpha Tona"			
	/note="Organ: embryo; Vector: pFLC1; Site_1: XhoI; Site_2:			
	BamHI; Library was kindly generated by Piero Carninci at			
	the RIKEN. The library was normalized and excised using			
	Cre recombinase. Plasmid cDNA library."			

BASE COUNT	94 a	58 c	78 g	67 t
ORIGIN				

	Query Match	59.0%;	Score 24.2;	DB 13;	Length 297;
	Best Local Similarity	78.4%;	Pred. No. 3e+02;	Mismatches	Indels
	Matches 29;	Conservative	0;	Mismatches	8; Indels 0; Gaps 0;
Oy	3	GGGACCGAGCGCAGGCCAAGGCTGTGGCCCCCGAG	39		
Db	153	GGGAACCTGGGGCAGCCCAAGGCTCACGTACCAGAG	189		
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	BIS89545				
	LOCUS				
	DEFINITION				
	RH02982.Prime RH Drosophila melanogaster normalized Head pfic-1				
	Drosophila melanogaster cDNA clone RH02982 5 similar to CG6084;				
	Pfano006084 GO: leuzyme (GO:0003824) located on: 3L 68C9-68C9;;				
	08/16/22001, mRNA sequence.				
	ACCESSION				
	BIS89545				
	VERSION				
	BIS89545.1				
	SOURCE				
	EST.				
	fruit fly.				
	Drosophila melanogaster				
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;				
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
	Ephydroidea; Drosophilidae; Drosophila.				
	1 (bases 1 to 393)				
	Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Carlson				
	,J., Champagne,M., Chavez,C., Dorsett,V., Farfan,D., Filse,E., George				
	,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Mistrá,S.,				
	Mungall,C.J., Nuno,J., Pacלב,J., Paragas,V., Park,S.,				
	Phouaneavong,S., Wan,K., Yu,C., Lewis,S.E., Celinker,S. and Rubin				
	,G.M.				
	BOGP/HMT RH Drosophila EST Project				
	Unpublished (2001)				
TITLE	Contact: Stapleton, M.				
JOURNAL	BDGP				
COMMENT	Lawrence Berkeley National Lab				
	One Cyclotron Rd, Berkeley, CA 94720, USA				
	Fax: 510 486 6798				
	Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu				
	hit genomic AE003544: arm:3L [11370031,11651899]				
	estimated-cyto:68C3-68C15: 08/16/2001				
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source	1..393				
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	pfic-1"				
	/sex="male and female"				
	/dev_stage="Adult"				
	/lab_host="DH5-alpha Tona"				
	/note="Organ: head; Vector: pfic1; Site.1: XhoI; Site.2:				
	BamHI; Library was kindly generated by Piero Carninci at				
	the RIKEN. The library was normalized and excised using				
	Cre recombinase. Plasmid cDNA library."				
BASE COUNT	119 a 80 c 102 g 91 t				
ORIGIN					
Query Match	59.0%; Score 24.2; DB 13; Length 393;				
Best Local Similarity	78.4%; Pred. No. 3.2e+02;				
Matches 29; Conservative	0; Mismatches 8; Indels 0; Gaps 0;				
Oy	3	GGGACCGAGCGCAGGCCAAGGCTGTGGCCCCCGAG	39		
Db	154	GGGAACCTGGGGCAGCCCAAGGCTCACGTACCAGAG	190		
RESULT 14					
LOCUS	BIS353926				
	438 bp				
	mRNA				
	linear				
	EST 31-JUL-2001				

DEFINITION	GM25615.5prlme GM Drosophila melanogaster ovary POT2 Drosophila melanogaster cDNA clone GM25615_5 similar to CG6084: FBan0006084 GO: [enzyme (GO:0003824)] located on: 3L 68C9-68C9; : 05/18/2001, mRNA sequence.
ACCESSION	B1353926
VERSION	B1353926.1 GI:15048368
KEYWORDS	EST.
SOURCE	fruit fly,
ORGANISM	Drosophila melanogaster. Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 438) Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M. BDGP/HHMT Drosophila EST Project Unpublished (2001)
REFERENCE	Authors
TITLE	JOURNAL
COMMENT	Contact: Stapleton, M. BDGP Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798 Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu hit genomic AE003544: arm:3L (11370031..11651891) estimated-cyto:68C3-68C15: 05/18/2001 plate: GM.256 row: B column: 3 High quality sequence stop: 243. Location/Qualifiers 1..438 /organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone="GM25615" /clone_11b="GM Drosophila melanogaster ovary POT2" /sex="female" /dev_stage="newly eclosed females: germarium-stage 6" /lab_host="X11 Blue" /note="Organ: ovary; Vector: POT2; Site_1: EcoRI; Site_2: XhoI. Sized fractionated cDNAs were directly ligated into POT2."
FEATURES	source
BASE COUNT	129 a 96 c 110 g 102 t 1 others
ORIGIN	
Query Match	59.0%; Score 24.2; DB 13; Length 438;
Best Local Similarity	78.4%; Pred. No. 3.2e+02;
Matches	29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Oy	3 GGCGACCGAGCCGAGGCCAAGGTCTGGCCCCGAG 39 Db 125 GGGACCTGGGCGAGCCCAAGGTCAGTCAACCGAG 161
RESULT 15	
B1241551	448 bp mRNA linear EST 12-JUL-2001
LOCUS	RE38647.5prlme RE Drosophila melanogaster normalized Embryo pfic-1
DEFINITION	Drosophila melanogaster cDNA clone RE38647 5 similar to CG6084: FBan0006084 "enzyme" located on: 3L 68C9-68C9; : 05/12/2001, mRNA sequence.
ACCESSION	B1241551
VERSION	B1241551.1 GI:14710247
KEYWORDS	EST.
SOURCE	fruit fly.
ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 448) Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mitra, S., Mungall, C.J., Nunoo, J., Pacleib, J., Paragas, V., Park, S., Phonaneavong, S., Wan, K., Yu, C., Lewis, S.E., Celinker, S. and Rubin G.M.

TITLE BDGP/HMI RE Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP

Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798

Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
hit genomic AE003544: arm:3L [11370031,11651899]

estimated-cyto:68C3-68C15: 05/12/2001

plate: RE 386 row: D column: 11

High quality sequence stop: 411.

FEATURES Location/Qualifiers

1..448

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone="RE38647"

/clone_lib="RE Drosophila melanogaster normalized Embryo

p1c-1"

/sex="male and female"

/dev_stage="0-24 hours mixed stage embryonic"

/lab_host="DH5-alpha Tona"

/note="Organ: embryo; Vector: p1c1; Site_1: XhoI; Site_2:

BamHI; Library was kindly generated by Piero Carninci at

the RIKEN. The library was normalized and excised using

Cre recombinase. Plasmid cDNA library."

BASE COUNT 132 a 99 c 111 g 106 t

ORIGIN

Query Match

Best Local Similarity 78.4%; Score 24.2; DB 13; Length 448;

Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 GGGCACCAGACCGCCCAAGGCTGGGCCCCGAG 39

DB 153 GGGAACTGGGGCGACCCCAAGGCTCAGCTACCGAG 189

Search completed: February 15, 2003, 18:03:11
Job time : 86.5273 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2003, 06:16:02 : Search time 2.19024 Seconds
(without alignments)
5740.812 Million cell updates/sec

Title: US-09-636-259B-2_COPY_730_770

Perfect score: 41
Sequence: 1 gggggcaccgagcgagcc.....aaggctctgggccccgagcg 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
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4: /cgn2_6/prodata/1/lna/6B.COMB.seq: *
5: /cgn2_6/prodata/1/lna/PCTUS.COMB.seq: *
6: /cgn2_6/prodata/1/lna/Backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22.2	54.1	35060	3 US-08-814-095-7	Sequence 7, Appl1
2	21.4	52.2	4190	3 US-08-938-291A-2	Sequence 2, Appl1
3	21.2	51.7	1008	4 US-09-091-097-38	Sequence 38, Appl1
4	20.6	50.2	3164	1 US-08-188-228-49	Sequence 49, Appl1
5	20.6	50.2	3164	1 US-08-332-643-43	Sequence 43, Appl1
6	20.6	50.2	3164	1 US-08-332-638-49	Sequence 49, Appl1
7	20.4	49.8	1312	1 US-08-205-506A-1	Sequence 1, Appl1
8	20.4	49.8	1312	5 PCT-US94-02389-1	Sequence 1, Appl1
9	20.4	49.8	3318	4 US-09-593-589-3	Sequence 3, Appl1
10	20.4	49.8	9775	4 US-08-977-171-1	Sequence 1, Appl1
11	20.4	49.8	9934	4 US-08-977-171-2	Sequence 1, Appl1
12	20.2	49.3	1068	5 PCT-US91-00899-13	Sequence 13, Appl1
13	20.2	49.3	1215	5 PCT-US91-00899-5	Sequence 9, Appl1
14	20.2	49.3	1488	1 US-07-914-281-9	Sequence 9, Appl1
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16	20.2	49.3	1488	1 US-08-525-058A-9	Sequence 9, Appl1
17	20.2	49.3	1488	2 US-08-696-731-9	Sequence 9, Appl1
18	20.2	49.3	1488	4 US-09-042-531-9	Sequence 9, Appl1
19	20.2	49.3	2175	4 US-08-487-073-9	Sequence 9, Appl1
20	20.2	49.3	2861	4 US-08-487-073-10	Sequence 10, Appl1
21	20.2	49.3	3647	1 US-07-914-281-7	Sequence 7, Appl1
22	20.2	49.3	3647	1 US-08-393-246-7	Sequence 7, Appl1
23	20.2	49.3	3647	1 US-08-525-058A-7	Sequence 7, Appl1
24	20.2	49.3	3647	1 US-08-696-731-7	Sequence 7, Appl1
25	20.2	49.3	3647	4 US-09-042-531-7	Sequence 4, Appl1
26	20.2	49.3	3854	5 PCT-US91-00899-4	Sequence 5, Appl1
27	20.2	49.3	3854	2 US-08-720-484A-1	Sequence 1, Appl1

28	20.2	49.3	3854	3 US-08-953-823A-1	Sequence 1, Appl1
29	20.2	49.3	3854	4 US-09-398-239-1	Sequence 1, Appl1
30	20	48.8	141	4 US-08-943-731-8	Sequence 8, Appl1
31	20	48.8	225	1 US-08-136-993-6	Sequence 6, Appl1
32	20	48.8	1218	1 US-08-136-993-8	Sequence 8, Appl1
33	20	48.8	1322	1 US-08-136-993-12	Sequence 12, Appl1
34	20	48.8	4772	4 US-09-484-970B-133	Sequence 133, App
35	20	48.8	18609	4 US-08-943-731-1	Sequence 1, Appl1
36	19.8	48.3	51	1 US-07-690-983D-17	Sequence 17, Appl1
37	19.8	48.3	54	1 US-07-690-983D-27	Sequence 27, Appl1
38	19.8	48.3	748	4 US-08-998-416-434	Sequence 434, App
39	19.8	48.3	987	2 US-08-891-837B-1	Sequence 1, Appl1
40	19.8	48.3	1349	1 US-08-451-777A-4	Sequence 4, Appl1
41	19.8	48.3	1349	1 US-08-451-777A-5	Sequence 5, Appl1
42	19.8	48.3	1349	1 US-08-451-777A-6	Sequence 6, Appl1
43	19.8	48.3	1349	2 US-08-451-778A-4	Sequence 4, Appl1
44	19.8	48.3	1349	2 US-08-451-778A-5	Sequence 5, Appl1
45	19.8	48.3	1349	2 US-08-451-778A-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-08-814-095-7
Sequence 7, Application US/08814095
Patent No. 6025183
GENERAL INFORMATION:
APPLICANT: Soreq, Hermona
APPLICANT: Zakut, Haim
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: KOHN & ASSOCIATES
STREET: 30500 No. 6025183Western Highway, Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: U.S.
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,095
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Montgomey, Ilene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2391,00066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 35060 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Cosmid including ACHÉ
DESCRIPTION: Promotor, ACHÉ gene and ARS gene"
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 7q22
FEATURE:

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NAME/KEY: promoter
LOCATION: 4089..22464
OTHER INFORMATION: /function= "ACHE Promotor"
OTHER INFORMATION: /standard_name= "ACHE Promotor"
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NAME/KEY: exon
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OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 1
FEATURE:
NAME/KEY: exon
LOCATION: 24090..25177
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function= "(translation start:
OTHER INFORMATION: 24110)"
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 2
FEATURE:
NAME/KEY: exon
LOCATION: 25524..26009
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 3
FEATURE:
NAME/KEY: exon
LOCATION: 27005..27274
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NAME/KEY: exon
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OTHER INFORMATION: /number= 16
US-08-814-095-7
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Best Local Similarity 77.1%; Pred. No. 25;
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 2 GGGGACCGAGCGGCGCCAGGCTGTGCGCCC 36
Db 22583 GGGGACCGAGCGGCGCCAGGCTGTGCGCCC 22617
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Thu Feb 20 09:21:37 2003

us-09-636-259b-2_copy_730_770.rml

RESULT 2
US-08-938-291A-2/C
Sequence 2, Application US/08938291A
Patent No. 6117673
GENERAL INFORMATION:
APPLICANT: Lev, Sima
APPLICANT: Plowman, Gregory D.
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: RDB PROTEINS AND RELATED
PRODUCTS AND METHODS
TITLE OF INVENTION: 11
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,291A
FILING DATE: September 26, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027,337
FILING DATE: October 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Walburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 228/172
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4190 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-938-291A-2

Query Match 52.2%; Score 21.4; DB 3; Length 4190;
Best Local Similarity 71.8%; Pred. No. 47; Indels 11; Gaps 0;
Matches 28; Conservative 0; Mismatches 11

QY 3 GGGCAGCGAGCGCGCCAGGCTGTGCGCCCGAGCG 41
DB 98 GGGCAGCGCGCGCGCCCGCTGTGCGAGCCCGAGCG 60

RESULT 3
US-09-091-097-38
Sequence 38, Application US/09091097
Patent No. 6432407
GENERAL INFORMATION:
APPLICANT: TAKESAKO, KAZUYOHI
APPLICANT: OKADO, TAKASHI
APPLICANT: YAGIHARA, TOMOYO
APPLICANT: KURODA, MASANOBU
APPLICANT: ONISHI, YOSHIMI
APPLICANT: KATO, IKUNOSHIN
APPLICANT: AKIYAMA, KAZUO
APPLICANT: YASUEDA, HIROSHI
APPLICANT: YAMAGUCHI, HIDEO
TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
MALASSEZIA

NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,097
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1422-0346P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8050
TELEFAX: 703-205-8050
INFORMATION FOR SEQ. ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1008 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
US-09-091-097-38

Query Match 51.7%; Score 21.2; DB 4; Length 1008;
Best Local Similarity 76.5%; Pred. No. 56; Indels 8; Gaps 0;
Matches 26; Conservative 0; Mismatches 8

QY 6 CACGAGCGAGCGCGCCAGGCTGTGCGCCCGAG 39
DB 657 CACGAGCGCGCTGCCCAAGGCTCTCGACGCTGAG 690

RESULT 4
US-08-188-228-49/C
Sequence 49, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA: US 07/872,643
APPLICATION NUMBER: 17 APR 1992

ATTORNEY/AGENT INFORMATION:
 NAME: No. 5597725and, Greta E.
 REGISTRATION NUMBER: 35,302
 TELECOMMUNICATION INFORMATION: 31340
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3164 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 US-08-188-228-49

Query Match
 Best Local Similarity 50.2%; Score 20.6; DB 1; Length 3164;
 Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 3 GGGACGACGAGCGAGCCCAAGGCTGTGGCCCG 37
 DB 2131 GGGGCTCCAGCGCGGCGCGGCGGCTTGGCCCG 2097

RESULT 5
 US-08-332-643-43/C
 Sequence 43, Application US/08332643
 Patent No. 5639634
 GENERAL INFORMATION:
 APPLICANT: Suzuki, Shintaro
 TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
 NUMBER OF SEQUENCES: 56
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 STREET: Two First National Plaza, 20 South Clark
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60603
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/332,643
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/872,643
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5639634and, Greta E.
 REGISTRATION NUMBER: 35,302
 TELECOMMUNICATION INFORMATION: 27866/30795
 TELEPHONE: (312) 346-5750
 TELEFAX: (312) 984-9740
 INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3164 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 US-08-332-643-43

Query Match

50.2%; Score 20.6; DB 1; Length 3164;

Best Local Similarity 74.3%; Pred No. 86;
 Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 3 GGGACGACGAGCGAGCCCAAGGCTGTGGCCCG 37
 DB 2131 GGGGCTCCAGCGCGGCGCGGCGGCTTGGCCCG 2097

RESULT 6
 US-08-332-638-49/C
 Sequence 49, Application US/08332638
 Patent No. 5646250
 GENERAL INFORMATION:
 APPLICANT: Suzuki, Shintaro
 TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
 NUMBER OF SEQUENCES: 62
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 STREET: 6300 Sears Tower, 233 S. Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/332,638
 FILING DATE: 01-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 435
 FILING DATE: 17 APR 1992
 APPLICATION NUMBER: US/07/872,643
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5646250and, Greta E.
 REGISTRATION NUMBER: 35,302
 TELECOMMUNICATION INFORMATION: 31340
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3164 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 US-08-332-638-49

Query Match
 Best Local Similarity 50.2%; Score 20.6; DB 1; Length 3164;
 Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 3 GGGACGACGAGCGAGCCCAAGGCTGTGGCCCG 37
 DB 2131 GGGGCTCCAGCGCGGCGCGGCGGCTTGGCCCG 2097

RESULT 7
 US-08-205-506A-1
 Sequence 1, Application US/08205506A
 Patent No. 5545563
 GENERAL INFORMATION:
 APPLICANT: Darlington, Gretchen J.
 APPLICANT: Wilson, Deborah R.
 APPLICANT: Wilde, Margaret
 TITLE OF INVENTION: THE HUMAN C/EBP GENE AND VECTORS FOR

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
;; STREET: 3100 No. 6232112west Center, 90 South 7th street
;; CITY: Minneapolis
;; STATE: MN
;; COUNTRY: USA
;; ZIP: 55402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FASTSEQ for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/977,171
;; FILING DATE: 24-NOV-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Skoog, Mark T
;; REGISTRATION NUMBER: 40,178
;; REFERENCE/DOCKET NUMBER: 10552.13US01
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 612-332-5300
;; TELEFAX: 612-332-9081
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9775 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: Genomic DNA
;; US-08-977-171-1

Query Match 49.8%; Score 20.4; DB 4; Length 9775;
Best Local Similarity 71.1%; Pred. No. 97;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 3 GGGCACCAGCGGCGCCCAAGGCTGCGGCCCGAGC 40
Db 2547 GGGCACCAGCGGCGGCAAGCATGACTCGGCCCAACC 2510

RESULT 11
US-08-977-171-2/C
; Sequence 2, Application US/08977171
; Patent No. 6232112
; GENERAL INFORMATION:
; APPLICANT: CATCHESIDE, DAVID E.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR DIVERSIFICATION
; TITLE OF INVENTION: OF DNA
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6232112west Center, 90 South 7th street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,171
; FILING DATE: 24-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Skoog, Mark T
;; REGISTRATION NUMBER: 40,178
;; REFERENCE/DOCKET NUMBER: 10552.13US01
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 612-332-5300
;; TELEFAX: 612-332-9081
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9934 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: Genomic DNA
;; US-08-977-171-2

Query Match 49.8%; Score 20.4; DB 4; Length 9934;
Best Local Similarity 71.1%; Pred. No. 97;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 3 GGGCACCAGCGGCGCCCAAGGCTGCGGCCCGAGC 40
Db 2651 GGGCACCAGCGGCGGCAAGCATGACTCGGCCCAACC 2614

RESULT 12
PCT-US91-00899-13/C
; Sequence 13, Application PCT/US9100899
; GENERAL INFORMATION:
; APPLICANT: Lowe, John B.
; TITLE OF INVENTION: Method and Products For the Synthesis of
; TITLE OF INVENTION: Oligosaccharide Structures on Glycoproteins, Glycolipids,
; TITLE OF INVENTION: or as Free Molecules, and For the Isolation of Cloned
; TITLE OF INVENTION: Genetic Sequences That Determine These Structures
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/00899
; FILING DATE: 19910214
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye Ph.D., Jean-Paul
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-021-55 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-5940
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1068 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; PCT-US91-00899-13

Query Match 49.3%; Score 20.2; DB 5; Length 1068;
Best Local Similarity 75.8%; Pred. No. 1.2e+02;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 7 ACCGAGCGAGCCCAAGGCTGTGGCCCCGAG 39
||| ||||| ||||| ||| ||||| |||
DB 356 ACCGAGCGCTGGCCCGGGGCGCTGGCGAG 324

RESULT 13

PCT-US91-00899-5/c
Sequence 5, Application PC/TUS9100899

GENERAL INFORMATION:

APPLICANT: LOWE, JOHN B.

TITLE OF INVENTION: Method and Products For the Synthesis of

TITLE OF INVENTION: Oligosaccharide Structures on Glycoproteins, Glycolipids,

TITLE OF INVENTION: or as Free Molecules, and For the Isolation of Cloned

TITLE OF INVENTION: Genetic Sequences That Determine These Structures

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

STREET: 1755 Jefferson Davis Highway, Suite 400

CITY: Arlington

STATE: Virginia

ZIP: 22202

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US91/00899

FILING DATE: 19910214

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Lavalleye Ph.D., Jean-Paul

REGISTRATION NUMBER: 31,451

REFERENCE/DOCKET NUMBER: 2363-021-55 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)521-5940

TELEFAX: (703)486-2347

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1215 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

PCT-US91-00899-5

Query Match 49.3%; Score 20.2; DB 5; Length 1215;

Best Local Similarity 75.8%; Pred. No. 1.2e+02;

Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 7 ACCGAGCGAGCCCAAGGCTGTGGCCCCGAG 39

||| ||||| ||||| ||| ||||| |||

DB 503 ACCGAGCGTGGCCCGGGGCGCTGGCGAG 471

RESULT 14

US-07-914-281-9/c

Sequence 9, Application US/07914281

Patent No. 5324663

GENERAL INFORMATION:

APPLICANT: LOWE, JOHN B.

TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS

TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,

TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION

TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

STREET: 1755 Jefferson Davis Highway, Fourth Floor

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/914,281

FILING DATE: 19920720

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Lavalleye, Jean-Paul M. P.

REGISTRATION NUMBER: 31,451

REFERENCE/DOCKET NUMBER: 2363-060-55

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)521-4500

TELEFAX: (703)486-2347

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 1488 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

US-07-914-281-9

Query Match 49.3%; Score 20.2; DB 1; Length 1488;

Best Local Similarity 75.8%; Pred. No. 1.2e+02;

Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 7 ACCGAGCGAGCCCAAGGCTGTGGCCCCGAG 39

||| ||||| ||||| ||| ||||| |||

DB 776 ACCGAGCGTGGCCCGGGGCGCTGGCGAG 744

RESULT 15

US-08-393-246-9/c

Sequence 9, Application US/08393246

Patent No. 5595900

GENERAL INFORMATION:

APPLICANT: LOWE, JOHN B.

TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS

TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,

TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION

TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

STREET: 1755 Jefferson Davis Highway, Fourth Floor

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/393,246

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/220,433

FILING DATE: 30-MAR-1994

APPLICATION NUMBER: US 07/914,281

FILING DATE: 20-JUL-1992

ATTORNEY/AGENT INFORMATION:

NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1488 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-393-246-9

Query Match 49.3%; Score 20.2; DB 1; Length 1488;
Best Local Similarity 75.8%; Pred. No. 1.2e+02;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 7 ACCGAGCGCAGGCCCAAGGGCTGTGGGCCCGAG 39
||| ||||| ||||| ||| ||||| |||
Db 776 ACCGAGCGCTGGCCCGGGGGCTGTGGGCTGTGAG 744

Search completed: February 13, 2003, 07:47:55
Job time : 17.1902 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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Run on: February 13, 2003, 06:22:49 ; Search time 2.82052 Seconds
        (without alignments)
        7403.688 Million cell updates/sec
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Title: US-09-636-259B-2_COPY_730_770

Sequence: 1 gggggcaccgagcgcaaggc.....aaggtcttggtcccgagcg 41

Scoring table: IDENTITY_NUC

Searched: 424239 seqs, 254661826 residues

Total number of hits satisfying chosen parameters: 848478

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 08

Listing first 45 summaries

Database :

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Published.Applications.NA.*
2:  /cgn2_6/plodata2/pubnpa/PCOT_NEW_PUB.seq.*
3:  /cgn2_6/plodata2/pubnpa/US06_NEW_PUB.seq.*
4:  /cgn2_6/plodata2/pubnpa/US06_PUBCOMB.seq.*
5:  /cgn2_6/plodata2/pubnpa/US07_NEW_PUB.seq.*
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14: /cgn2_6/plodata2/pubnpa/US06_PUBCOMB.seq.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	23	56.1	410	10	US-09-983-965-4927	Sequence 4927, Appl
2	22.2	54.1	15504	9	US-10-026-188-6	Sequence 6, Appl
3	22	53.7	2622	10	US-09-815-242-7871	Sequence 7871, Appl
4	21.8	53.2	440	10	US-09-960-352-868	Sequence 868, Appl
5	21.8	53.2	967	10	US-09-764-877-2208	Sequence 2208, Appl
6	21.2	51.7	224	10	US-09-294-093B-3768	Sequence 3768, Appl
7	21.2	51.7	3667	9	US-09-974-298-64	Sequence 64, Appl
8	20.8	50.7	946	10	US-09-864-761-1226	Sequence 1226, Appl
9	20.8	50.7	487	10	US-09-764-877-2858	Sequence 2858, Appl
10	20.8	50.7	2033	10	US-09-759-777-134	Sequence 134, Appl
11	20.8	50.7	2033	10	US-09-947-316-3	Sequence 3, Appl
12	20.8	50.7	2033	12	US-10-044-090-777	Sequence 777, Appl
13	20.8	50.7	7521	9	US-09-819-104A-3	Sequence 3, Appl
14	20.8	50.7	8686	9	US-09-819-104A-1	Sequence 1, Appl
15	20.6	50.2	239	10	US-09-764-860-216	Sequence 216, Appl
16	20.6	50.2	366	10	US-09-783-590-4787	Sequence 4787, Appl
17	20.6	50.2	2750	10	US-09-905-983-51	Sequence 51, Appl
18	20.6	50.2	4000	10	US-09-954-456-2153	Sequence 2153, Appl
19	20.6	50.2	4000	10	US-09-860-107-3803	Sequence 3803, Appl

20	20.4	49.8	1598	10	US-09-815-242-1770	Sequence 7770, App
21	20.4	49.8	6143	10	US-09-880-107-1536	Sequence 1536, App
22	20.4	49.8	9775	10	US-09-751-962-1	Sequence 1, App11
23	20.4	49.8	9775	10	US-09-751-962-2	Sequence 2, App11
24	20.4	49.8	4354	10	US-09-864-761-15679	Sequence 15679, App
25	20.2	49.3	1687	10	US-09-764-877-2209	Sequence 2209, App
26	20.2	49.3	968	10	US-09-863-475A-9	Sequence 9, App1
27	20.2	49.3	1966	9	US-09-764-868-152	Sequence 152, App
28	20.2	49.3	2466	12	US-10-044-090-051	Sequence 251, App
29	20.2	49.3	3387	10	US-09-789-481C-3	Sequence 3, App11
30	20.2	49.3	3647	10	US-09-863-475A-7	Sequence 7, App11
31	20.2	49.3	3500	10	US-09-789-481C-1	Sequence 1, App11
32	20	48.8	179	9	US-09-783-590-280	Sequence 280, App
33	20	48.8	491	9	US-09-854-133-305	Sequence 305, App
34	20	48.8	491	10	US-09-738-973-305	Sequence 305, App
35	20	48.8	1809	9	US-10-124-429-3	Sequence 3, App11
36	20	48.8	5597	10	US-09-865-872-4	Sequence 4, App11
37	20	48.8	5597	10	US-09-966-552-4	Sequence 4, App11
38	19.8	48.3	430	10	US-09-960-552-4	Sequence 4, App11
39	19.8	48.3	463	10	US-09-764-869-1603	Sequence 4598, App
40	19.8	48.3	578	10	US-09-864-761-9336	Sequence 1603, App
41	19.8	48.3	658	9	US-09-883-125-11	Sequence 9336, App
42	19.8	48.3	1002	9	US-09-995-225-1	Sequence 11, App1
43	19.8	48.3	1002	9	US-09-990-960-3	Sequence 1, App11
44	19.8	48.3	1051	10	US-09-917-800A-1473	Sequence 3, App11
45	19.8	48.3	1436	9	US-09-975-719-131	Sequence 1473, App
						Sequence 131, App

ALIGNMENTS

RESULT 1

```

: Sequence 4927, Application US/09983965
: Patent No. US20020137160A1
: GENERAL INFORMATION:
: APPLICANT: Warren, Wesley C.
: APPLICANT: Tao, Nengping
: APPLICANT: Byatt, John C.
: APPLICANT: Mathialagan, Nagappan
: TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
: TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
: FILE REFERENCE: 37-21(10297)C
: CURRENT APPLICATION NUMBER: US/09/983,965
: CURRENT FILING DATE: 2001-10-26
: PRIOR APPLICATION NUMBER: US 09/465,221
: PRIOR FILING DATE: 1999-12-15
: PRIOR APPLICATION NUMBER: US 60/113,678
: PRIOR FILING DATE: 1998-12-17
: NUMBER OF SEQ ID NOS: 5912
: SEQ ID NO 4927
: LENGTH: 410
: TYPE: DNA
: ORGANISM: Bos taurus
: FEATURE:
: OTHER INFORMATION: Clone ID: 25-LIB34-026-Q1-E1-G9
: US-09-983-965-4927

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Query Match	56.18;	Score 23;	DB 10;	Length 410;
Best Local Similarity	74.48;	Pred. No. 16;		
Matches 29;	Conservative	0;	Mismatches 10;	Indels 0;
			Gaps	0

QY 2 GGGCACCAGCGCAGGCCCAAGGCTGTGCCCCGAGC 40
||||| ||| ||||| ||| ||||| |||||
Db 10 GGGCCCCAAGCAGCAGCTGGCAGGCTTGCGCCCTGAGC 48

RESULT 2
US-10-026-188-6/c
Sequence 6, Application US/10026188
; Patent No. US20020164645A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.

```
APPLICANT: Zhang, Yifeng
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
TITLE OF INVENTION: Ion Channel
FILE REFERENCE: 02307E-114910US
CURRENT APPLICATION NUMBER: US/10/026,188
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US 60/259,379
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 155074
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human genomic region containing Itprc5
OTHER INFORMATION: (Human Chromosome 11p15.5 PAC clone PD0915f1)
OTHER INFORMATION: containing KVLQT1 gene)
US-10-026-188-6
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Query Match          54.1%; Score 22.2; DB 9; Length 155074;
Best Local Similarity 77.1%; Pred. No. 29;
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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QY 6 CACCGAGCGAGCCCGAGGCTCTGGGCCCCGAGC 40
Db 51942 CTCACGCGCCGAGCCGAGGCTCTGGGCCCCGAGTGC 51908
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RESULT 3
US-09-815-242-7871
Sequence 7871, Application US/09815242
Patent No. US2002006159A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: EITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7871
LENGTH: 2622
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2622)
US-09-815-242-7871
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Query Match          53.7%; Score 22; DB 10; Length 2622;
Best Local Similarity 73.7%; Pred. No. 34;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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QY 4 GGCACCGAGCGCAGGCCCAAGGCTCTGGGCCCCGAGCG 41
Db 1228 GGCAGCGACGCTCGAGGCCCAAGGCTCTGGGCCCCGAGCG 1265
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RESULT 4
US-09-960-352-3868
Sequence 3868, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengping
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 3868
LENGTH: 440
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 17-LIB3058-018-Q1-K1-E9
US-09-960-352-3868
```

```
Query Match          53.2%; Score 21.8; DB 10; Length 440;
Best Local Similarity 70.7%; Pred. No. 40;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
```

```
QY 1 GGGGCGACCGAGCGCAGGCCCAAGGCTCTGGGCCCCGAGCG 41
Db 22 GGGGCGCGGAGCGCAGGACGAGCGACCGCGCGCTGAGCG 62
```

```
RESULT 5
US-09-764-877-2208/C
Sequence 2208, Application US/09764877
Patent No. US20020147140A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2208
LENGTH: 967
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-877-2208
```

```
Query Match          53.2%; Score 21.8; DB 10; Length 967;
Best Local Similarity 78.8%; Pred. No. 39;
Matches 26; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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```
QY 8 CCGAGCGCAGGCCCAAGGCTCTGGGCCCCGAGC 40
Db 543 CTTCTCTAGAGCCAGGAGGCTCTGGGCCCGCAGC 511
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```
RESULT 6
US-09-294-093B-3768
Sequence 3768, Application US/09294093B
Patent No. US20010051335A1
GENERAL INFORMATION:
```

```
; APPLICANT: Laljudi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 3768
; LENGTH: 224
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700282543H2
; NAME/KEY: unsure
; LOCATION: 2, 19, 27, 35, 46, 51-52, 57, 102, 119, 122, 124, 127, 131, 165, 185,
; OTHER INFORMATION: a, t, c, g, or other
; US-09-294-093B-3768
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```
Query Match          51.7%; Score 21.2; DB 10; Length 224;
Best Local Similarity 74.3%; Pred. No. 63;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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```
OY 7 ACCGACGCGAGCCCAAGGCTGTGGCCCGCG 41
    | | | | | | | | | | | | | | | | | |
Db 138 AGCTGGCGACGCGCCCAAGGCTATCGACNCCCGCG 172
```

```
RESULT 7
; US-09-974-298-64
; Sequence 64, Application US/09974298
; Patent No. US20020156263A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Huel-mei
; TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
; FILE REFERENCE: PA-0037 P
; CURRENT APPLICATION NUMBER: US/09/974,298
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,331
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 64
; LENGTH: 3667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020156263A1 234537.3
; US-09-974-298-64
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```
Query Match          51.7%; Score 21.2; DB 9; Length 3667;
Best Local Similarity 76.5%; Pred. No. 62;
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
OY 2 GGGGACCGAGCGCGCCCAAGGCTGTGGGCC 35
    | | | | | | | | | | | | | | | | | |
Db 65 GGGGACCGAGCGCGCCCGCTTAGCTGTGCCCC 98
```

```
RESULT 8
; US-09-864-761-1226/c
; Sequence 1226, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
```

```
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 1226
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006328.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.9
; OTHER INFORMATION: EXPRESSED IN HL100, SIGNAL = 5.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.9
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 9.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 8.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.6
; US-09-864-761-1226
```

```
Query Match          50.7%; Score 20.8; DB 10; Length 487;
Best Local Similarity 70.0%; Pred. No. 85;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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```
OY 2 GGGGACCGAGCGCGCCCAAGGCTGTGGCCCGCG 41
    | | | | | | | | | | | | | | | | | |
Db 186 GGGGACCGAGCGCGCGCTAGAGTGTGAGCCAGGTGAG 147
```

```
RESULT 9
; US-09-764-877-2858
; Sequence 2858, Application US/09764877
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```
/ Patent No. US20020147140A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PC005
/ CURRENT APPLICATION NUMBER: US/09/764,877
/ CURRENT FILING DATE: 2001-01-17
/ PRIOR APPLICATION data removed - refer to PALM or file wrapper
/ NUMBER OF SEQ ID NOS: 4031
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2858
/ LENGTH: 946
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-764-877-2858

Query Match
Best Local Similarity 50.7%; Score 20.8; DB 10; Length 946;
                          70.0%; Pred. No. 85;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2 GGGGACCGAGCGCGAGCCCAAGGCTGTGGCCCGGAGCG 41
DB 185 GGGGACCGAGCGCGAGCGCTCAAGAGCTGTGAGCCAGGTGAG 224

RESULT 10
US-09-799-777-134/C
/ Sequence 134, Application US/09799777
/ Patent No. US20020091244A1
/ GENERAL INFORMATION:
/ APPLICANT: Lal, Preeti
/ Hillman, Jennifer L.
/ Corley, Neil C.
/ Guegler, Karl J.
/ Baugh, Marian
/ Sather, Susan
/ Shah, Purvi
/ TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
/ NUMBER OF SEQUENCES: 154
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/799,777
/ FILING DATE: 06-Mar-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/002,485
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BILLINGS, LUCY J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0459 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 134:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2033 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: BRAITUT21
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/ CLONE: 2518547
/ SEQUENCE DESCRIPTION: SEQ ID NO: 134 :
/ US-09-799-777-134

Query Match
Best Local Similarity 50.7%; Score 20.8; DB 10; Length 2033;
                          70.0%; Pred. No. 85;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 GGGGACCGAGCGCGAGCCCAAGGCTGTGGCCCGGAGCG 40
DB 371 GGGGACCTGGCGCGGAGATCAAGGCTGTGACACTGAGC 332

RESULT 11
US-09-947-316-3/C
/ Sequence 3, Application US/09947316
/ Patent No. US20020103339A1
/ GENERAL INFORMATION:
/ APPLICANT: Jennifer L. Hillman
/ Hillman, Preeti Lal
/ APPLICANT: Neil C. Corley
/ Corley, Karl J. Guegler
/ Guegler, Chandra Patterson
/ TITLE OF INVENTION: INTERFERON-RESPONSIVE PROTEIN
/ FILE REFERENCE: PF-0459-1 CIP
/ CURRENT APPLICATION NUMBER: US/09/947,316
/ CURRENT FILING DATE: 2001-09-05
/ PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/157,091
/ PRIOR FILING DATE: 1998-09-18
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PERL Program
/ SEQ ID NO 3
/ LENGTH: 2033
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE: -
/ OTHER INFORMATION: 2518547
/ US-09-947-316-3

Query Match
Best Local Similarity 50.7%; Score 20.8; DB 10; Length 2033;
                          70.0%; Pred. No. 85;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 GGGGACCGAGCGCGAGCCCAAGGCTGTGGCCCGGAGCG 40
DB 371 GGGGACCTGGCGCGGAGATCAAGGCTGTGACACTGAGC 332

RESULT 12
US-10-044-090-777/C
/ Sequence 777, Application US/10044090
/ Patent No. US20020137081A1
/ GENERAL INFORMATION:
/ APPLICANT: Olga Bandman
/ TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
/ FILE REFERENCE: PA-0028 US
/ CURRENT APPLICATION NUMBER: US/10/044,090
/ CURRENT FILING DATE: 2002-01-09
/ NUMBER OF SEQ ID NOS: 850
/ SOFTWARE: PERL Program
/ SEQ ID NO 777
/ LENGTH: 2033
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ OTHER INFORMATION: Incyte ID NO. US20020137081A1 2518547CBI
/ US-10-044-090-777

Query Match
Best Local Similarity 50.7%; Score 20.8; DB 12; Length 2033;
                          70.0%; Pred. No. 85;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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Qy 1 GGGGACCGAGCGAGCCCAAGGCTGTGCGCCCGAGC 40
|||||
Db 371 GGGGACACTGGCGCGGGAATCAAGGCTGTGACACTGAGC 332

RESULT 13
US-09-819-104A-3/C
; Sequence 3, Application US/09819104A
; Publication No. US20030027137A1
; GENERAL INFORMATION:
; APPLICANT: Chen, J. Don
; TITLE OF INVENTION: NOVEL NUCLEAR RECEPTOR COREPRESSOR MOLECULES
; FILE REFERENCE: UMG-030
; CURRENT APPLICATION NUMBER: US/09/819,104A
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/193,138
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 7521
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(7521)
US-09-819-104A-3

Query Match
Best Local Similarity 50.7%; Score 20.8; DB 9; Length 7521;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 2 GGGGACCGAGCGAGCCCAAGGCTGTGCGCCCGAGC 41
|||
Db 4577 GGCTTACCGACGCTCAGCAGCAATGACCGGCGCCGCGC 4538

RESULT 14
US-09-819-104A-1/C
; Sequence 1, Application US/09819104A
; Publication No. US20030027137A1
; GENERAL INFORMATION:
; APPLICANT: Chen, J. Don
; TITLE OF INVENTION: NOVEL NUCLEAR RECEPTOR COREPRESSOR MOLECULES
; FILE REFERENCE: UMG-030
; CURRENT APPLICATION NUMBER: US/09/819,104A
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/193,138
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8686
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (157)..(7677)
US-09-819-104A-1

Query Match
Best Local Similarity 50.7%; Score 20.8; DB 9; Length 8686;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 2 GGGGACCGAGCGAGCCCAAGGCTGTGCGCCCGAGC 41
|||
Db 4733 GGCTTACCGACGCTCAGCAGCAATGACCGGCGCCGCGC 4694

RESULT 15
US-09-764-860-216

; Sequence 216, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; PRIOR FILING DATE: 2001-01-17
; PRIOR application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 216
; LENGTH: 239
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (55)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-860-216

Query Match
Best Local Similarity 50.2%; Score 20.6; DB 10; Length 239;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 5 GCACCGAGCGAGCCCAAGGCTGTGCGCCCGAGC 39
|||||
Db 72 GCACCGAGCTCAGCAGCAGGCGCCGAGCGCCGAG 106

Search completed: February 13, 2003, 07:51:28
Job time : 54.8205 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 15, 2003, 13:41:57 ; Search time 47 Seconds

(without alignments)
1275.804 Million cell updates/sec

Title: us-09-636-259b-4

Perfect score: 2380
Sequence: 1 MGSIQPDAGNASWNGTEAPG.....HDFRAFKKILCRGRKRTV 450

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2380	100.0	450	22	AAW52123
2	2375	99.8	450	22	AAW52122
3	1553	65.3	324	10	AAW50552
4	1537	64.6	330	15	AAW48700
5	1537	64.6	330	17	AAW02672
6	1523	64.0	334	15	AAW48701
7	1523	64.0	334	17	AAW02673
8	1454.5	61.1	307	22	AAW08334
9	1171	49.2	458	15	AAW54834
10	1139.5	48.7	461	22	AAW52124
					Human alpha-2CAR p

11	1150.5	48.3	457	22	AAW52126	Human alpha-2CAR v
12	1126.5	47.3	450	22	AAW52117	Human alpha-2BAR t
13	1126.5	47.3	450	22	AAE00990	Human alpha2B-adre
14	1126	47.3	447	22	AAW52118	Human alpha-2BAR t
15	1126	47.3	447	22	AAE00989	Human alpha2B-adre
16	1094.5	46.0	487	12	AAW14149	Human alpha-2 beta
17	1094.5	46.0	487	18	AAW11804	Human alpha-2b adr
18	1046.5	44.0	330	15	AAW48698	G-protein coupled
19	1046.5	44.0	330	17	AAW02670	G-protein coupled
20	1029	43.2	330	15	AAW48699	G-protein coupled
21	1029	43.2	330	17	AAW02671	G-protein coupled
22	895	37.6	437	22	AAW52119	G-protein coupled
23	881.5	38.6	379	18	AAW33185	Sheep/guinea pig c
24	652	27.4	476	18	AAW24089	Corn barnacle G-pr
25	649	27.3	601	13	AAW21931	Balanus amphitrite
26	649	27.3	601	22	ABW63318	D.melanogaster oct
27	649	27.3	601	23	AAW80701	Drosophila melanog
28	649	27.3	601	23	AAW17036	D. melanogaster oc
29	627	26.3	414	12	AAW11800	Drosophila melanog
30	621.5	26.1	443	11	AAW05549	Human retinal dopa
31	621.5	26.1	443	12	AAW11497	Human pituitary do
32	621.5	26.1	443	20	AAW01600	Human dopamine D2 r
33	621.5	26.1	443	22	AAW76292	Human D2 dopamine
34	621.5	26.1	443	22	AAW69075	Human D2 dopamine
35	621.5	26.1	443	23	AAW51019	Human D2 dopamine
36	618.5	26.0	415	11	AAW05539	Human D2 dopamine
37	618.5	26.0	415	20	AAW01598	Rat D2 dopamine re
38	617.5	25.9	415	17	AAW09388	Rat D2 dopamine re
39	615.5	25.9	415	22	AAW08332	Rat D2 dopamine re
40	615.5	25.9	415	23	AAW51017	Rat D2 dopamine re
41	614.5	25.8	443	22	ABW56348	Non-endogenous hum
42	613	25.8	444	12	AAW10544	D2 dopamine recept
43	613	25.8	444	17	AAW09387	Mouse dopamine D2
44	590	24.8	422	22	AAW70249	HTR1A protein. Ho
45	589	24.7	637	20	AAW13445	Invertebrate octop

ALIGNMENTS

RESULT 1	AAW52123	standard; Protein: 450 AA.
ID	AAW52123	
AC	AAW52123;	
XX		
DT	18-FEB-2002 (first entry)	
XX		
DE	Human alpha-2AAR variant protein.	
XX		
KW	Human: genotyping; alpha-2B; alpha-2C; adrenergic receptor;	
KW	polymorphic site; allelic variant; cardiovascular disease;	
KW	central nervous system disease; adenylyl cyclase; MAP kinase activity;	
KW	phosphorylation; inositol phosphate; alpha-2AAR.	
OS	Homo sapiens.	
XX		
FH		
FT	Key	Location/Qualifiers
XX	Misc-difference 251	/note= "Wild-type Asn substituted by Lys"
XX		
XX	WO200179561-A2.	
XX		
PD	25-OCT-2001.	
XX		
PF	17-APR-2001; 2001WO-0512575.	
XX		
PR	17-APR-2000; 2000US-0551744.	
PR	10-AUG-2000; 2000US-0636259.	
PR	19-OCT-2000; 2000US-0692077.	
XX		
XX	(LIGG/) LIGGETT S B.	
PA	(SMAL/) SMALL K M.	

```

XX  Liggett SB, Small KM;
PI
XX
XX  WPI: 2001-611728/70.
DR  N-PSDB; AAI99918.
PT  Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT  determining whether an individual is at increased risk of developing a
PT  disease associated with the corresponding receptor comprises detecting
PT  a polymorphic site -
XX
XX  Claim 48: Page 154-155; 163pp; English.
PS
XX  The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
XX  receptor gene (I)-(III) by detecting a polymorphic site, comprising:
XX  (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
XX  alpha2A or alpha2C or fragment or complement of; and
XX  (b) detecting a polymorphic site comprising nucleotide positions 901-909
XX  of (I), a site comprising cytosine or guanine at position 753 of (II)
XX  or a site comprising (A) (99ggcg9g9ccg) or (B) (99ggcg9ct9ag) at
XX  positions 961-972 of (III). The method may be used for genotyping an
XX  alpha2B, alpha2A or alpha2C receptor gene and further used to determine
XX  whether an individual is at increased risk of developing a disease
XX  associated with alpha2B, alpha2A or alpha2, comprising detecting a
XX  polymorphic site which correlate to disease selected from cardiovascular
XX  disease, central nervous system disease and combinations of these. In
XX  addition, the technique may be used to predict an individual's response
XX  to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
XX  norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
XX  combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
XX  rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of
XX  these) by detecting the polymorphic site and correlating the site to a
XX  predetermined response (where the response is correlated to adenylyl
XX  cyclase, MAP kinase activity, phosphorylation or inositol phosphate
XX  levels). The present sequence is that of the human alpha-2AAR variant
XX
XX  Sequence 450 AA;
SQ
XX  Query Match 100.0%; Score 2380; DB 22; Length 450;
XX  Best Local Similarity 100.0%; Pred. No. 3.3e-172;
XX  Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSLOPDGNSMNGTEAPGGARATPYSLQVTLTLCAGLMLTFVGNVLTIVFT 60
DB 1 MGSLOPDGNSMNGTEAPGGARATPYSLQVTLTLCAGLMLTFVGNVLTIVFT 60
QY 61 SRALKAPQNLFLVSLASADILVATLVTFPSLANEVMGYWFGKWCETIYALDVLCTSS 120
DB 61 SRALKAPQNLFLVSLASADILVATLVTFPSLANEVMGYWFGKWCETIYALDVLCTSS 120
QY 121 IVHCAISLDKRYWSTQAIENLNKTRPRKAIITTWVWISAVISFPPLISIEKKGGGG 180
DB 121 IVHCAISLDKRYWSTQAIENLNKTRPRKAIITTWVWISAVISFPPLISIEKKGGGG 180
QY 121 IVHCAISLDKRYWSTQAIENLNKTRPRKAIITTWVWISAVISFPPLISIEKKGGGG 180
DB 121 IVHCAISLDKRYWSTQAIENLNKTRPRKAIITTWVWISAVISFPPLISIEKKGGGG 180
QY 181 POPAPRCEINDOKWYVSSICGSFPAFLIMILVYRITQIAKRRTRVPSRGPDAVA 240
DB 181 POPAPRCEINDOKWYVSSICGSFPAFLIMILVYRITQIAKRRTRVPSRGPDAVA 240
QY 241 APPGCTERRPKGLPERSAGFGAEAEPLPTQNLGAGCEPAPAPRDTADLDESSSSD 300
DB 241 APPGCTERRPKGLPERSAGFGAEAEPLPTQNLGAGCEPAPAPRDTADLDESSSSD 300
QY 301 HAERPGRPRERGRGKARASQVKKPGDSLPRGPGANGIGTPAGPGERVGAAKAS 360
DB 301 HAERPGRPRERGRGKARASQVKKPGDSLPRGPGANGIGTPAGPGERVGAAKAS 360
QY 361 RMRGQNRKERTFVLAVIVGVFVVCWPFPTTLTAVGCSVRLTFFKFFMFGYCNSS 420
DB 361 RMRGQNRKERTFVLAVIVGVFVVCWPFPTTLTAVGCSVRLTFFKFFMFGYCNSS 420
QY 421 LNPVYITFNHDFRRAFKILCRGDKRIV 450
DB 421 LNPVYITFNHDFRRAFKILCRGDKRIV 450

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DB 421 LNPVYITFNHDFRRAFKILCRGDKRIV 450
XX
XX  RESULT 2
XX  AAM52122
XX  AAM52122 standard; Protein: 450 AA.
XX
XX  AAM52122:
XX  18-FEB-2002 (first entry)
XX
XX  Human alpha-2AAR protein.
XX
XX  Human: genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
XX  polymorphic site; allelic variant; cardiovascular disease;
XX  central nervous system disease; adenylyl cyclase; MAP kinase activity;
XX  phosphorylation; inositol phosphate; alpha-2AAR.
XX
XX  Homo sapiens.
XX
XX  WO200179561-A2.
XX
XX  25-OCT-2001.
XX
XX  17-APR-2001; 2001WO-US12575.
XX
XX  17-APR-2000; 2000US-0551744.
XX  10-AUG-2000; 2000US-0636259.
XX  19-OCT-2000; 2000US-0692077.
XX
XX  (LIGG/) LIGGETT S B.
XX  (SMAL/) SMALL K M.
XX
XX  Liggett SB, Small KM;
XX
XX  WPI: 2001-611728/70.
XX  N-PSDB; AAI99917.
XX
XX  Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
XX  determining whether an individual is at increased risk of developing a
XX  disease associated with the corresponding receptor comprises detecting
XX  a polymorphic site -
XX
XX  Claim 48: Page 152-154; 163pp; English.
PS
XX  The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
XX  receptor gene (I)-(III) by detecting a polymorphic site, comprising:
XX  (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
XX  alpha2A or alpha2C or fragment or complement of; and
XX  (b) detecting a polymorphic site comprising nucleotide positions 901-909
XX  of (I), a site comprising cytosine or guanine at position 753 of (II)
XX  or a site comprising (A) (99ggcg9g9ccg) or (B) (99ggcg9ct9ag) at
XX  positions 961-972 of (III). The method may be used for genotyping an
XX  alpha2B, alpha2A or alpha2C receptor gene and further used to determine
XX  whether an individual is at increased risk of developing a disease
XX  associated with alpha2B, alpha2A or alpha2, comprising detecting a
XX  polymorphic site which correlate to disease selected from cardiovascular
XX  disease, central nervous system disease and combinations of these. In
XX  addition, the technique may be used to predict an individual's response
XX  to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
XX  norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
XX  combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
XX  rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of
XX  these) by detecting the polymorphic site and correlating the site to a
XX  predetermined response (where the response is correlated to adenylyl
XX  cyclase, MAP kinase activity, phosphorylation or inositol phosphate
XX  levels). The present sequence is that of the human alpha-2AAR protein.
XX
XX  Sequence 450 AA;
SQ
XX  Query Match 99.8%; Score 2375; DB 22; Length 450;
XX  Best Local Similarity 99.8%; Pred. No. 8e-172;
XX  Matches 449; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MSLQPDAGNASMNGTEAPGGARATPYSLQVTLTVCLAGLMLTVFGNVLTIAVFT 60
   |||||
Db 1 MSLQPDAGNASMNGTEAPGGARATPYSLQVTLTVCLAGLMLTVFGNVLTIAVFT 60
OY 61 SRALKAPONLFLVSLASADILVATLVIPFSLANEVWGTYFGKAMCEIYIALDLVLEFCTSS 120
   |||||
Db 61 SRALKAPONLFLVSLASADILVATLVIPFSLANEVWGTYFGKAMCEIYIALDLVLEFCTSS 120
OY 121 IVHLCALISLDRYWSTQIAIEYNLKRTPRRIKAIITVWVISAVISFPPLISIEKKGCGG 180
   |||||
Db 121 IVHLCALISLDRYWSTQIAIEYNLKRTPRRIKAIITVWVISAVISFPPLISIEKKGCGG 180
OY 181 POPAEPCEINDQKMYVVISCSIGSFAPCLIMLVYRIYQIAKRRTRVPSRRGPDAVA 240
   |||||
Db 181 POPAEPCEINDQKMYVVISCSIGSFAPCLIMLVYRIYQIAKRRTRVPSRRGPDAVA 240
OY 241 APPGTERPKGLCPERSAGPGAEAEPLPTQLNGAPGEPAAPAGPRDTDALDLESSSSD 300
   |||||
Db 241 APPGTERPKGLCPERSAGPGAEAEPLPTQLNGAPGEPAAPAGPRDTDALDLESSSSD 300
OY 301 HAERPPGPRPERGPRGKGARASQVKGDSLPRRGGATGCTPAAGPEERVGAKAKAS 360
   |||||
Db 301 HAERPPGPRPERGPRGKGARASQVKGDSLPRRGGATGCTPAAGPEERVGAKAKAS 360
OY 361 RWRGRONREKRFTFVLAVVIGVFCWFPPEFTYTLTAVGCSVPRTLKFFFMFGYCNS 420
   |||||
Db 361 RWRGRONREKRFTFVLAVVIGVFCWFPPEFTYTLTAVGCSVPRTLKFFFMFGYCNS 420
OY 421 LNPVITYITFNHDFRRAFKKILCRGDRKRIY 450
   |||||
Db 421 LNPVITYITFNHDFRRAFKKILCRGDRKRIY 450

RESULT 3
AAP90552
ID AAP90552 standard; protein: 324 AA.
XX
AC AAP90552:
XX
DT 16-FEB-1990 (first entry)
XX
DE Hamster beta-2 -adrenergic receptor.
XX
KW Alpha-2 -adrenergic receptor; 5HT1c receptor.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 38..58
FT /label=I
FT /note="transmembrane domain"
FT 70..90
FT /label=II
FT /note="transmembrane domain"
FT 107..128
FT /label=III
FT /note="transmembrane domain"
FT 148..172
FT /label=IV
FT /note="transmembrane domain"
FT 192..215
FT /label=V
FT /note="transmembrane domain"
FT 249..271
FT /label=VI
FT /note="transmembrane domain"
FT 281..303
FT /label=VII
FT /note="transmembrane domain"
FT 327
FT /note="125 bp cytoplasmic loop"
XX

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PN W08918149-A.
XX
XX 08-SEP-1989.
PD
XX
XX 28-FEB-1989; 89MO-US00808.
PF
XX
XX 29-FEB-1988; 88US-0162654.
PR
XX
XX (UYCO-) COLUMBIA UNIVERSITY.
PA
XX
XX Axel R, Jessell TM;
PI
XX
XX WPI; 1989-278308/38.
DR
XX
XX DNA encoding serotonin 5HT1c receptor - used for producing protein,
PT antibodies and probes for studying receptor binding and screening drugs.
XX
XX Disclosure; Fig 11; 84pp; English.
XX
XX Sequence codes for human alpha 2 adrenergic receptor.
CC
CC See also AAP90549-p90554, AAP92111 and AAN90955.
XX
XX Sequence 324 AA:
SQ

Query Match          65.3%; Score 1553; DB 10; Length 324;
Best Local Similarity 70.4%; Pred. No. 9,8e-110;
Matches 317; Conservative 0; Mismatches 7; Indels 126; Gaps 4;

OY 1 MSLQPDAGNASMNGTEAPGGARATPYSLQVTLTVCLAGLMLTVFGNVLTIAVFT 60
   |||||
Db 1 MSLQPDAGNASMNGTEAPGGARATPYSLQVTLTVCLAGLMLTVFGNVLTIAVFT 60
OY 61 SRALKAPONLFLVSLASADILVATLVIPFSLANEVWGTYFGKAMCEIYIALDLVLEFCTSS 120
   |||||
Db 61 SRALKAPONLFLVSLASADILVATLVIPFSLANEVWGTYFGKAMCEIYIALDLVLEFCTSS 119
OY 121 IVHLCALISLDRYWSTQIAIEYNLKRTPRRIKAIITVWVISAVISFPPLISIEKKGCGG 180
   |||||
Db 121 IVHLCALISLDRYWSTQIAIEYNLKRTPRRIKAIITVWVISAVISFPPLISIEKKGCGG 178
OY 181 POPAEPCEINDQKMYVVISCSIGSFAPCLIMLVYRIYQIAKRRTRVPSRRGPDAVA 240
   |||||
Db 181 POPAEPCEINDQKMYVVISCSIGSFAPCLIMLVYRIYQIAKRRTRVPSRRGPDAVA 240
OY 179 POPAEPCEINDQKMYVVISCSIGSFAPCLIMLVYRIYQIAKRRTRVPSRRGPDAVA 226
   |||||
OY 241 APPGTERPKGLCPERSAGPGAEAEPLPTQLNGAPGEPAAPAGPRDTDALDLESSSSD 300
   |||||
Db 227 -----
OY 301 HAERPPGPRPERGPRGKGARASQVKGDSLPRRGGATGCTPAAGPEERVGAKAKAS 360
   |||||
Db 227 -----XSGLPRRRAGA----- 237
OY 361 RWRGRONREKRFTFVLAVVIGVFCWFPPEFTYTLTAVGCSVPRTLKFFFMFGYCNS 420
   |||||
Db 238 ---GGQNRKREKRTFVLAVVIGVFCWFPPEFTYTLTAVGCSVPRTLKFFFMFGYCNS 294
   |||||
OY 421 LNPVITYITFNHDFRRAFKKILCRGDRKRIY 450
   |||||
Db 295 LNPVITYITFNHDFRRAFKKILCRGDRKRIY 324

RESULT 4
AAR48700
ID AAR48700 standard; Protein: 330 AA.
XX
XX
AC AAR48700;
XX
DT 05-JUN-1996 (first entry)
XX
DE G-protein coupled human alpha-2 C10 adrenergic receptor protein.
XX
XX G-protein coupled receptor; ligand binding assay; transmembrane domain;
KW psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin;

```

KW muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;
 KW rhodopsin; opsin; odorant; cytomegalovirus.
 XX Homo sapiens.
 OS
 XX WO9405695-A1.
 PN
 XX 17-MAR-1994.
 PD
 XX 09-SEP-1993; 93WO-US08528.
 PF
 XX 10-SEP-1992; 92US-0943236.
 PR
 XX (UYNV) UNIV NEW YORK STATE.
 PA
 XX Murphy RB, Schuster DI;
 PI
 XX WPI; 1994-101120/12.
 DR
 XX Polypeptides of G-coupled receptor proteins (GPRs) - useful for
 PT binding GPR ligands or modulating GPR binding
 PS Disclosure; Page 73-74; 160pp; English.
 XX
 CC Proteins AAR48685-R48758 represent a range of G-protein coupled receptor
 CC proteins selected from cAMP, adenosine, muscarinic acetylcholine,
 CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
 CC odorant, cytomegaloviral and other G-protein coupled receptors. The
 CC receptor proteins were used to design polypeptides, pref. based on the
 CC transmembrane domains, for use in G-protein coupled receptor ligand
 CC binding assays. The polypeptide fragments retain biological activity
 CC such as binding a GPR ligand or modulating GPR ligand binding to a GPR
 CC (see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples
 CC of polypeptide fragments). The polypeptide fragments can be used in
 CC compositions for treating subjects suffering from a pathology related to
 CC a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
 XX
 SQ Sequence 330 AA;
 Query Match 64.6%; Score 1537; DB 15; Length 330;
 Best Local Similarity 74.2%; Pred. No. 1.6e-108;
 Matches 310; Conservative 7; Mismatches 13; Indels 88; Gaps 6;
 QY 33 TLTVACGLMLTVFNGNVLTIAVFTSRALKAPQNLFLVYSASADIVATVIFPSLA 92
 DB 1 TLTVACIA--CLSLTFNGNVLTIAVFTSRALKAPQNLFLVYSASADIVATVIFPSLA 58
 QY 93 NEVMGYWYFGKAWCEIYALDVLCTSSIVHLCALISLDRYWSTIQALEYINKRTPRRIKA 152
 DB 59 NEVMGYWYFGK-WCEIYALDVLCTSSIVHLCALISLDRYWSTIQALEYINKRTPRRIKA 117
 QY 153 IITVWVISAIVISFPPLISIEKKGGGGGPOAPRCEINDOKWYVYSSICISFFAPCLIM 212
 DB 118 IITVWVISAIVISFPPLISIEKKGGGGGPOAPRCEINDOKWYVYSSICISFFAPCLIM 177
 QY 213 ILVYVRIYQIAKRRTRVPPSRGPDVAAPPGGTERPCKGLGPERSGAGGAEAPLPQ 272
 DB 178 -LVYVRIYQIAKRRTRVPPSRGPDVAAPPGGTERPCKGLGPERSGAGGAEAPLPQ----- 227
 QY 273 LMGAPGEPAPGPRDLDLDESSSSDHAERPPGPRRPPGPRGCKGKARASQVKKPGDSL 332
 DB 228 -----GGRHS-----ASGL 236
 QY 333 PRRGATGATGTPAAGPGBERYGAAKARMGRONRERKFTFVLAVGVFVWCFPPFF 392
 DB 237 PRRRGA-----GGQNRKRTFTVIAVAVIGVFVWCFPPFF 272
 QY 393 TTTTAVGCVSPRTLKFEFFWEGYCNSSINPIYITIFNHDFRAAFKTLGDRKRIY 450
 DB 273 TTTTAVGCVSPRTLKFEFFWEGYCNSSINPIYITIFNHDFRAAFKTLGDRKRIY 330

AAW02672
 ID AAW02672 standard; peptide; 330 AA.
 XX
 AC AAW02672;
 XX
 DT 12-NOV-1996 (first entry)
 DE
 XX G-protein coupled human alpha-2 C10 adrenergic receptor.
 XX
 KW G-protein coupled receptor; ligand binding assay; transmembrane domain;
 KW schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin;
 KW muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;
 KW odorant; cytomegalovirus; serotonergic.
 XX
 OS Homo sapiens.
 XX
 PN US5508384-A.
 XX
 PD 16-APR-1996.
 XX
 PF 10-SEP-1992; 92US-0943236.
 PR
 XX 09-SEP-1993; 93US-0118270.
 PR 10-SEP-1992; 92US-0943236.
 XX
 PA (UYNV) UNIV NEW YORK STATE.
 XX
 XX Murphy RB, Schuster DI;
 DR WPI; 1996-208785/21.
 XX
 PT New dopamine receptor peptide - useful as antipsychotic agent, e.g.
 XX for treating schizophrenia
 PS Disclosure; Column 71-74; 184pp; English.
 XX
 CC Proteins AAW02657-W02720 represent a range of G-protein coupled receptor
 CC (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine,
 CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
 CC odorant, cytomegaloviral and other GPR proteins. The receptor proteins
 CC were used to design polypeptides, pref. based on the transmembrane
 CC domains, for use in G-protein coupled receptor ligand binding assays.
 CC The polypeptide fragments retain biological activity such as binding a
 CC GPR ligand or modulating GPR ligand binding to a GPR (see
 CC AAW02747-W02999 for examples of polypeptide fragments). The polypeptide
 CC fragments can be used in compositions for treating subjects suffering
 CC from a pathology related to a GPR abnormality e.g. a psychotic disorder
 CC such as schizophrenia.
 XX
 SQ Sequence 330 AA;
 Query Match 64.6%; Score 1537; DB 17; Length 330;
 Best Local Similarity 74.2%; Pred. No. 1.6e-108;
 Matches 310; Conservative 7; Mismatches 13; Indels 88; Gaps 6;
 QY 33 TLTVACGLMLTVFNGNVLTIAVFTSRALKAPQNLFLVYSASADIVATVIFPSLA 92
 DB 1 TLTVACIA--CLSLTFNGNVLTIAVFTSRALKAPQNLFLVYSASADIVATVIFPSLA 58
 QY 93 NEVMGYWYFGKAWCEIYALDVLCTSSIVHLCALISLDRYWSTIQALEYINKRTPRRIKA 152
 DB 59 NEVMGYWYFGK-WCEIYALDVLCTSSIVHLCALISLDRYWSTIQALEYINKRTPRRIKA 117
 QY 153 IITVWVISAIVISFPPLISIEKKGGGGGPOAPRCEINDOKWYVYSSICISFFAPCLIM 212
 DB 118 IITVWVISAIVISFPPLISIEKKGGGGGPOAPRCEINDOKWYVYSSICISFFAPCLIM 177
 QY 213 ILVYVRIYQIAKRRTRVPPSRGPDVAAPPGGTERPCKGLGPERSGAGGAEAPLPQ 272
 DB 178 -LVYVRIYQIAKRRTRVPPSRGPDVAAPPGGTERPCKGLGPERSGAGGAEAPLPQ----- 227
 QY 273 LMGAPGEPAPGPRDLDLDESSSSDHAERPPGPRRPPGPRGCKGKARASQVKKPGDSL 332

QY	153	IIITWVIVAVISFEP-LTISTEKGGGPOPAEPCEINDOKWYVISCIGSFAPCL	211		
Db	120	IIVTWVIVAVISFPLPLISTEKKGAGGQQAEPESCKINDOKMYVISSISFPA	179		
QY	212	MLLVYRITQIAKKRTRPPSRRGPDVAVAAPGTERRRKGLGSPERSAGPGAEAP	271		
Db	180	NHLVYRITQIAKKRTRPPSRRGPDVACAPGADRRNAGPERRAGTAG	231		
QY	272	QLNGAPGEPAAPGPRDTDALDLESSSDHAERPPGPRPEGPRGKKARASQYK	331		
Db	232	-----	231		
QY	332	LPRRPGATGICTPAAGDEEERVGAAKASRMGRONREKREFVLAVYIGVFV	391		
Db	232	-----GGGEERAGGAKASRMGRONREKREFVLAVYIGVFVCMPPFF	275		
QY	392	FIITLTAVGCSVPRTLFFKFFEFVGYCNSLNPVYITINHDPRAFKIILRGDK	450		
Db	276	FIITLTAVGCSVPYQLEFFEFVGYCNSLNPVYITINHDPRAFKIILRGDK	334		
RESULT 7					
ID	AAW02673				
XX	AAW02673	standard; peptide; 334 AA.			
XX	AAW02673;				
DT	12-NOV-1996	(first entry)			
DE	G-protein coupled rat alpha-2 adrenergic receptor.				
XX					
KW	G-protein coupled receptor; ligand binding assay; transmembrane domain;				
KW	schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin;				
KW	muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;				
KW	odorant; cytomegalovirus; serotonergic.				
OS	Rattus rattus.				
PN	US5508384-A.				
PD	16-APR-1996.				
XX					
PF	10-SEP-1992;	92US-0943236.			
XX					
PR	09-SEP-1993;	93US-0118270.			
XX	10-SEP-1992;	92US-0943236.			
PA	(UYNV) UNIV NEW YORK STATE.				
PI	Murphy RB, Schuster DI;				
DR	WPI; 1996-208785/21.				
PT	New dopamine receptor peptide - useful as antipsychotic agent, e.g.				
PS	for treating schizophrenia				
XX					
XX	Disclosure; Column 73-76; 184pp; English.				
CC	Proteins AAW02657-W02730 represent a range of G-protein coupled receptor				
CC	(GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine,				
CC	adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,				
CC	odorant, cytomegaloviral and other GPR proteins. The receptor proteins				
CC	were used to design polypeptides, pref. based on the transmembrane				
CC	domains, for use in G-protein coupled receptor ligand binding assays.				
CC	The polypeptide fragments retain biological activity such as binding a				
CC	GPR ligand or modulating GPR ligand binding to a GPR (see				
CC	AAW02747-W02999 for examples of polypeptide fragments). The polypeptide				
CC	fragments can be used in compositions for treating subjects suffering				
CC	from a pathology related to a GPR abnormality e.g. a psychotic disorder				
CC	such as schizophrenia.				
XX					
XX	Sequence 334 AA:				

Query Match	Similarity	Score	DB ID	Length
Best Local Similarity	71.6%	1523	DB 17	334
Matches 300	Conservative 10	Mismatches 23	Indels 86	Gaps

Query	Match	Similarity	Score	DB ID	Length
QY	33	TLTLVLCAGLIMLTFFEGNVLTIAVFTSRALKAPQNLTVLSIASADILVATLVIPFSLA	92		
Db	1	TLTLVLCAGLIMLTFFEGNVLTIAVFTSRALKAPQNLTVLSIASADILVATLVIPFSLA	60		
QY	93	NEVGVYVPEKAWCEIYALDVLCFSSSYIHLCAISLDKRWSTIOALEVNLKRTPPRIKA	152		
Db	61	NEVGVYVPEKAWCEIYALDVLCFSSSYIHLCAISLDKRWSTIOALEVNLKRTPPRIKA	119		
QY	153	IITVWVISAIVISPP-LISIEKKGSGGPQAPAPRCEINDOKWYVSISSCSFFAPCLI	211		
Db	120	IITVWVISAIVISPP-LISIEKKGSGGPQAPAPRCEINDOKWYVSISSCSFFAPCLI	179		
QY	212	MLIVYVRIYQAKKRTVPSPSRGPDVAAPPGTEPRGKGLPERSAGAGAEPLPT	271		
Db	180	NHLVYVRIYQAKKRTVPSPSRGPDVAAPPGTEPRGKGLPERSAGAGAEPLPT	231		
QY	272	QLNGAPGEPAAGPRDLDLLESSSSDHAERPPGPRPERGPRGKARASQVXPGDS	331		
Db	232	QLNGAPGEPAAGPRDLDLLESSSSDHAERPPGPRPERGPRGKARASQVXPGDS	231		
QY	332	LPRGPGATGIGTIPAGPGEERVAAKASRRGQNRKKEFTVYLAIVIGVFWCPEPF	391		
Db	232	LPRGPGATGIGTIPAGPGEERVAAKASRRGQNRKKEFTVYLAIVIGVFWCPEPF	275		
QY	392	FTYTLTAVGCSVPRTLEKFFEFWFCYCNSSLPLVYITTFNHDFFRAFEKILCRGDRKRIV	450		
Db	276	FTYTLTAVGCSVPRTLEKFFEFWFCYCNSSLPLVYITTFNHDFFRAFEKILCRGDRKRIV	334		

RESULT 8	AAU08334
AAU08334	standard; Protein; 307 AA.
XX	AAU08334;
XX	21-MAY-2002 (first entry)
DE	Human alpha 2 adrenergic receptor.
XX	Human; D2 dopamine receptor; RGB-2; antiparkinsonian; hormone secretion;
KW	G-protein coupled receptor; schizophrenia; drug addiction;
KW	Parkinson's disease; Tourette syndrome; Tardive dyskinesia;
KW	receptor; neuroleptic.
XX	Homo sapiens.
OS	
XX	
XX	Key
FT	Location/Qualifiers
FT	37..59
FT	/note= "Transmembrane domain I"
FT	71..96
FT	/note= "Transmembrane domain II"
FT	108..129
FT	/note= "Transmembrane domain III"
FT	151..173
FT	/note= "Transmembrane domain IV"
FT	190..213
FT	/note= "Transmembrane domain V"
FT	238..261
FT	/note= "Transmembrane domain VI"
FT	269..292
FT	/note= "Transmembrane domain VII"
XX	
XX	US6277591-B1.
XX	21-AUG-2001.
XX	07-JUN-1995;
XX	95US-0480390.

20-NOV-1989: 89US-0438544.
 09-NOV-1992: 92US-0973588.
 18-NOV-1988: 88US-0273373.
 (UYOR-) UNIV OREGON HEALTH SCI.
 Clivelli O, Bunzow JR, Grandy DK, Machida CA:
 WPI: 2001-540405/60.
 New isolated mammalian G-protein coupled D2 dopamine receptor polynucleotide, useful in gene therapy and for treating schizophrenia, drug addiction, Parkinson's disease, Tourette syndrome and Tardive dyskinesia -
 Claim 1; Fig 2; 71pp: English.
 This invention relates to the nucleotide and polypeptide sequences of an isolated mammalian G-protein coupled D2 dopamine receptor. This protein binds to G proteins to inhibit cyclic AMP generation and hormone secretion. The nucleotide sequences of the invention are useful as oligonucleotide probes and to screen nucleic acid libraries containing dopamine receptor nucleic acid sequences. These probes are also useful in hybridisation methods to locate the dopamine gene positions in various mammalian chromosomal maps or to determine the levels of mRNA or receptor concentrations in a sample. The nucleic acid sequences can also be used to identify dopamine receptor gene disorders (defective or aberrant genes) and for in vitro diagnostic procedures on DNA samples in given patients. A composition comprising the nucleic acid may be used for increasing the concentration of the receptor or its gene in a sample, or for in vivo uses such as gene therapy to render a defective gene or gene product inactive or to provide an increased concentration of dopamine receptor in a given location. The nucleotide sequences are useful for treating disease conditions associated with abnormalities in the structure, expression or concentration of the dopamine receptor or its gene, where the disease conditions are selected from neurological CC and other disorders, including schizophrenia, drug addiction, CC Parkinson's disease, Tourette syndrome, and Tardive dyskinesia. The CC polynucleotide sequence is also useful for preparing the corresponding CC transgenic animals, in particular nonhuman mammals and to inject CC oocytes from frogs, which can then be conventionally used in blinding or second messenger analyses. This sequence represents the human alpha 2 CC adrenergic receptor which has homology to the rat D2 dopamine CC receptor of the invention.

SQ Sequence 307 AA:
 Query Match 61.1%; Score 1454.5; DB 22; Length 307;
 Best Local Similarity 65.7%; Pred. No. 2.7e-102;
 Matches 291; Conservative 7; Mismatches 8; Indels 137; Gaps 1;

QY	1	MKSLQPDAGNASMNGTEAPGCGARATPTYSLOYTLTVLCAGLMLLTGVNGNLYIAVPT	60
DB	1	MKSLQPDAGNASMNGTEAPGCGARATPTYSLOYTLTVLCAGLMLLTGVNGNLYIAVPT	60
QY	61	SRATKAPQULFVYSLASADILVATLYPPSLNENVMGYVFGKAMCEIYLAIDVLEFCTSS	120
DB	61	SRATKAPQULFVYSLASADILVATLYPPSLNENVMGYVFGKAMCEIYLAIDVLEFCTSS	120
QY	121	IYHLCASIDRWYSITQALEYENLKRTPRRIKAIITVWVYSAVISFPLISIEKKGGGG	180
DB	121	IYHLCASIDRWYSITQALEYENLKRTPRRIKAIITVWVYSAVISFPLISIEKKGGGG	180
QY	181	PGAPAEKRLINQKWKVVISCTGSPFAPCLIMLVYVRYQIAKRTTRVPPSRGPDAVA	240
DB	181	PGAPAEKRLINQKWKVVISCTGSPFAPCLIMLVYVRYQIAKRTTRP-----	230
QY	241	APPGGTERRPKIGLSPERSAPGCGAEAEPYPTOLNGAPGEPAPGPRDOTALDEESSSD	300
DB	231	-----	230
QY	301	HAERPGRPRPEGPGKKGKARASQYKPDDSLPRRGPMATGICTPAAGGGEERYGAAKAS	360


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Db 221 ----- 230
QY 361 RMRGRONREKREFTVLAVIGVYVCMPEFFETTLTAVGCSVPRTLFKFEFPGYCNSS 420
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 221 -----REKRFIVIAVIGMFVVCMPFFETTLTAVGCSVPRTLFKFEFPGYCNSS 283
QY 421 LNPVITITFNHDFRRAFKILCR 443
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 284 LNPVITITFNHDFRRAFKILCR 306

RESULT 9
AARS4834
ID AARS4834 standard; Protein; 458 AA.
AC AARS4834;
XX
DT 01-FEB-1995 (first entry)
DE Human derived adrenaline alpha 2CII receptor.
XX
KW adrenaline receptor; alpha CII; screening; detection; pharmacology;
KM drug.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT MISC-difference 1
FT /note= "may or may not be present, but is only
FT present if amino acid residues 2-17 are
FT present."
FT Peptide 2..17
FT /label= "N-terminal-peptide
FT /note= "may or may not be present"
XX
PN JP06121686-A.
XX
PD 06-MAY-1994.
XX
PF 12-OCT-1992; 92JP-0272744.
XX
PR 12-OCT-1992; 92JP-0272744.
XX
PA (ASAH ) ASAH KASEI KOGYO KK.
XX
DR WPI: 1994-185923/23.
DR N-PSDB; AA064890.
XX
PT Adrenaline receptor gene encoding alpha 2CII receptor - for
PT screening drugs reactive to the alpha 2CII receptor
XX
PS Claim 1: Page 9-11; 13pp; Japanese.
XX
CC AA064890 encodes the amino acid sequence of a polypeptide
CC (AARS4834) that constitutes human derived adrenaline alpha 2CII
CC receptor. The DNA can be used for the study of the pharmacological
CC importance of the gene expression in humans.
XX
SQ Sequence 458 AA;

Query Match 49.2%; Score 1171; DB 15; Length 458;
Best Local Similarity 52.3%; Pred. No. 1.2e-80;
Matches 252; Conservative 38; Mismatches 102; Indels 90; Gaps 9;
QY 10 NASMNGTEAPGGGARAT-----PYSIQVTLVCLAGLMLTVEGNVLTIAVFT 60
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 19 NASGAGERSGGVANASGSMGPRGQYSAGAVAGLAIVGGLIVFTVGNVLTIAVLT 78
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 SIALAPQNLFLVSLASADIVATLVIPPSLANEYVGYGKAWCEITYLADVLCCTS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 79 SIALAPQNLFLVSLASADIVATLVIPPSLANEIMAYVGYGQVYGLADVLCCTS 138
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 IVHLCALSIDRWYSITQAEVNLKTRPRRIKAITTVIVISAVISFPLISIEKKGGGG 180

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Db 139 IVHLCALSIDRWYSITQAEVNLKTRPRRYKATIVAWLISAVISFPLVSLYKPDGA- 197
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 POPAEPRCEINDQKWYVSSICISGFAPCLIMLVYRIYQIAKRTTRVPSRGPDAVA 240
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 198 ---AYPOGGLNDETWYILSSCISGFAPCLINGLVARIYRAKLTRTLSEKRAP---V 251
QY 241 APPGTERPRKGLGPERKSGPGCAEAPLPQLNGCAPGPAPAGPRDLDLESSSSD 300
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 252 GPDGASPTTENGIGAAAGAGENGHCA-----PPPA-----DVEPDESSA 290
QY 301 HAERPPGRRPRGPRGKAKARASQVKGPDSLPRGPGATGCTPAAGGGERVAAKAS 360
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 291 AAE-----RRRRGALRRG-----GRRRAGAGAGAGDGGAAESGALTRAS 332
QY 361 RMRG-----RQNRKREFTVLAVIGVYVCMF 388
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 333 RSPGPGRLSRASRSVEFFLSRRRRARSVCRRVAQAREKRTFVLAVMGVFLCMF 392
QY 389 PEEFTYTLTAV---GCSVPRTLFKFEFPGYCNSSLNPVITITFNHDFRRAFKILCRGD 445
    |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 393 PEEFSTLYGICREACQVGPPLFKFEFMYGICNSSLNPVITVFNQDFRRSEKILFRRR 452
QY 446 RK 447
    | :
Db 453 RR 454

RESULT 10
AAM52124
ID AAM52124 standard; Protein; 461 AA.
XX
PN AAM52124;
XX
DT 18-FEB-2002 (first entry)
DE Human alpha-2CAR protein.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2CAR.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 205..409
FT /note= "featured in figure 12"
FT Domain 208..231
FT /label= "transmembrane_domain"
FT Region 321..324
FT /label= "polymorphic-site"
FT /note= "Polymorphic site absent in the variant protein
FT (AAM52126)"
FT Domain 383..406
FT /label= "transmembrane_domain"
XX
PN WO200179561-A2.
XX
PD 25-OCT-2001.
XX
PF 17-APR-2001; 2001WO-US12575.
XX
PR 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
XX
PA (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
PI Liggett SB, Small KM;
DR WPI: 2001-611728/70.

```

DR N-PSDB: AAI99931.
 XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 PT determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting
 PT a polymorphic site -
 XX
 PS Claim 78: Page 158-160; 163pp; English.
 XX
 CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC of (I), a site comprising cytosine or guanine at position 753 of (II)
 CC or a site comprising (A) (999gcg99gcg) or (B) (999gcgctgag) at
 CC positions 961-972 of (III). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
 CC polymorphic site which correlate to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g., epinephrine,
 CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
 CC combinations of these) or antagonist (e.g., yohimbine, prazosin, ARC 239,
 CC rauwolfscine, idazoxan, tolazoline, phenolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC levels). The present sequence is that of the human alpha-2CAR protein,
 CC the sequence includes a 4 amino acid polymorphic site at residues 321-324
 CC (GAGP), absent in the alpha-2CAR variant protein (AAM52126).
 CC
 XX
 SQ Sequence 461 AA:
 Query Match 48.7%; Score 1159.5; DB 22; Length 461;
 Best Local Similarity 51.7%; Pred. No. 9,1e-80;
 Matches 254; Conservative 37; Mismatches 95; Indels 105; Gaps 12;
 QY 10 NASWNGTEAPGCGARAT-----PYSLOVITLVCLAGLMLTFEENVYIIAVFT 60
 DB 19 NASGAGERGSGVANASGASWGPREGQYSAGAVAGLAAGVGLFVFNWGNVIAVLVT 78
 QY 61 SRAKAPONTFLVSLASADILVATLVTPFSLANVGVWYEGKAMCIYATLDTCTSS 120
 DB 79 SRAIRAPONTFLVSLASADILVATLVTPFSLANVGVWYEGKAMCIYATLDTCTSS 138
 QY 121 IVHCAISLDRYWSITQAIENYLMKTRPRRIKATITWVWISAVISFPPLISIEKKGGGG 180
 DB 139 IVHCAISLDRYWSITQAIENYLMKTRPRRIKATITWVWISAVISFPPLISIEKKGGGG 197
 QY 181 PQPAPRCETIDQKWIYSSCTGSPFAPCLIMILVYRIYQIAKRRIRVPPSRGPDVA 240
 DB 198 ---AYPOGLNDEWYILISCTGSPFAPCLIMGLVYRIYKAVAKRRITSEKAP---- 250
 QY 241 APPGTERPRGICPERSAGGAEBPLPTOLNG---APGE--PADAGPRDITDALDLE 295
 DB 251 -----VGPDGS-----PTTEGLGAAGAEATGARARRP-----PT 282
 QY 296 SSSSDHAERP---PGRRPRRPGRGKAKARASGVKGDLSLRPGCATGICPAPGGE 351
 DB 283 WSRIRRAQRPGRGAPGLR--RGGRRRAGAG-----GAGGADGGAGAPGA 326
 QY 352 ERVGAARASRWKG-----RQNRERREFVLAAY 379
 DB 327 AESGALTRSRSPGGGRLSRASSSVVEFLSRRRRASVCCRRAVAAERKREFVLAAY 386
 QY 380 IGVFVWCAEPFFFTYTLAV---GCSVPRTLKFEFMEFGYCNSSLNVIYITFNHDFRA 436
 DB 387 MGVFVLCMFPFFFTYSLGICRGACQVGPFLKFFFWIGYCNSSLNVIYITFVQNDPRPS 446
 QY 437 FKILCRGDRK 447

DB 447 FKILFRRRRR 457
 RESULT 11
 ID AAM52126
 XX AAM52126 standard; Protein; 457 AA.
 AC
 XX AAM52126;
 XX
 DE 18-FEB-2002 (first entry)
 DE Human alpha-2CAR variant protein.
 KM Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
 KM polymorphic site; allelic variant; cardiovascular disease;
 KM central nervous system disease; adenylyl cyclase; MAP kinase activity;
 KM phosphorylation; inositol phosphate; alpha-2CAR.
 XX
 OS Homo sapiens.
 FH
 FT Key Location/Qualifiers
 FT Domain 208..231
 FT /label= transmembrane_domain
 FT Domain 379..402
 FT /label= transmembrane_domain
 XX
 PN WO200179561-A2.
 PD 25-OCT-2001.
 PD 17-APR-2001; 2001WO-US12575.
 PF 17-APR-2000; 2000US-0551744.
 PR 10-AUG-2000; 2000US-0636259.
 PR 19-OCT-2000; 2000US-0692077.
 XX
 PA (LIGG/) LIGGETT S B.
 PA (SMAL/) SMALL K M.
 PI Liggett SB, Small KM;
 DR WPT. 2001-611728/70.
 DR N-PSDB: AAI99933.
 XX
 PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 PT determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting
 PT a polymorphic site -
 XX
 PS Claim 78: Page 160-162; 163pp; English.
 XX
 CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC of (I), a site comprising cytosine or guanine at position 753 of (II)
 CC or a site comprising (A) (999gcg99gcg) or (B) (999gcgctgag) at
 CC positions 961-972 of (III). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
 CC polymorphic site which correlate to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g., epinephrine,
 CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
 CC combinations of these) or antagonist (e.g., yohimbine, prazosin, ARC 239,
 CC rauwolfscine, idazoxan, tolazoline, phenolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate


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QY 206 FAPCLIMLVYVRLIYOLAKRRTRPRRRGRPDVAAMPQGTERRPKGLGPREBAGCGAE 265
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 182 FAPCLIMLVYLRILYLIATKR-----SNRRKPRAAAGCGGCGESKOPR--PDHGALASAK 233
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 266 AEPRLPT-----QLNG---AGCEPAPA-GPRDPTALDDEES-----SS 298
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 234 LPALASVASAREVHGSHKSTGKEGEPTPDTGTBALPRSMALPNSGQGEKGVGASP 293
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 299 SDHAERPRGPRRPRERGRGCKAKAASQYKCGD--SLPRRGRG-----ATGTGPPAAGPRE 351
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 294 EDEAEE-----EEEEEEEECEPDPAVVPSPASACSPPLQDPQGSRYLATLRGVLLGRG- 348
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 352 ERVAKAASRWKRGRO--NREKRFEFLVAVYIGVFWVCWPFPEFFTYTLTAV---GCSVPRT 406
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 349 --VGAIGGQWMMRRRAQTLREKRPFVLAVYIGVFLCWMFPFFSYSGAICPCHKCVPHG 406
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 407 LFKFFPFVFGYCNSSLNVPYITITFNHDDRRAFKILCR 443
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 407 LFOFFFWGICYNSSLNVPYITITFNQDRRRAFRILCR 443
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Accession	Protein Name	Organism	Gene Name	Protein Size (aa)	Protein Weight (kDa)	Protein pI	Protein pKa	Protein pKb	Protein pKc	Protein pKd	Protein pKe	Protein pKf	Protein pKg	Protein pKh	Protein pKi	Protein pKj	Protein pKk	Protein pKl	Protein pKm	Protein pKn	Protein pKo	Protein pKp	Protein pKq	Protein pKr	Protein pKs	Protein pKt	Protein pKu	Protein pKv	Protein pKw	Protein pKx	Protein pKy	Protein pKz	Protein pKa1	Protein pKa2	Protein pKa3	Protein pKa4	Protein pKa5	Protein pKa6	Protein pKa7	Protein pKa8	Protein pKa9	Protein pKa10	Protein pKa11	Protein pKa12	Protein pKa13	Protein pKa14	Protein pKa15	Protein pKa16	Protein pKa17	Protein pKa18	Protein pKa19	Protein pKa20	Protein pKa21	Protein pKa22	Protein pKa23	Protein pKa24	Protein pKa25	Protein pKa26	Protein pKa27	Protein pKa28	Protein pKa29	Protein pKa30	Protein pKa31	Protein pKa32	Protein pKa33	Protein pKa34	Protein pKa35	Protein pKa36	Protein pKa37	Protein pKa38	Protein pKa39	Protein pKa40	Protein pKa41	Protein pKa42	Protein pKa43	Protein pKa44	Protein pKa45	Protein pKa46	Protein pKa47	Protein pKa48	Protein pKa49	Protein pKa50	Protein pKa51	Protein pKa52	Protein pKa53	Protein pKa54	Protein pKa55	Protein pKa56	Protein pKa57	Protein pKa58	Protein pKa59	Protein pKa60	Protein pKa61	Protein pKa62	Protein pKa63	Protein pKa64	Protein pKa65	Protein pKa66	Protein pKa67	Protein pKa68	Protein pKa69	Protein pKa70	Protein pKa71	Protein pKa72	Protein pKa73	Protein pKa74	Protein pKa75	Protein pKa76	Protein pKa77	Protein pKa78	Protein pKa79	Protein pKa80	Protein pKa81	Protein pKa82	Protein pKa83	Protein pKa84	Protein pKa85	Protein pKa86	Protein pKa87	Protein pKa88	Protein pKa89	Protein pKa90	Protein pKa91	Protein pKa92	Protein pKa93	Protein pKa94	Protein pKa95	Protein pKa96	Protein pKa97	Protein pKa98	Protein pKa99	Protein pKa100	Protein pKa101	Protein pKa102	Protein pKa103	Protein pKa104	Protein pKa105	Protein pKa106	Protein pKa107	Protein pKa108	Protein pKa109	Protein pKa110	Protein pKa111	Protein pKa112	Protein pKa113	Protein pKa114	Protein pKa115	Protein pKa116	Protein pKa117	Protein pKa118	Protein pKa119	Protein pKa120	Protein pKa121	Protein pKa122	Protein pKa123	Protein pKa124	Protein pKa125	Protein pKa126	Protein pKa127	Protein pKa128	Protein pKa129	Protein pKa130	Protein pKa131	Protein pKa132	Protein pKa133	Protein pKa134	Protein pKa135	Protein pKa136	Protein pKa137	Protein pKa138	Protein pKa139	Protein pKa140	Protein pKa141	Protein pKa142	Protein pKa143	Protein pKa144	Protein pKa145	Protein pKa146	Protein pKa147	Protein pKa148	Protein pKa149	Protein pKa150	Protein pKa151	Protein pKa152	Protein pKa153	Protein pKa154	Protein pKa155	Protein pKa156	Protein pKa157	Protein pKa158	Protein pKa159	Protein pKa160	Protein pKa161	Protein pKa162	Protein pKa163	Protein pKa164	Protein pKa165	Protein pKa166	Protein pKa167	Protein pKa168	Protein pKa169	Protein pKa170	Protein pKa171	Protein pKa172	Protein pKa173	Protein pKa174	Protein pKa175	Protein pKa176	Protein pKa177	Protein pKa178	Protein pKa179	Protein pKa180	Protein pKa181	Protein pKa182	Protein pKa183	Protein pKa184	Protein pKa185	Protein pKa186	Protein pKa187	Protein pKa188	Protein pKa189	Protein pKa190	Protein pKa191	Protein pKa192	Protein pKa193	Protein pKa194	Protein pKa195	Protein pKa196	Protein pKa197	Protein pKa198	Protein pKa199	Protein pKa200	Protein pKa201	Protein pKa202	Protein pKa203	Protein pKa204	Protein pKa205	Protein pKa206	Protein pKa207	Protein pKa208	Protein pKa209	Protein pKa210	Protein pKa211	Protein pKa212	Protein pKa213	Protein pKa214	Protein pKa215	Protein pKa216	Protein pKa217	Protein pKa218	Protein pKa219	Protein pKa220	Protein pKa221	Protein pKa222	Protein pKa223	Protein pKa224	Protein pKa225	Protein pKa226	Protein pKa227	Protein pKa228	Protein pKa229	Protein pKa230	Protein pKa231	Protein pKa232	Protein pKa233	Protein pKa234	Protein pKa235	Protein pKa236	Protein pKa237	Protein pKa238	Protein pKa239	Protein pKa240	Protein pKa241	Protein pKa242	Protein pKa243	Protein pKa244	Protein pKa245	Protein pKa246	Protein pKa247	Protein pKa248	Protein pKa249	Protein pKa250	Protein pKa251	Protein pKa252	Protein pKa253	Protein pKa254	Protein pKa255	Protein pKa256	Protein pKa257	Protein pKa258	Protein pKa259	Protein pKa260	Protein pKa261	Protein pKa262	Protein pKa263	Protein pKa264	Protein pKa265	Protein pKa266	Protein pKa267	Protein pKa268	Protein pKa269	Protein pKa270	Protein pKa271	Protein pKa272	Protein pKa273	Protein pKa274	Protein pKa275	Protein pKa276	Protein pKa277	Protein pKa278	Protein pKa279	Protein pKa280	Protein pKa281	Protein pKa282	Protein pKa283	Protein pKa284	Protein pKa285	Protein pKa286	Protein pKa287	Protein pKa288	Protein pKa289	Protein pKa290	Protein pKa291	Protein pKa292	Protein pKa293	Protein pKa294	Protein pKa295	Protein pKa296	Pro
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mediate many of the physiological effects of the catecholamines, norepinephrine and epinephrine. An antagonist of α 1-adrenoceptor is useful for treating a mammal suffering from vascular contraction of coronary arteries and a disease involving vascular contraction of coronary arteries which is clinically expressed as coronary heart disease (CHD), unstable chronic angina pectoris which is clinically expressed as Prinzmetal's variant form or acute myocardial infarction (AMI). α 1-adrenoceptor gene is used in gene therapy.

Query Match	47.3%;	Score 1126.5;	DB 22;	Length 450;
Best Local Similarity	53.2%;	Pred. No. 2.8e-77;		
Matches 243; Conservative	50;	Mismatches 105;	Indels 59;	Gaps 14;

```

0Y 27 PYSLOVITLYVCLAGLMLTLTVEGNVYIIANFISRAKAPOMFLYSLASADITVATLY 86
Db 6 PYSVQATATAIAATTFLLFFLFGNALVYIALLVTSRLRQPMFLVSLAAADITVATLY 65
0Y 87 IPFSIANEVMGYWYFGKAMCEIYALALVLECTSSIVHCAISLDRWYSINQIAEYMLKRT 146
Db 66 IPFSIANELLETQWYFRKRCWCYIYALDVLCTSSIVHCAISLDRWYASRALEYSKRT 125
0Y 147 PRRIKAIITWVYISAVISFPPILSIEKKGGGGGPOP-ABPCEIINDQWYIISCTIGSF 205
Db 126 PRRICTILITWYILAAVVISLPELT-----YKDDQOPQRCGRPOCKLINEAWYIIASSIGSF 181
0Y 206 FAPCIIIMLYVYRIYQIARKRTTRPSPRGDVAAPRGERTKGLGERSAAGPAG 265
Db 182 FAPCIIIMLYVRIYRIYLIANKR-----SNRGRRAAGGPGQGESKOPR---PDHGALASAK 223
0Y 266 AEPILPT-----QUNG--APGEPAPA-GPRDUTDALDEES-----SS 298
Db 234 LPALASVASARENVGHKSGSTGEGETBEDTGTRALPRSMALPNBSGQCEKGVASCAP 293
0Y 299 SDHAEPRPPGRRPERGPRGSKAKAASQYKPED-SLPRRGPG-----ATGIGPAPGPG 351
Db 294 EDEAEE-----EEEEEHEEECEPAPVSPASACSPLOOPQGSRYLATLRGOVLLGRG- 348
0Y 352 ERVGAKASRRRGRO--RREKRTFFVLAVYGVGVCMQFFFFFYTLTAV--GCSVPRT 406
Db 349 --VGAIGOMMRRRARQTLREKRRTFFVLAVYGVVLCVDMFFFFFSYLGALICPRHCKVPHG 406
0Y 407 LKFEFFWFYCNSSLNPIYIYIINHDPRAAKLLCR 443
Db 407 LFOEFFWYIGYCNSSLNPIYIYIIFODPRRFRRLICR 443

```

RESULT 14	
AA052118	
ID	AA052118 standard; Protein; 447 AA.
XX	
XX	
AC	AA052118;
XX	
XX	
DT	18-FEB-2002 (first entry)
XX	
DE	Human alpha-2BAR third intracellular loop variant.
XX	
XX	
KW	Human: genotyping; alpha-2B: alpha-2A; adrenergic receptor;
KW	polymorphic site; allelic variant; cardiovascular disease;
KW	central nervous system disease; adenylyl cyclase; MAP kinase activity
KW	phosphorylation; inositol phosphate; alpha-2BAR.
XX	
OS	Homo sapiens.
XX	
XX	
EH	Key
FT	Location/Qualifiers
FT	170..193
FT	/label= transmembrane_domain
FT	307..309
FT	/label= polymorphic_site
FT	370..393
FT	/label= transmembrane_domain
XX	

PN WO200179561-A2.
 XX 25-OCT-2001.
 XX 17-APR-2001: 2001WO-US12575.
 XX 17-APR-2000; 2000US-0551744.
 PR 10-AUG-2000; 2000US-0636259.
 PR 19-OCT-2000; 2000US-0692077.
 XX (LIGGETT S B.
 PA (SMAL/) SMALL K M.
 XX LIGGETT SB, Small KM;
 PI WPI: 2001-611728/70.
 DR N-PSDB; AA199906.
 XX
 PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 PT determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting
 PT a polymorphic site -
 XX
 PS Claim 20: Page 147-149; 163pp; English.
 XX
 CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
 CC or a site comprising (A) (999gcgagcg) or (B) (999gcgctgag) at
 CC positions 961-972 of (III). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2C, comprising detecting a
 CC polymorphic site which correlate to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g., epinephrine,
 CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
 CC combinations of these) or antagonist (e.g., yohimbine, prazosin, ARC 239,
 CC rauwolfazine, idazoxan, tolazoline, phenoltamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC levels). The present sequence is that of the third intracellular loop of
 CC the human alpha-2BAR variant protein, the sequence is deleted for the 3
 CC amino acid polymorphic site at residues 301-303 (EEE) of the wildtype
 CC protein (AAM52117).
 XX
 SQ Sequence 447 AA:
 Query Match 47.3%; Score 1126; DB 22; Length 447;
 Best Local Similarity 53.2%; Pred. No. 3e-77;
 Matches 243; Conservative 50; Mismatches 102; Indels 62; Gaps 14;
 OY 27 PYSIQVTLVLCAGLMLTYPGVNVIYIAFTSRALKAPONLPLVSLASDILVATLV 86
 DB 6 PISVQVTAIAIAATFFLITFGNALVTLAVLTSTRSLRAPONLPLVSLAADIIVATLI 65
 OY 87 IPFSLANEVGYWYFGKACETIYLDVFCSSIVHICATISLDYRWSTQIAEYNLRT 146
 DB 66 IPFSLANELGMYFRMRFCCEYVIALDVLCFSSIVHICATISLDYRWSTQIAEYNLRT 125
 OY 147 PRRIATITVWVIAVSVFPLISIEKKGGGQGP- AEPRCETINDQKVVYISSCISF 205
 DB 126 PRRICTIITVWVIAVSVFPLISIEKKGGGQGP- AEPRCETINDQKVVYISSCISF 181
 OY 206 FAPCLIMILVYRIQVIRKRRTRVPSRGPAAVAPRGCTERRKKGCGPERSAGPGAE 265
 DB 189 FAPCLIMILVYRIQVIRKRRTRVPSRGPAAVAPRGCTERRKKGCGPERSAGPGAE 233

OY 266 AEPPLPT-----QLNG---ADGEPAPA-GPRDTPALDLEES-----SS 298
 DB 234 LPALASVASAREVNGSHSKSTGEKEGETPEDTCTRALPSPMALPNSGGGQKGVGASAP 293
 OY 299 SDHAERPPGRRRPERPRGCKARASQVPRGD--SLPRGPG-----ANGIGTPAAGPEE 351
 DB 294 EDPAEE-----EEEBEECEPQAVPSPASCSPPDQPGOSRYLATLRQVLLGRG- 345
 OY 352 ERYGAAKASRMGRQ--NREKRTFVLAVIGVGVCMFPPEFTYTLTAV--GGSVPRT 406
 DB 346 --VGAIGGQWMMRRRAQLTREKRTFVLAVIGVGVCMFPPEFTYSLGAIKCKKVPBG 403
 OY 407 LKFFFFMFCYCNLSLNPVYITTFNHDPRRAFKKILCR 443
 DB 404 LFOFFFMFCYCNLSLNPVYITTFNODFRRAFRILCR 440
 RESULT 15
 AAEO0989
 ID AAEO0989 standard; Protein: 447 AA.
 AC AAEO0989;
 XX
 DT 04-JUL-2001 (first entry)
 XX
 DE Human alpha2B-adrenoceptor (alpha2B-AR) variant protein.
 KW Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
 KW glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
 KW norepinephrine; epinephrine; therapy; vascular contraction; variant;
 KW coronary artery; coronary heart disease; CHD; chronic angina pectoris;
 KW acute myocardial infarction; AMI; Prinzmetal's variant.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 298..306
 FT /note="Glutamic acid repeat"
 XX
 PN WO200129082-A1.
 PD 26-APR-2001.
 PF 20-OCT-2000; 2000WO-FI00913.
 PR 22-OCT-1999; 99US-0422985.
 XX
 PA (JUVA-) JUVANTIA PHARMA LTD OY.
 PI Snapir A, Heinonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U;
 PI Scheinin M, Salonen JT, Tuomalahti T, Lakka TA, Nyssönen K;
 PI Salonen R, Kauppinen J, Valkonen V;
 DR WPI: 2001-300318/31.
 DR N-PSDB; AAD04761.
 PT New DNA molecule encoding variant specific adrenoceptor protein with
 PT deletion of specific amino acids located in the third intracellular
 PT loop of the polypeptide, for treating vascular contraction of coronary
 PT arteries -
 XX
 PS Claim 8; Page 26-27; 37pp; English.
 XX
 CC The present sequence is human alpha2B-adrenoceptor (alpha2B-AR) variant
 CC protein. Alpha2B-AR has a glutamic acid repeat element (amino acids
 CC 298-309) of 12 glutamates, in an acidic stretch of 18 amino acids (amino
 CC acids 294-311), located in the third intracellular loop of the receptor
 CC polypeptide. The variant is obtained by deletion of three glutamates from
 CC the Glu repeat (amino acids 307-309). Alpha2B-AR gene is located on
 CC chromosome 2. Alpha2-AR mediate many of the physiological effects of the
 CC catecholamines, norepinephrine and epinephrine. An antagonist of the
 CC alpha2B-adrenoceptor is useful for treating a mammal suffering from
 CC vascular contraction of coronary arteries and a disease involving from

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 15, 2003, 16:56:00 ; Search time 24.5 Seconds
(without alignments)
1765.734 Million cell updates/sec

Title: US-09-636-259B-4

Perfect score: 2360

Sequence: 1 MGSLOPDAGNASWNGTEAPG.....HDFRRAFKKILCRGDRKRIY 450

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2221	93.3	450	2	A38316
2	2216	93.1	450	2	A34169
3	2193	92.1	450	2	I49481
4	2126	86.3	450	2	B40392
5	2105	86.4	450	2	JH0190
6	1173	49.3	458	2	I49480
7	1169	49.1	458	2	A40392
8	1167	49.0	458	2	A48392
9	1167	49.0	458	2	A37869
10	1160.5	48.8	450	2	A31237
11	1127.5	47.4	450	2	A37223
12	1126.5	47.3	432	2	I50829
13	1121.5	47.1	455	2	S48221
14	1111.5	46.7	448	2	I51883
15	1100.5	46.2	453	2	A35642
16	693.5	29.1	484	2	S58868
17	681.5	28.6	379	2	JC6178
18	652	27.4	476	2	JC5042
19	649	27.3	601	2	S12004
20	649	27.3	601	2	JH0170
21	624	26.2	444	1	DYB0D2
22	621.5	26.1	443	1	DYHND2
23	617	25.9	511	2	C56849
24	613	25.8	444	1	DYMSD2
25	613	25.8	444	1	S08146
26	611	25.7	377	2	B30341
27	608.5	25.6	442	1	DYXLD2
28	594.5	25.0	430	2	T16079
29	590	24.8	422	2	I38209

30	587	24.7	421	2	I49375	serotonin receptor
31	586.5	24.6	377	2	S68423	serotonin receptor
32	585.5	24.6	377	2	A53279	serotonin receptor
33	579.5	24.3	514	2	D56849	dopamine receptor-
34	578	24.3	422	2	JH0315	serotonin receptor
35	577.5	24.3	390	2	JN0268	serotonin receptor
36	573.5	24.1	517	2	A45121	alpha-1B adrenergic
37	564	23.7	374	2	I77467	serotonin receptor
38	562	23.6	564	2	A38271	serotonin receptor
39	561.5	23.6	389	2	S68422	serotonin receptor
40	560	23.5	387	1	DYHND4	serotonin receptor
41	560	23.5	515	2	A40491	dopamine receptor
42	559.5	23.5	390	2	S58126	alpha-1-adrenergic
43	558.5	23.5	501	2	T18863	serotonin receptor
44	558	23.4	386	2	A42688	hypothetical prote
45	556.5	23.4	315	2	JC1525	serotonin receptor
						alpha-1B-adrenergic

ALIGNMENTS

RESULT 1

A38316

alpha-2-adrenergic receptor - pig

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999

C:Accession: A38316

R:Guyer, C.A.; Horstman, D.A.; Wilson, A.L.; Clark, J.D.; Craige Jr., E.J.; Limbird, J. Biol. Chem. 265, 17307-17317, 1990

A:Title: Cloning, sequencing, and expression of the gene encoding the porcine alpha-2

A:Reference number: A38316; MUID:91009167; PMID:2170371

A:Accession: A38316

A:Molecule type: DNA

A:Residues: 1-450 <GUY>

A:Cross-references: GB:U05652; NID:q164303; PIDN:AAA30984.1; PID:q164304

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match	Score	DB 2:	Length	450:
Best Local Similarity	93.8%	Pred. No. 3.1e-134;		
Matches 422;	Conservative	3;	Mismatches 25;	Indels 0;
Gaps 0;				
QY	1	MGSLOPDAGNASWNGTEAPG	ATPYSLOVTLTVCLAGLMLTVFGNVLIIVFT	60
DB	1	MGSLOPDAGNASWNGTEAPG	ATPYSLOVTLTVCLAGLMLTVFGNVLIIVFT	60
QY	61	SRALKAPONLFLVSLASADII	VATVIPFSLANFVWYFGKAWCEIYALDVLCTSS	120
DB	61	SRALKAPONLFLVSLASADII	VATVIPFSLANFVWYFGKAWCEIYALDVLCTSS	120
QY	121	IVHICATSLDHYWGITQAI	IEVNLKRTPRRIKATITVWVISAVISPPPLISTEKKGGG	180
DB	121	IVHICATSLDHYWGITQAI	IEVNLKRTPRRIKATITVWVISAVISPPPLISTEKKGGG	180
QY	181	POAPEPCREINDOKWYI	SSCIGSFAPCLIMLVYRIQIAKRRTRVPSRRGPDVA	240
DB	181	QOAPPCREINDOKWYI	SSCIGSFAPCLIMLVYRIQIAKRRTRVPSRRGPDVA	240
QY	241	APPGCTRRRPGGLGPE	RSAGGAEAPLPQLNGAGBPAPGPRDTDLDESSSSD	300
DB	241	ALPGEAERPPGGLGPE	RSAGGAEAPLPQLNGAGBPAPGPRDTDLDESSSSS	300
QY	301	HAEPGPRPRERPRCK	KARASOVPRGSLPRGGAGIGPAPGPEERYGAKAS	360
DB	301	HAEPGPRPRERPRCK	KARASOVPRGSLPRGGAGIGPAPGPEERYGAKAS	360
QY	361	RWGRQNRKRFETFL	AVVIGVFVWCPPEFFTYTLTAVCCSVPTLKFEEFGYCNS	420
DB	361	RWGRQNRKRFETFL	AVVIGVFVWCPPEFFTYTLTAVCCSVPTLKFEEFGYCNS	420
QY	421	LNPIYITIFNDFRR	AFKKILCRGDRKRIY	450
DB	421	LNPIYITIFNDFRR	AFKKILCRGDRKRIY	450

RESULT 2

A34169

alpha-2A-adrenergic receptor - human
N:Alternate names: alpha-2C10-adrenergic receptor

C:Species: Homo sapiens (man)

C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 29-Oct-1999

C/Accession: A34169; A40132; S14311

R:Fraser, C.M.; Arakawa, S.; McCombie, W.R.; Venter, J.C.

J. Biol. Chem. 264, 11754-11761, 1989

A:Title: Cloning, sequence analysis, and permanent expression of a human alpha2-adrenergic cyclase attenuation and activation.

A:Reference number: A34169; MUID:8930857; PMID:2568356

A:Accession: A34169

A:Molecule type: DNA

A:Residues: 1-450 <FRA>

A:Cross-references: GB:M23533; NID:g178195; PIDN:AA51665.1; PID:g178196

R:Koblika, B.K.; Matsui, H.; Koblika, T.S.; Yang-Peng, T.L.; Francke, U.; Caron, M.G.; I Science 238, 650-656, 1987

A:Title: Cloning, sequencing, and expression of the gene coding for the human platelet A:Reference number: A40132; MUID:86042785; PMID:2823383

A:Accession: A40132

A:Molecule type: DNA

A:Residues: 1-103, 'T', 105-156, 'C', 158-367, 'L', 369-450 <KOB>

A:Cross-references: GB:M18415; NID:g178191; PIDN:AA51664.1; PID:g178192

A:Note: the authors translated the codon TGT for residue 157 as Val, and CTC for residue R:Chajlant, V.; Rangel, N.; Uhlen, S.; Wikberg, J.E.S.

FEBS Lett. 280, 241-244, 1991

A:Title: Identification of an additional gene belonging to the alpha(2) adrenergic recep

A:Reference number: S14308; MUID:91192139; PMID:1849485

A:Accession: S14311

A:Molecule type: DNA

A:Residues: 77-123, 'P', 125-209 <CHN>

C:Genetics:

A:Gene: GDB:ADRA2A; ADRA2; ADRA2R

A:Cross-references: GDB:120538; OMIM:104210

A:Map position: 10q25-10q25

A:introns: #status absent

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 93.1%; Score 2216; DB 2; Length 450;
Best local similarity 94.2%; Pred. No. 6.5e-134;
Matches 424; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

```
QY 1 MGSIQPDAGNASWNGTEAPGGARATPYSLOVTLTVCLAGLMLTVFGNVLIIAVFT 60
    |||||||
DB 1 MGSIQPDAGNASWNGTEAPGGARATPYSLOVTLTVCLAGLMLTVFGNVLIIAVFT 60

QY 61 SRALKAPQNLFLVSLASADIIIVATLVIPFSLANEMGVYFGKAMCEIYALDVLFCISS 120
    |||||||
DB 61 SRALKAPQNLFLVSLASADIIIVATLVIPFSLANEMGVYFGKAMCEIYALDVLFCISS 120

QY 121 IYHLCALISLDKRWYSITQALEYLNKRTPRRIKAIITVWVISAIVSPPLISIEKKGCGG 180
    |||||||
DB 121 IYHLCALISLDKRWYSITQALEYLNKRTPRRIKAIITVWVISAIVSPPLISIEKKGCGG 180

QY 181 PQAPRCEINDQKWIYVSSICISGFAPCLIMILVYVRIYIAKRRTRVPPSRGPDAYA 240
    |||||||
DB 181 PQAPRCEINDQKWIYVSSICISGFAPCLIMILVYVRIYIAKRRTRVPPSRGPDAYA 240

QY 241 APPGTERPRKGLGPERBAGGAAEPPLPTQUNGAPPEPAPAPROTDALDLESSSSD 300
    |||||||
DB 241 APPGTERPRKGLGPERBAGGAAEPPLPTQUNGAPPEPAPAPROTDALDLESSSSD 300

QY 301 HAERPGRRRPRGPRGKGKARASQVYKPGDSLPRRGPGATIGTPAAGPGEERYGAAKAS 360
    |||||||
DB 301 HAERPGRRRPRGPRGKGKARASQVYKPGDSLPRRGPGATIGTPAAGPGEERYGAAKAS 360

QY 361 RWRGRONREKRFTFVLAVVIGVFVVCWPFPEFTYTLTAVGCSVPRTLKFFPFMGYCNS 420
    |||||||
DB 361 RWRGRONREKRFTFVLAVVIGVFVVCWPFPEFTYTLTAVGCSVPRTLKFFPFMGYCNS 420
```

```
DB 361 AGAGQONREKRFTFVLAVVIGVFVVCWPFPEFTYTLTAVGCSVPRTLKFFPFMGYCNS 420
QY 421 LNPVYITIFNHDFRRRAFKKILCRGDRKRIV 450
    |||||||
DB 421 LNPVYITIFNHDFRRRAFKKILCRGDRKRIV 450
```

RESULT 3

I49481

alpha-2 adrenergic receptor - mouse
C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999

C/Accession: I49481

R:Link, R.; Daut, D.; Barsch, G.S.; Chruscinski, A.; Koblika, B.

Mol. Pharmacol. 42, 16-27, 1992

A:Title: Cloning of two mouse genes encoding alpha-2 adrenergic receptor subtypes and in antagonist binding.

A:Reference number: I49480; MUID:92342131; PMID:1353249

A:Accession: I49481

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-450 <RES>

A:Cross-references: GB:M93377; NID:g191882; PIDN:AA37213.1; PID:g191883

C:Superfamily: vertebrate rhodopsin

C:Keywords: neurotransmitter receptor

Query Match 92.1%; Score 2193; DB 2; Length 450;
Best local similarity 92.0%; Pred. No. 1.9e-132;
Matches 414; Conservative 8; Mismatches 28; Indels 0; Gaps 0;

```
QY 1 MGSIQPDAGNASWNGTEAPGGARATPYSLOVTLTVCLAGLMLTVFGNVLIIAVFT 60
    |||||||
DB 1 MGSIQPDAGNASWNGTEAPGGARATPYSLOVTLTVCLAGLMLTVFGNVLIIAVFT 60

QY 61 SRALKAPQNLFLVSLASADIIIVATLVIPFSLANEMGVYFGKAMCEIYALDVLFCISS 120
    |||||||
DB 61 SRALKAPQNLFLVSLASADIIIVATLVIPFSLANEMGVYFGKAMCEIYALDVLFCISS 120

QY 121 IYHLCALISLDKRWYSITQALEYLNKRTPRRIKAIITVWVISAIVSPPLISIEKKGCGG 180
    |||||||
DB 121 IYHLCALISLDKRWYSITQALEYLNKRTPRRIKAIITVWVISAIVSPPLISIEKKGCGG 180

QY 181 PQAPRCEINDQKWIYVSSICISGFAPCLIMILVYVRIYIAKRRTRVPPSRGPDAYA 240
    |||||||
DB 181 PQAPRCEINDQKWIYVSSICISGFAPCLIMILVYVRIYIAKRRTRVPPSRGPDACS 240

QY 241 APPGTERPRKGLGPERBAGGAAEPPLPTQUNGAPPEPAPAPROTDALDLESSSSD 300
    |||||||
DB 241 APPGADRRPRNGLGPERBAGPTGAEAPLPTQUNGAPPEPAPAPROTDALDLESSSSE 300

QY 301 HAERPGRRRPRGPRGKGKARASQVYKPGDSLPRRGPGATIGTPAAGPGEERYGAAKAS 360
    |||||||
DB 301 HAERPGRRRPRGPRGKGKARASQVYKPGDSLPRRGPGATIGTPAAGPGEERYGAAKAS 360

QY 361 RWRGRONREKRFTFVLAVVIGVFVVCWPFPEFTYTLTAVGCSVPRTLKFFPFMGYCNS 420
    |||||||
DB 361 RWRGRONREKRFTFVLAVVIGVFVVCWPFPEFTYTLTAVGCPVPSOLFNFPMFGYCNS 420

QY 421 LNPVYITIFNHDFRRRAFKKILCRGDRKRIV 450
    |||||||
DB 421 LNPVYITIFNHDFRRRAFKKILCRGDRKRIV 450
```

RESULT 4
B40392
alpha-2-adrenergic receptor (clone RG10) - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 06-Dec-1991 #sequence_revision 03-Apr-1992 #text_change 13-Aug-1999
C/Accession: B40392
R:Lanier, S.M.; Downing, S.; Duzic, E.; Homcy, C.J.
J. Biol. Chem. 266, 10470-10478, 1991
A:Title: Isolation of rat genomic clones encoding subtypes of the alpha-2-adrenergic A:Reference number: A40392; MUID:91244823; PMID:1645350

A:Accession: B40392
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-450 <LAN>
 A:Cross-references: GB:M62372; NID:q206615; PIDN:AAA42034.1; PID:q206616
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 89.3%; Score 2126; DB 2; Length 450;
 Best Local Similarity 89.6%; Pred. No. 3.4e-128;
 Matches 403; Conservative 10; Mismatches 37; Indels 0; Gaps 0;

QY 1 MGSLOPDAGNSWNGTEAPGGARATPSLOYTLVLCAGLMLTLVFGNVLIIVFT 60
 Db 1 MGSLOPDAGNSWNGTEAPGGARATPSLOYTLVLCAGLMLTLVFGNVLIIVFT 60
 QY 61 SRALKAPQNLFLVSLASADILVATLVPFSLANEVGVYFGKWCETIYALDVLFTSS 120
 Db 61 SRALKAPQNLFLVSLASADILVATLVPFSLANEVGVYFGKWCETIYALDVLFTSS 120
 QY 121 IVHLCALISLDKRWSTQAEYNLKRTPRIKAITVWVISAIVSPPLISTEKKGGGG 180
 Db 121 IVHLCALISLDKRWSTQAEYNLKRTPRIKAITVWVISAIVSPPLISTEKKGGGG 180
 QY 181 POAPEPCINDDKMWYISSIGSFAPCLIMLVYVRIYQIAKRTVPSPRRGPDAA 240
 Db 181 POAPEPCINDDKMWYISSIGSFAPCLIMLVYVRIYQIAKRTVPSPRRGPDAA 240
 QY 241 APPGTERRRPGKLPERSAGGAEAPLPQLNGAPGAPAPGPRDTALDLEESSSD 300
 Db 241 APPGTERRRPGKLPERSAGGAEAPLPQLNGAPGAPAPGPRDTALDLEESSSD 300
 QY 301 HAERPGRRPRERPRGKARASQVKGDSLPFRGPGATGIGTPAAGPGEERGAAKAS 360
 Db 301 HAERPGRRPRERPRGKARASQVKGDSLPFRGPGATGIGTPAAGPGEERGAAKAS 360
 QY 361 RWRGRONREKRFETVLAVVIGVYVCPPEFTYTLAVGSCVPRTLKFFFMFGYCNS 420
 Db 361 RWRGRONREKRFETVLAVVIGVYVCPPEFTYTLAVGSCVPRTLKFFFMFGYCNS 420
 QY 421 LNPVITYTFNHDFRRAFKKILCRGDKRRIY 450
 Db 421 LNPVITYTFNHDFRRAFKKILCRGDKRRIY 450

RESULT 5

alpha-2-adrenergic receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Feb-1997
 C:Accession: JH0190
 R:Chalberg, S.C.; Duda, T.; Rhine, J.A.; Sharma, R.K.
 Mol. Cell. Biochem. 97, 161-172, 1990
 A:Title: Molecular cloning, sequencing and expression of an alpha2-adrenergic receptor
 A:Reference number: JH0190; MUID:91125329; PMID:217834
 A:Accession: JH0190
 A:Molecule type: mRNA
 A:Residues: 1-450 <CHA>
 A:Experimental source: brain
 C:Comment: Alpha-2-adrenergic receptor is a predominant catecholamine receptor. It mediates
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein
 F:34-59/Domain: hydrophobic <HD1>
 F:71-96/Domain: hydrophobic <HD2>
 F:106-131/Domain: hydrophobic <HD3>
 F:150-175/Domain: hydrophobic <HD4>
 F:193-218/Domain: hydrophobic <HD5>
 F:375-400/Domain: hydrophobic <HD6>
 F:405-430/Domain: hydrophobic <HD7>

Query Match 88.4%; Score 2105; DB 2; Length 450;
 Best Local Similarity 89.1%; Pred. No. 7.4e-127;
 Matches 401; Conservative 9; Mismatches 40; Indels 0; Gaps 0;

QY 1 MGSLOPDAGNSWNGTEAPGGARATPSLOYTLVLCAGLMLTLVFGNVLIIVFT 60
 Db 1 MGSLOPDAGNSWNGTEAPGGARATPSLOYTLVLCAGLMLTLVFGNVLIIVFT 60
 QY 61 SRALKAPQNLFLVSLASADILVATLVPFSLANEVGVYFGKWCETIYALDVLFTSS 120
 Db 61 SRALKAPQNLFLVSLASADILVATLVPFSLANEVGVYFGKWCETIYALDVLFTSS 120
 QY 121 IVHLCALISLDKRWSTQAEYNLKRTPRIKAITVWVISAIVSPPLISTEKKGGGG 180
 Db 121 IVHLCALISLDKRWSTQAEYNLKRTPRIKAITVWVISAIVSPPLISTEKKGGGG 180
 QY 181 POAPEPCINDDKMWYISSIGSFAPCLIMLVYVRIYQIAKRTVPSPRRGPDAA 240
 Db 181 POAPEPCINDDKMWYISSIGSFAPCLIMLVYVRIYQIAKRTVPSPRRGPDAA 240
 QY 241 APPGTERRRPGKLPERSAGGAEAPLPQLNGAPGAPAPGPRDTALDLEESSSD 300
 Db 241 APPGTERRRPGKLPERSAGGAEAPLPQLNGAPGAPAPGPRDTALDLEESSSD 300
 QY 301 HAERPGRRPRERPRGKARASQVKGDSLPFRGPGATGIGTPAAGPGEERGAAKAS 360
 Db 301 HAERPGRRPRERPRGKARASQVKGDSLPFRGPGATGIGTPAAGPGEERGAAKAS 360
 QY 361 RWRGRONREKRFETVLAVVIGVYVCPPEFTYTLAVGSCVPRTLKFFFMFGYCNS 420
 Db 361 RWRGRONREKRFETVLAVVIGVYVCPPEFTYTLAVGSCVPRTLKFFFMFGYCNS 420
 QY 421 LNPVITYTFNHDFRRAFKKILCRGDKRRIY 450
 Db 421 LNPVITYTFNHDFRRAFKKILCRGDKRRIY 450

RESULT 6

alpha-2 adrenergic receptor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
 C:Accession: I49480
 R:Link, R.; Daunt, D.; Barsh, G.S.; Chrusciel, A.; Kobilka, B.
 Mol. Pharmacol. 42, 16-27, 1992
 A:Title: Cloning of two mouse genes encoding alpha-2 adrenergic receptor subtypes and
 A:Reference number: I49480; MUID:92342131; PMID:1353249
 A:Accession: I49480
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-458 <RES>
 A:Cross-references: GB:M99376; NID:9191880; PIDN:AAA37212.1; PID:9191881
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: neurotransmitter receptor

Query Match 49.3%; Score 1173; DB 2; Length 458;
 Best Local Similarity 53.5%; Pred. No. 1.4e-67;
 Matches 251; Conservative 46; Mismatches 104; Indels 68; Gaps 11;

QY 14 NGTEA-----PGGARRAT-----PSLOYTLVLCAGLMLTLVFGNVLIIVFT 60
 Db 19 NSDAGEKSGSGGANSQTDWVPPPGQYSAVAGLAAYGFLIVTVGVNLVIAVLT 78
 QY 61 SRALKAPQNLFLVSLASADILVATLVPFSLANEVGVYFGKWCETIYALDVLFTSS 120
 Db 79 SRALKAPQNLFLVSLASADILVATLVPFSLANEVGVYFGKWCETIYALDVLFTSS 138
 QY 121 IVHLCALISLDKRWSTQAEYNLKRTPRIKAITVWVISAIVSPPLISTEKKGGGG 180
 Db 139 IVHLCALISLDKRWSTQAEYNLKRTPRIKAITVWVISAIVSPPLISTEKKGGGG 197
 QY 181 POAPEPCINDDKMWYISSIGSFAPCLIMLVYVRIYQIAKRTVPSPRRGPDAA 240
 Db 198 --APQCGLNDETWYISSIGSFAPCLIMLVYVRIYQIAKRTVPSPRRGPDAA 250

FEBS Lett. 278, 45-50, 1991

A:Title: The rat alpha(2)-adrenoceptor gene encodes a novel pharmacological subunit

A:Reference number: S13023; MUID:91130536; PMID:1704314

A:Accession: S13023

A:Molecule type: DNA

A:Residues: 1-39, 'G', '41-68, 'N', '70-154, 'E', '156-244, 'S', '246-458 <VOI>

A:Cross-references: GB:557659; NID:9288044; PIDN:CAA0861.1; PID:9288045

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match

Best Local Similarity 53.3%; Pred. No. 3, 4e-67; Matches 250; Conservative 46; Mismatches 105; Indels 68; Gaps 11;

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14 NGTEA-----PGGARAT-----PYSLOVTLTVCLAGLMLTVFGNTVLIATFT 60
19 NSGAGEMSGGGANASGTMAPPQGYSAAGAAVAGLAAYGFLVFGVTVLVIATVLT 78
61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEMVGMVFGKACEITVLDVLCCTSS 120
79 SRALKAPQNLFLVSLASADILVATLVIPFSLANEMVGMVFGKACEITVLDVLCCTSS 138
121 IVHLCASIDRWYSITQAIENLKRTPRIKAIITVWVISAIVISPPPLISIEKKGGCGG 180
139 IVHLCASIDRWYSITQAIENLKRTPRIKAIITVWVISAIVISPPPLISIEKKGGCGG 197
181 POPAEPCIEINDOKWYVISCISGFAPCLIMLVYVRYQAKRRTRVPSRGGDAVA 240
198 ---AYPGGLNDEWYITLSSICISFFAPCLIMGLVARIYAKKRLTRITLTERGP--- 250
241 APPGCTERRPKGLGPKRSAGPGAEEPLPTQLNG---APGEPAAPRDTALDLEES 297
251 -----AGPDGAS---PTTEGLGKAENGHCAPRTE-VEPDESS 287
298 SSQDAERPGRPRERPRRKGKARASQVKSPLRRSGAGATGTPAAGPEEYKGA 357
288 AAEERRRRRGLKRGGRREGAEDTGSADGPGCLAEDGARTASNSP--GPGRLSRAS 345
358 KAS-----RMGR-----QNRKRTFLVAVISGVVCFPFPTTTLTAV-- 399
346 SRSEVFPLSRRRARSSVCRRKVAQAAREKFTFLVAVMGVFLVLCFPPFFSSSLGICR 405
400 -GGSVPRTLEKFFFWGCGSSLNPIYITFNHDFRAEKKILCRDRK 447
406 EACQLPEPLKFFFWGCGSSLNPIYITFNHDFRAEKKILCRDRK 454

```

RESULT 10

A31237

alpha-2C-adrenergic receptor - human

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1990 #sequence-revision 31-Mar-1990 #text-change 13-Aug-1999

C:Accession: A31237; S14309; S14310

R:Regan, J.W.; Koblika, T.S.; Yang-Feng, T.L.; Garon, M.G.; Lefkowitz, R.J.; Koblika, B.

Proc. Natl. Acad. Sci. U.S.A. 85, 6301-6305, 1988

A:Title: Cloning and expression of a human kidney cDNA for an alpha-2-adrenergic receptor

A:Reference number: A31237; MUID:88320430; PMID:2842764

A:Accession: A31237

A:Molecule type: mRNA

A:Residues: 1-461 <RRG>

A:Cross-references: GB:J03853; NID:9178193; PIDN:AAA35513.1; PID:9178194

R:Chhajlani, V.; Rangel, N.; Uhlen, S.; Wikberg, J.E.S.

FEBS Lett. 280, 241-244, 1991

A:Title: Identification of an additional gene belonging to the alpha(2) adrenergic receptor

A:Reference number: S14308; MUID:91192139; PMID:1849485

A:Accession: S14309

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 95-223 <CHH>

A:Accession: S14310

A:Molecule type: DNA

A:Residues: 95-223 <CH2>

C:Genetics:

A:Gene: GDB:ADRA2C; ADRA2L2; ADRA2RL2

A:Cross-references: GDB:120540; OMIM:104250

A:Map position: 4p16.3-4p15

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match

Best Local Similarity 48.8%; Score 1160.5; DB 2; Length 461; Matches 254; Conservative 38; Mismatches 94; Indels 105; Gaps 12;

```

10 NSMNGTEAPGGGARAT-----PYSLOVTLTVCLAGLMLTVFGNTVLIATFT 60
19 NSGAGEMSGGGANASGSMCKPQGYSAAGAAVAGLAAYGFLVFGVTVLVIATVLT 78
61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEMVGMVFGKACEITVLDVLCCTSS 120
79 SRALKAPQNLFLVSLASADILVATLVIPFSLANEMVGMVFGKACEITVLDVLCCTSS 138
121 IVHLCASIDRWYSITQAIENLKRTPRIKAIITVWVISAIVISPPPLISIEKKGGCGG 180
139 IVHLCASIDRWYSITQAIENLKRTPRIKAIITVWVISAIVISPPPLISIEKKGGCGG 197
181 POPAEPCIEINDOKWYVISCISGFAPCLIMLVYVRYQAKRRTRVPSRGGDAVA 240
198 ---AYPGGLNDEWYITLSSICISGFAPCLIMGLVARIYAKKRLTRITLTERGP--- 250
241 APPGCTERRPKGLGPKRSAGPGAEEPLPTQLNG---APGE--PAPAGPRDTALDLEE 295
251 -----VGPDGAS---PTTEGLGKAAGCARGTARPR-----PT 282
296 SSQDAERPGRPRERPRRKGKARASQVKSPLRRSGAGATGTPAAGPEEYKGA 351
283 AAEERRRRRGLKRGGRREGAEDTGSADGPGCLAEDGARTASNSP--GPGRLSRAS 326
352 ERYGAKASRMWG-----QNRKRTFLVAVISGVVCFPFPTTTLTAV-- 379
327 AQSGLALTASRSPGGRRLSRASSRSEVFPLSRRRARSSVCRRKVAQAAREKFTFLVAV 386
400 -GGSVPRTLEKFFFWGCGSSLNPIYITFNHDFRAEKKILCRDRK 447
406 EACQLPEPLKFFFWGCGSSLNPIYITFNHDFRAEKKILCRDRK 457

```

RESULT 11

A37223

alpha-2B-adrenergic receptor - human

N:Alternate names: alpha-2C2-adrenergic receptor

C:Species: Homo sapiens (man)

C:Date: 22-Jan-1993 #sequence-revision 22-Jan-1993 #text-change 29-Oct-1999

C:Accession: A37223; S19407; S14308; A36158

R:Weinstein, R.L.; Zagon, J.M.; Macchi, M.; Adham, N.; Lichtblau, H.; Branchek, T.

Mol. Pharmacol. 38, 681-688, 1990

A:Title: Cloning, expression, and pharmacological characterization of a human alpha-2

A:Reference number: A37223; MUID:91042469; PMID:2172775

A:Accession: A37223

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-450 <WEI>

R:Tomasey, J.W.; Lorenz, W.; Allen, L.F.; King, R.; Regan, J.W.; Yang-Feng, T.L.; Ca

Proc. Natl. Acad. Sci. U.S.A. 87, 5094-5098, 1990

A:Title: Expansion of the alpha 2-adrenergic receptor family: cloning and characteriz

A:Reference number: S19407; MUID:90311349; PMID:2164221

A:Accession: S19407

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-450 <LOW>

A:Cross-references: GB:M34041; NID:9178197; PIDN:AAA51666.1; PID:9178198

R:Chhajlani, V.; Rangel, N.; Uhlen, S.; Wikberg, J.E.S.

FEBS Lett. 280, 241-244, 1991

A:Title:	Identification of an additional gene belonging to the alpha(2) adrennergic recep
A:Reference number:	514308; MUID:91192139; PMID:1849485
A:Accession:	514308
A:Status:	preliminary
A:Molecule type:	DNA
A:Residues:	56-185 <CH>
A:Cross-references:	GB:X59684; NID:g28635
A>Note:	This translation is not annotated in GenBank entry H5ALRH218, release 111.0
R:Chang, A.C.;	Ho, T.F.; Chan, N.C.
Biochem. Biophys. Res. Commun.	172, 817-823, 1990
A:Title:	In vitro amplification by polymerase chain reaction of a partial gene encoding
A:Reference number:	A36158; MUID:91054503; PMID:2173582
A:Accession:	A36158
A:Molecule type:	DNA
A:Residues:	95-361, 'QL', 364-389 <CHA>
A:Cross-references:	GB:M8742; NID:g177867; PIDN:AAA62823.1; PID:g177868
C:Genetics:	
A:Gene:	GDB:ADRA2B; ADRA2L1; ADRA2RL1
A:Cross-references:	GDB:120539; OMIM:104260
A:Map position:	2p13-2q13
C:Superfamily:	vertebrate rhodopsin
C:Keywords:	G protein-coupled receptor; glycoprotein; transmembrane protein
Query Match	47.4%; Score 1127.5; DB 2; Length 450;
Best Local Similarity	53.2%; Pred. No. 1,16-64;
Matches	243; Conservative 51; Mismatches 104; Indels 59; Gaps 14;
OY	27 PYSLOYTLVLCAGLMLLVFGNVLVITVFSRAKAPONFLVSLASDILVATLY 86
Db	6 PYSVQATAAIAAATFTLFTFTFGNALVILAVLSRSRAQONFLVSLAADILVATLY 65
OY	87 IPFSLANFVGMGYFGKAMCEIYALADVLCNSSLIVHCAISLDKWSITQAIENLKRT 146
Db	66 IPFSLANELGWMYRRFMCEVYALADVLCNSSLIVHCAISLDKWMVSRALTEYNSKRT 125
OY	147 PRRIKAITITVWISAVISFPPPLISIEKKGGGGQGP-AERCELENDQKWTYISCTISF 205
Db	126 PRRIKIIITVWLVLAIVSLPLI---YKGDGQGPGRPCCKINQMAVITLASSISF 181
OY	206 FAPCIIIMLVYRIQIAKKRTRVPPSRGPDAAVAPGGETERERKGLGPEKSAAGGAE 265
Db	162 FAPCIIIMLVYRIITLIRK-----SNRRGPRAKGPGQGESKQPR---PDHGALASAK 233
OY	266 AEPLEPT-----QLNG---APGEPAAP-GPRDTDALDLES-----SS 298
Db	234 IPALASVASARAEVNHSKSTGEKEGETPEPTGTALPSPWALDPSNGOGKEVCGASP 293
OY	299 SDHARPPGPRPERGPRGKAKARAOVKPGD--SLPRRPG-----ATGIGTPAAGGE 351
Db	294 EDEAE-----EEEEEEECPEQAVPVSPASACSPILQOPGGSVLAFTLRQVLLGG- 348
OY	352 ERVGAAKASRMGRON--REKRFETVLAVVIGVAVVCMPPFEFTYTLAV--GCSVPT 406
Db	349 --VGAIGGCMRRRAHVRREKRFETVLAVVIGVFLCMFPFEFTSLGAIKPKCKVPHG 406
OY	407 LEKFEFMFGYCNSSLNPVYITFNHDFRAFKIICR 443
Db	407 LFQFFFWIGYCNSSLNPVYITFTFNDFRAFRRIICR 443
RESULT 12	
alpha 2-adrenoceptor - cuckoo wrasse	
C:Species:	Labrus ossifagus (cuckoo wrasse)
C:Date:	04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 13-Aug-1999
C:Accession:	150829
R:Swenson, S.P.;	Bailey, T.J.; Pepperl, D.J.; Grundstrom, N.; Ala-Dotila, S.; Scheinin
Br. J. Pharmacol.	110, 54-60, 1993
A:Title:	Cloning and expression of a fish a2-adrenoceptor.
A:Reference number:	150829; MUID:94035926; PMID:7693288
A:Accession:	150829
A:Status:	preliminary;
A:Molecule type:	DNA
A:Molecule type:	translated from GB/EMBL/DBJ

A:Residues: 1-132 <SV>		47.3%, Score 1126.5; DB 2; Length 432;	
A:Cross-references: EMBL:U07743; NID:9467287; PIDN:AAA17386.1; PID:9467288		Best Local Similarity 53.0%, Pred. No. 1.2e-64;	
C:Superfamily: vertebrate rhodopsin		Matches 240; Conservative 50; Mismatches 108; Indels 55; Gaps 11;	
Query Match			
10	MSNMGTAEPGGCAATATPYSLOVTLTLYCAGLMLTFVGVNLTIVFTSRALKAPON 69		
18	MSWS-----ADSG-----YSTLAATASIALYSLFLLFTVVGNIIVAVLTSRLKAPN 68		
70	LEFVLSASADILVATLVIPFSLANEVGYWYFGKACEIYALDVLFTSSIVHLCAISL 129		
69	LEFVLSATADILVATLVMPFSLANELMGYWGKWCIGYALDVLFTSSIVHLCAISL 128		
130	DRYWTQTQAEVNLKRTPRKATITVWVTSAVTSPPFLSIIEKGGGGGPQAPRPE 189		
129	DRYWTQTQAEVNLKRTPRKATITVWVTSAVTSPPFLSIID-----SNNTISSQPCM 184		
190	INDQKVVYVSSCIGSFPAFLIMLVYVRIYIAKRTFRVPSRRGPDVAAPGQTERR 249		
185	LMDDTWYLISSMASFEACLMILVYIRIYVATFRR-----SMGKRP 231		
250	PKGL-----GPERSGAP-----GGAERAPLPITLNGAPGEPAPAGRPDLDLESS 297		
232	PGVVTQTENGLKANSPCGHGRENGHCQPPPSQRTVITGQ-----QTDADAMDESF 284		
298	SSDHAEKRPGRPRPRGPRGKARASGVKPPDSLPKRGPCATIGTPAAGGEEERYAA 357		
285	SSEGGCHKRQRODSQRAKR-PGLKSSISIKSGARISRYSNKSYDLFASRRKRRESIAEK 343		
358	KASRMGRGNRKRKFTFLVAVIGVYVCAPEPFETTYLLAV--GGSVPRLTKFFWF 414		
344	KVS-----QAREKREFFLVAVMGVFWVCWPFPEFSYSLHAYCRDYCKIPDTLTK-FPM 397		
415	GYCNSSLNPVITYTFNHDFRAFKRLICRGDK 447		
398	GYCNSSLNPATITYTFNDRFRAPFKILCKSMK 430		
RESULT 13			
S28221			
alpha-2-C2 adrenergic receptor - mouse			
C:Species: Mus musculus (house mouse)			
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 13-Aug-1999			
C:Accession: S28221; JH0693			
R:Chem. W.M.; Chang, A.C.; Shie, B.-J.; Chang, Y.H.; Chang, N.C.A.			
R:Biochem. Biophys. Res. Commun. 186, 1280-1287, 1992			
A:Note: The authors translated the codon CCA for residue 161 as Phe, ACT for residue R.Chruschinski, A.J.; Link, R.E.; Daunt, D.A.; Barsh, G.S.; Koblika, B.K.			
A:Title: Cloning and expression of the mouse homolog of the human alpha2-C2 adrenergic			
A:Reference number: JH0693; MUID:92378586; PMID:1354956			
A:Accession: S28221			
A:Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1-455 <CHE>			
A:Cross-references: EMBL:M94583			
C:Keywords: G protein-coupled receptor; transmembrane protein			
F:18-43/Domain: transmembrane #status predicted <TM1>			
F:55-115/Domain: transmembrane #status predicted <TM2>			
F:134-158/Domain: transmembrane #status predicted <TM3>			
F:173-199/Domain: transmembrane #status predicted <TM4>			
F:377-402/Domain: transmembrane #status predicted <TM5>			

Thu Feb 20 09:21:44 2003

us-09-636-259b-4.rpt

Page 8

Db 411 FOFFWIGYONSLNPVITYVFNODFRRAFRRIICR 446

Search completed: February 15, 2003, 18:08:04
Job time : 25.5 secs

. . .

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 15, 2003, 14:30:52 ; Search time 50 Seconds

(without alignments)
1854.424 Million cell updates/sec

Title: US-09-636-259b-4

Perfect score: 2380

Sequence: 1 MGSLQPDAGNASWNGTEAPG.....HDFRRAFKKILCRGDRKRTV 450

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2380	100.0	450	4	Q9BZK1
2	1305.5	54.9	388	13	Q90WY4
3	1174.5	49.3	432	13	Q90WY6
4	1132	47.6	510	13	Q90WY5
5	1126	47.3	447	4	Q9BZK0
6	1116.5	46.9	448	11	Q925K7
7	1113.5	46.8	448	11	Q925K6
8	1112.5	46.7	453	11	Q925E4
9	969.5	40.7	393	11	Q9JTW2
10	943	39.6	392	6	Q95N80
11	940	39.5	390	6	Q9GLI9
12	938.5	39.5	391	6	Q8SOQ0
13	938.5	39.4	389	6	Q9GK25
14	938.5	39.4	395	6	Q9GLI2
15	938	39.4	390	6	Q9GK26
16	937.5	39.4	379	6	Q9GLI3

17	935.5	39.3	393	6	Q9GLI1	Q9G111 nycticebus
18	933.5	39.2	395	6	Q95N91	Q95n91 tonatia bid
19	933	39.2	388	6	Q9GLI8	Q9G118 alceros bic
20	932.5	39.2	389	6	Q9GL07	Q9G107 phoca vitul
21	932	39.2	390	6	Q95N89	Q95n89 taphozous s
22	931.5	39.1	387	6	Q9GLI7	Q9G117 felis silve
23	929.5	39.1	393	6	Q95N92	Q95n92 myotis daub
24	928.5	39.0	393	6	Q9GL20	Q9G120 cynopterus
25	928.5	39.0	393	6	Q9GL15	Q9G115 macrotus ca
26	928	39.0	392	6	Q9GL35	Q9G135 balaenopter
27	925.5	38.9	393	6	Q9GL16	Q9G116 hippopotamu
28	924.5	38.8	391	6	Q9GL06	Q9G106 sus scrofa
29	923.5	38.8	385	6	Q9GL14	Q9G114 micropotamo
30	922.5	38.8	389	6	Q95N94	Q95n94 hipposidero
31	922	38.7	388	6	Q95O91	Q95o91 nycteris th
32	921.5	38.7	385	6	Q9GK27	Q9Gk27 tenrec ecan
33	920.5	38.7	391	6	Q95O93	Q95o93 antrozous gr
34	919	38.6	388	6	Q95O93	Q95o93 nycteris th
35	919	38.6	396	6	Q95O97	Q95o97 rhogeessa t
36	914.5	38.4	395	6	Q95O94	Q95o94 megalodonta
37	913	38.4	392	6	Q9GL28	Q9G128 bradydus tr
38	910.5	38.3	383	6	Q95O91	Q95o91 desmodus ro
39	910	38.2	394	6	Q95O92	Q95o92 natalus str
40	910	38.2	398	6	Q95O95	Q95o95 nyctimene a
41	909.5	38.2	389	6	Q95O95	Q95o95 pleiopus ra
42	907.5	38.1	383	6	Q95N93	Q95n93 rhinolophus
43	904	38.0	365	6	Q95O98	Q95o98 rhinolophus
44	900.5	37.8	389	6	Q95O98	Q95o98 boophilus m
45	684.5	28.8	419	5	077254	

ALIGNMENTS

RESULT 1

Q9BZK1 PRELIMINARY; PRT; 450 AA.
AC Q9BZK1;
DT 01-JUN-2001 (TREMUREL. 17, Created)
DT 01-JUN-2001 (TREMUREL. 17, Last sequence update)
DT 01-MAR-2002 (TREMUREL. 20, Last annotation update)
DE Alpha 2A adrenergic receptor.
GN ADRA2A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20556293; Pubmed=10948191;
RA Small K.M., Forbes S.L., Brown K.M., Liggett S.B.;
RT "An asn to lys polymorphism in the third intracellular loop of the
RT human alpha 2A-adrenergic receptor imparts enhanced agonist-promoted
RT GI coupling.";
RL J. Biol. Chem. 275:38518-38523(2000).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF116994; AK01034.1; -.
DR HSP; P29274; IWH.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G-PROTEIN_RECPT_F1_1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECPT_F1_2; 1.
KW G-PROTEIN coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT VARIANT 251 251 K -> N.
SQ SSQUNCE 450 AA; 48970 MW; 94E02E227CE5ECFE CRC64;

Query Match 100.0%; Score 2380; DB 4; Length 450;
Best Local Similarity 100.0%; Pred. No. 5.8e-165;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSLQPDAGNASWNGTEAPGAGATPYSLQVTLTVLCIAGLIMLTJVGWLVITAVPT 60

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|||||
Db 1 MCSLDPDAGNAGMNGTEAPGGARATPYSLQYTLTVLCLAGLMLLTVEGNVLIAVFT 60
Qy 61 SRALAPQMLFVLSASADILVATVTPSTLANEMGWYEGKAMCEIYALDVLCFTSS 120
Db 61 SRALAPQMLFVLSASADILVATVTPSTLANEMGWYEGKAMCEIYALDVLCFTSS 120
Qy 121 IYHLCASIDRYWSTIQAEIENYMLKTPRRIRKAIITVWVISAIVISFPLISIEKKGGGG 180
Db 121 IYHLCASIDRYWSTIQAEIENYMLKTPRRIRKAIITVWVISAIVISFPLISIEKKGGGG 180
Qy 181 POPAEPRCEINDQKTVYVSSCTGSPAPCLIMLVYVRIYQIAKRRTRVPSRRGPDVA 240
Db 181 POPAEPRCEINDQKTVYVSSCTGSPAPCLIMLVYVRIYQIAKRRTRVPSRRGPDVA 240
Qy 241 APGGTERPRKGLGPEPSAGPGAEPPLPTQLNGAPGPAPAGPRDTDLDESSSSD 300
Db 241 APGGTERPRKGLGPEPSAGPGAEPPLPTQLNGAPGPAPAGPRDTDLDESSSSD 300
Qy 301 HAERPPGPRRPERGPRGKARASQVCPGDSLPRGPGATGIGTPAAGGEERVAAKAS 360
Db 301 HAERPPGPRRPERGPRGKARASQVCPGDSLPRGPGATGIGTPAAGGEERVAAKAS 360
Qy 361 RMGRONREKREFVLAVYGVVCMPEFFTYTLTAVGCSVPRLTFKFFWFGYCNSS 420
Db 361 RMGRONREKREFVLAVYGVVCMPEFFTYTLTAVGCSVPRLTFKFFWFGYCNSS 420
Qy 421 LNPVIYTIENHDEPRRAFKILCRGDRRIY 450
Db 421 LNPVIYTIENHDEPRRAFKILCRGDRRIY 450
```

RESULT 2

```
Q90WY4 PRELIMINARY: PRT; 388 AA.
ID 090WY4:
AC 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
GN Alpha2A-adrenergic receptor.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Ruuskanen J., Xhaard H., Marjamäki A., Salaneck E., Salminen T.,
RA Van Y.L., Postlethwait J.H., Johnson M.S., Larhammar D., Schein M.;
RT "Origin of Alpha2-Adrenergic Receptor Subtypes as Revealed by Cloning
RT and Mapping of Three Receptor Subtype Genes in the Zebrafish (Danio
RT rerio).";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY048971; AL07510.1;
DR InterPro: IPR00276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECPT_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECPT_F1_2; 1.
KW Receptor.
SQ SEQUENCE 388 AA; 43996 MW; 431965A04E1986DD CRC64;
```

Query Match 54.9%; Score 1305.5; DB 13; Length 388;

Best Local Similarity 60.5%; Pred. No. 4.6e-87; Mismatches 78; Indels 59; Gaps 8;

```
Qy 15 GTEAPGGARATPYSLQYTLTVLCLAGLMLLTVEGNVLIAVTSRALKAPQNLFLVS 74
Db 4 GANNATNGNATKEYTLVALPLSTAVGLILILIFGNVLIAVTSRALKAPQNLFLVS 63
Qy 75 LASADILVATVTPSTLANEMGWYEGKAMCEIYALDVLCFTSSIVHCAISLDRYWS 134
Db 64 LASADILVATVTPSTLANEMGWYEGKAMCEIYALDVLCFTSSIVHCAISLDRYWS 123
```

```
Qy 135 ITQAEIENYMLKTPRRIRKAIITVWVISAIVISFPLISIEKKGGGGQPAEPRCEINDOK 194
Db 124 ITQAEIENYMLKTPRRIRKAIITVWVISAIVISFPLISIEKKGGGGQPAEPRCEINDOK 175
Qy 195 WYVSSCTGSPAPCLIMLVYVRIYQIAKRRTRVPSRRGPDVAAPGGTERPRKGLG 254
Db 176 WYVSSCTGSPAPCLIMLVYVRIYQIAKRRTRVPSRRGPDVAAPGGTERPRKGLG 213
Qy 255 PERSAGPGAEPPLPTQLNGAPGPAPAGPRDTDLDESSSSDHAERPPGPRR 311
Db 214 DHRKNVEGKKENPD-HEKLNQIQN---AEPDDKDELINGVDMESSSDHKVSNPSCCLK 268
Qy 312 ERGRGPGKARASQVCPGDSLPRGPGATGIGTPAAGGEERVAAKASRMGRONREK 371
Db 269 K---SSGKTKLSQIKFD-----GDKTEACQTTAKSRMKGRONREK 308
Qy 372 FTFLAVYGVVCMPEFFTYTLTAVGCSVPRLTFKFFWFGYCNSSLNPVIYTIEN 430
Db 309 FTFLAVYGVVCMPEFFTYTLTAVGCSVPRLTFKFFWFGYCNSSLNPVIYTIEN 368
Qy 431 HDPRRAFKILCRGDRRIY 450
Db 369 NDFRSEFKILCRGDRRIY 388
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RESULT 3

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Q90WY6 PRELIMINARY: PRT; 432 AA.
ID 090WY6:
AC 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
GN Alpha2C-adrenergic receptor.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Ruuskanen J., Xhaard H., Marjamäki A., Salaneck E., Salminen T.,
RA Van Y.L., Postlethwait J.H., Johnson M.S., Larhammar D., Schein M.;
RT "Origin of Alpha2-Adrenergic Receptor Subtypes as Revealed by Cloning
RT and Mapping of Three Receptor Subtype Genes in the Zebrafish (Danio
RT rerio).";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY048968; AL07508.1;
DR InterPro: IPR00276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECPT_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECPT_F1_2; 1.
KW Receptor.
SQ SEQUENCE 432 AA; 49137 MW; 1A52F0283C63DA7 CRC64;
```

Query Match 49.3%; Score 1174.5; DB 13; Length 432;

Best Local Similarity 56.4%; Pred. No. 1.6e-77; Mismatches 113; Indels 29; Gaps 8;

```
Qy 20 GGGARATPYSLQYTLTVLCLAGLMLLTVEGNVLIAVTSRALKAPQNLFLVSASAD 79
Db 22 GNSNTSTYSPATITIGLAVSFLILFTVGNVLIAVTSRALKAPQNLFLVSASAD 81
Qy 80 ILVATVTPSTLANEMGWYEGKAMCEIYALDVLCFTSSIVHCAISLDRYWSITQAI 139
Db 82 ILVATVTPSTLANEMGWYEGKAMCEIYALDVLCFTSSIVHCAISLDRYWSITQAV 141
Qy 140 EYNLKRTPRRIRKAIITVWVISAIVISFPLISIEKKGGGGQPAEPRCEINDQKMYIS 199
Db 142 EYNLKRTPRRIRKAIITVWVISAIVISFPLISMDR---NTVDERRPMQCLNDHWTYILY 197
Qy 200 SCIGSFAPCLIMLVYVRIYQIAKRRTR-VPSRRGPDVAAPGGTERPRKGLGPEPS 258
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Db      198  SSGISFFAPCVIMILYIRIYQAKTRTNMSSEKRRDPDS-----GSGTPLFENGLSREDS 253
QY      259  AGPGAAEAPLPTQNLNGAGEPAPAGPRDPTDALDLESSSDH-AERPPRPREPGPRG 317
Db      254  RRENG-----HCSSSPGEKPPA--EDNPDADLESDSSDDEKARSONETAAPSKDRR 303
QY      318  KGARASQVKGPSDLPKPRPGATGIGTPAAGPEERVGAAKASRWGRQNRKERTFVLA 377
Db      304  SSRKSSSSKHSKRKRASKSLDFS-----SRKRRTIRTKITISQAREKRTFVLA 357
QY      378  VLVGVFVWCFFPEFFTYTLTAV---GCSVRTLFKRFPEFGYCNSSLNPVYITFNHDER 434
Db      358  VVGVGVFVWCFFPEFFSYSLYGICREPCALPDLFKFFEFWIGYCNSSLNPVYITFNODPR 417
QY      435  RAFFKIICR 443
Db      418  RAFOKILICK 426

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RESULT 4

```

Q90WY5  PRELIMINARY: PRT; 510 AA.
AC      090WY5;
DT      01-DEC-2001 (TREMBlrel. 19, Created)
DT      01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT      01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE      Alpha2B-adrenergic receptor.
GN      ADRA2B.
OS      Brachydanio rerio (Zebrafish) (Zebra danio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC      Cyprinidae; Danio.
OX      NCBI_TaxId=7955;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Ruuskanen J., Xhaard H., Marjamaki A., Salaneck E., Salminen T.,
RA      Yan Y.L., Postelthwait J.H., Johnson M.S., Larhammar D., Scheinlin M.;
RT      Origin of Alpha2-Adrenergic Receptor Subtypes as Revealed by Cloning
RT      and Mapping of Three Receptor Subtype Genes in the Zebrafish (Danio
RT      rerio).
RL      Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
DR      EMBL; AY048970; AAL07509.1;
DR      InterPro; IPR000276; GPCR_Rhodopsn.
DR      Pfam; PF00001; 7tm_1; 1.
DR      PROSITE; PS00237; G_PROTEIN_RECEPTOR_FL_1; UNKNOWN_1.
DR      PROSITE; PS50262; G_PROTEIN_RECEPTOR_FL_2; 1.
KW      Receptor.
SQ      SEQUENCE 510 AA; 55971 MW; 1CB07C0AFC6DE3D3 CRC64;

```

Query Match 47.6%; Score 1132; DB 13; Length 510;

Best Local Similarity 48.5%; Pred. No. 2.4e-74;

Matches 249; Conservative 58; Mismatches 104; Indels 102; Gaps 15;

```

QY      14  NCTEAPGCGARKT-----PYSIQVTLTLYVCLAGLMLTLFQNVLYITAVTTSAL 64
Db      16  NCT-----GGTSPTCQMSMIKILAPYSPEATAFATITMLTLTIGNILVIITAVTSRL 72
QY      65  KAPONLFLVSLASADILVTLVIPSFLANVMGYFGKAWCEIYLAIDLVECTSSIVHL 124
Db      73  RGPONLFLVSLAADIIVATLTIIPSLANELMGYTFPSWCETIYLAIDLVECTSSIVHL 132
QY      125  CAISIDRWSTQATIEYLNKRTPRRIKAIITVWVISAIVISFPPLISTIEKGGGGGPPA 184
Db      133  CAISIDRWYSISRATVYGRKTPRKIKCALIVWVLSAIVISFPPLSM-NNKKGGGEGSA 191
QY      185  BPERCEINDQKWVIVSSCGSPFAPCLIMIVYVRIYQAKRTRVPPS---RQGDVAAA 241
Db      192  LPQCOLNDERKTIITLSTGSEFAPCLIMILVYRIYQAKRTRCPPEPRKEAPANAT 251
QY      242  P-----PGTER--RPKGLGERSAGPGAAEAPLPTQNLNGAGEP----- 279
Db      252  PQHKIONGDETPGTGLQKAPRPPLAVSQVESVQAANTPIANNLDAQPSTTLTPTT 311

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QY      280  PAPAGPRDPTDALDLESSSDHAERPPRPREPGPRGKGARASQV-----PGDS 331
Db      312  PPS-----PSNSSEVA-----PSKSEKKEKKKKNNKKNKKEPPNNNS 355
QY      332  L-----PRRPGATGIGTP-----AAGPGERV-----GA 356
Db      356  MSSDSPTDEGGGGLVPCPTPTP--SGHSPTAQKTRDMATATKAKKLVARRAKQDGT 413
QY      357  AKASRWGRQNRKERTFVLAIVGVFVWCFFPEFFTYTLTAV---GCSVRTLFKFFFW 413
Db      414  PMSARRKAVVNRKERTFVLAIVGVFVWCFFPEFFSYSLQAVCESCALDEPLKFFFW 473
QY      414  FGYCNSSLNPVYITFNHDERAFKIIICRGDR 446
Db      474  IGYCNSSLNPVYITFNHDERAFKIIICKMKR 506

```

RESULT 5

```

Q9BZK0  PRELIMINARY: PRT; 447 AA.
AC      Q9BZK0;
DT      01-JUN-2001 (TREMBlrel. 17, Created)
DT      01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT      01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE      Alpha 2B adrenergic receptor.
GN      ADRA2B.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX      NCBI_TaxId=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      MEDLINE-21265012; PubMed-11056163;
RA      Small K.M., Brown K.M., Forbes S.L., Liggett S.B.;
RT      "Polymorphic Deletion of Three Intracellular Acidic Residues of the
RT      alpha 2B-adrenergic Receptor Decreases G Protein-coupled Receptor
RT      Kinase-mediated Phosphorylation and Desensitization."
RL      J. Biol. Chem. 276:4917-4922(2001).
CC      1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC      1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR      EMBL; AF316895; AAK01635.1;
DR      HSSP; P29274; 1MMH.
DR      InterPro; IPR000276; GPCR_Rhodopsn.
DR      Pfam; PF00001; 7tm_1; 1.
DR      PRINTS; PR00237; GPCR_RHODOPSN.
DR      PROSITE; PS00237; G_PROTEIN_RECEPTOR_FL_1; 1.
DR      PROSITE; PS50262; G_PROTEIN_RECEPTOR_FL_2; 1.
KW      G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT      VARIANT 298 EEE -> KRR.
SQ      SEQUENCE 447 AA; 49566 MW; B3DAB5B719C1C45 CRC64;

```

Query Match 47.3%; Score 1126; DB 4; Length 447;

Best Local Similarity 53.2%; Pred. No. 5.6e-74;

Matches 243; Conservative 50; Mismatches 102; Indels 62; Gaps 14;

```

QY      27  PYSIQVTLTLYVCLAGLMLTLFQNVLYITAVTSRLKAPONLFLVSLASADILVATLV 86
Db      6  PYSQATRAIAAATFTFLTIFGNALVILAVLTSRLAPQNLFLVSLAADIIVATL 65
QY      87  IPEFLANVMGYFGKAWCEIYLAIDLVECTSSIVHLCASIDRWYSITQATIEYLNKRT 146
Db      66  IPEFLANELGMYFRRFTWCVEYIALDLVLTCTSSIVHLCASIDRWYAVSRALEYNSKRT 125
QY      147  PRKIKCIITVWVISAIVISFPPLISTIEKGGGGGPP-APRCEINDQKWVIVSSICGSP 205
Db      126  PRKIKCIITVWVLSAIVISFPPLI-----YKGDGPQPRGAPQCKLQEAAYIIASSIGSP 181
QY      206  FAPCLIMILYVRIYQAKRTRVPSRGPDAVAAPGTEPRKGLGERSAGGAGAE 265
Db      182  FAPCLIMILYVRIYLAIAK-----SNRKGPRAKGFGGEGSKQPR---PDHGGALASAK 233
QY      266  AEPLPT-----QLNG--APGEPA-GRPDPTDALDEES-----SS 298

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      234 LPLASVASKREYNGSKSGEKEBEDTETDITRALPPSWALPNSSGGOKEGVGSAP 293
      299 SDHAERPPGRRPGRPGKAKASQVPGD--SLPRGPG----ATGIGTPAAGPGE 351
      294 EDAAEE-----EEEBEECEPOAVPSPASCSPLQOPGSRVLTATLRGVLLGRG- 345
      352 ERGAKAKASWRGRQ--NREKRTFVLAVIGVFVCMFPPEFTYTLAV---GCSVPT 406
      346 --VGALGGQWRRRAQLTRKRTFVLAVIGVFVCMFPPEFTYSLGALCPKCKVPHG 403
      407 LKFFWFYGCNSSLNPIVITYTFNHDFRRRAFKKILCR 443
      404 LFOFFFWIGYCNSLNPIVITYTFNHDFRRRAFKKILCR 440

RESULT 6
ID 0925K7 PRELIMINARY; PRT; 448 AA.
AC 0925K7;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Adrenergic receptor alpha 2B.
GN ADRA2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ISS;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.,
RT "High-Throughput Sequence Identification of Gene Coding Variants
RT within Alcohol-Related QTLs.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332049; AAK56078.1; -.
DR MGI; MGI:87935; Adra2b.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECPR_F1.1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECPR_F1.2; 1.
KW Receptor.
SQ
SEQUENCE 448 AA; 50018 MW; 1B5ED9456C0B2B73 CRC64;

Query Match 46.9%; Score 1116.5; DB 11; Length 448;
Best Local Similarity 52.7%; Pred. No. 2,8e-73;
Matches 241; Conservative 50; Mismatches 105; Indels 61; Gaps 14;

      27 PYSLOVTLTVCLAGLMLTLVFGNVLYIAVFTSRALKAPONLFVLSASADILVATLV 86
      6 PYSVQATRAIASATFLIFTIFGNALVILAVLSRSLRAPONLFVLSAADIIVATLI 65
      87 IFFSLANEVMGWYFGKAMCEIYALDVLFCSTSVHLCALSLDRYWSITQAIENYKRT 146
      66 IFFSLANELLGWYFWRAMCEVYALDVLFCSTSVHLCALSLDRYWAASRALEYNSKRT 125
      147 PRRIKAIITVWYISAVISFPPLISIEKKGGGCGPQ--APRCINQKQWYVSSCIGSF 205
      126 PRRIKCIITLTVMLIAVILYIAKR-----YKGDQRPBPHGLPQCLNEAWYTLASSISGSF 181
      206 FAPCLIMLVVRYIOAKRTRVPPSRGPDVAAPPGTERPRKGLGERSAGPGGAE 265
      182 FAPCLIMLVLYRIYIAKR-----SHCRGLGAKRSGEGESKPR---PAAGVPAASAK 233
      266 AEPPLTQUNG---APGEPAPAPRDTALDLESSSSSDHAER---PPG---PRRPERGP 315
      234 VPTLVSPLSVSGEANGHHP--PREK-----EEGETPEDPEARALPWNMSALPRSVQDOK 286
      316 RKGKARASQVPGD-----SLPRGPGATGIGTPAAGGEER----- 353
      287 KGTSGATAEKGAEBDEEVECEPQTLP--ASPASVFNPLQOPQTSRVLTATLRGVLLS 344
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      354 --VGAKAKASWRGRQ--NREKRTFVLAVIGVFVCMFPPEFTYTLAV---GCSVPT 406
      345 KNVGAASQWRRRRQQLSRKRTFVLAVIGVFVCMFPPEFTYSLGALCPQCKVPHG 404
      407 LKFFWFYGCNSSLNPIVITYTFNHDFRRRAFKKILCR 443
      405 LFOFFFWIGYCNSLNPIVITYTFNHDFRRRAFKKILCR 441

RESULT 7
ID 0925K6 PRELIMINARY; PRT; 448 AA.
AC 0925K6;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Adrenergic receptor alpha 2B.
GN ADRA2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ISS;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.,
RT "High-Throughput Sequence Identification of Gene Coding Variants
RT within Alcohol-Related QTLs.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332050; AAK56079.1; -.
DR MGI; MGI:87935; Adra2b.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECPR_F1.1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECPR_F1.2; 1.
KW Receptor.
SQ
SEQUENCE 448 AA; 49998 MW; B37E5E21B0EC4625 CRC64;

Query Match 46.8%; Score 1113.5; DB 11; Length 448;
Best Local Similarity 52.7%; Pred. No. 4,6e-73;
Matches 241; Conservative 49; Mismatches 106; Indels 61; Gaps 14;

      27 PYSLOVTLTVCLAGLMLTLVFGNVLYIAVFTSRALKAPONLFVLSASADILVATLV 86
      6 PYSVQATRAIASATFLIFTIFGNALVILAVLSRSLRAPONLFVLSAADIIVATLI 65
      87 IFFSLANEVMGWYFGKAMCEIYALDVLFCSTSVHLCALSLDRYWSITQAIENYKRT 146
      66 IFFSLANELLGWYFWRAMCEVYALDVLFCSTSVHLCALSLDRYWAASRALEYNSKRT 125
      147 PRRIKAIITVWYISAVISFPPLISIEKKGGGCGPQ--APRCINQKQWYVSSCIGSF 205
      126 PRRIKCIITLTVMLIAVILYIAKR-----YKGDQRPBPHGLPQCLNEAWYTLASSISGSF 181
      206 FAPCLIMLVVRYIOAKRTRVPPSRGPDVAAPPGTERPRKGLGERSAGPGGAE 265
      182 FAPCLIMLVLYRIYIAKR-----SHCRGLGAKRSGEGESKPR---PAAGVPAASAK 233
      266 AEPPLTQUNG---APGEPAPAPRDTALDLESSSSSDHAER---PPG---PRRPERGP 315
      234 VPTLVSPLSVSGEANGHHP--PREK-----EEGETPEDPEARALPWNMSALPRSVQDOK 286
      316 RKGKARASQVPGD-----SLPRGPGATGIGTPAAGGEER----- 353
      287 KGTSGATAEKGAEBDEEVECEPQTLP--ASPASVFNPLQOPQTSRVLTATLRGVLLS 344
      354 --VGAKAKASWRGRQ--NREKRTFVLAVIGVFVCMFPPEFTYTLAV---GCSVPT 406
      345 KNVGAASQWRRRRQQLSRKRTFVLAVIGVFVCMFPPEFTYSLGALCPQCKVPHG 404
      407 LKFFWFYGCNSSLNPIVITYTFNHDFRRRAFKKILCR 443
```

Db 405 LFOFFFWIGYCNSSLNPIYITIFNODFRRAFRILCR 441

RESULT 8

0925E4 PRELIMINARY; PRT; 453 AA.
AC 0925E4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Alpha2B-adrenergic receptor.
GN RRG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Schack S., Cusack D., Paris H.;
RT *Cloning and characterization of the rat alpha2B-adrenergic receptor
RT gene promoter*;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL:AF366899; AAK53388.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KM Receptor.
SQ SEQUENCE 453 AA; 50369 MW; CBA69CE23EACB511 CRC64;

Query Match 46.7%; Score 1112.5; DB 11; Length 453;
Best Local Similarity 52.5%; Pred. No. 5,4e-73;
Matches 240; Conservative 51; Mismatches 105; Indels 61; Gaps 14;

27 PYSIQYTLVLCAGLMLITVGNVLIIVFTSRALAPQNLFLVSLASADIVATLV 86
11 PYSQATAIASAITPLLETITGNALVLIIVFTSRALAPQNLFLVSLASADIVATLV 70
87 IPFSLANWGVYFGKANCEIYALDVLCSTSIYHLCALISDRYMSITQAIENYLNKRT 146
11 IPFSLANWGVYFGKANCEIYALDVLCSTSIYHLCALISDRYMSITQAIENYLNKRT 130
147 PRITKAITTWYISAVISPPILISTEKKGGGGPOP AEPCEINDQKWYISSCIGSF 205
131 PRRIKCIITLVWLIIVLISLPDI---YKGDQRPGRGLPQCELNQEAAMYLASSIGSF 186
206 FAPCLIMILVYVRIQIAKRRTRVPSRRGPDVAAPPGSTRBRPGGLGPEKSGAGAE 265
187 FAPCLIMILVYVRIQIAKRRTRVPSRRGPDVAAPPGSTRBRPGGLGPEKSGAGAE 238
266 AEPPLPQNG--AGEPAPAGPRDTALDLESSSSDHAER---PPG---PRRPERGP 315
239 VPLVPLSLSSVGEANGHPKP--PREK---EEGETPEDPEARALPPTMSALPRSGOGK 291
316 RGKRGARASQVPRG-----SLPRGCGATGIGPAAGPGEER----- 353
292 KGTSGATAEGDEDEEVECEPQTLR--ASPASVCNPLDQOPTSRVLTATLRQVLLG 349
354 --VGAAKASRMGRQ--NRKRRTEFLAVVIGFVVCMPFFFTYTLAV---GCSVPRT 406
350 KNGVVASGGWMRRRQJLSKRRFTYLAIVIGFVVCMPFFFTYSLGAIQPHCKVPHG 409
407 LKREFFWPGYCNSSLNPIYITIFNODFRRAFRILCR 443
410 LFOFFFWIGYCNSSLNPIYITIFNODFRRAFRILCR 446

RESULT 9
09JW2 PRELIMINARY; PRT; 393 AA.
AC 09JW2;
ID 09JW2;
OX 09JW2;

DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Alpha adrenergic receptor 2b (fragment).
GN AAR2B.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA Madsen O.;
RT *Molecular evolution of alpha adrenergic receptor 2B.*;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AJ271336; CAB66895.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT NON_TER 1
FT NON_TER 393
SQ SEQUENCE 393 AA; 42921 MW; 5399B7175A53BD48 CRC64;

Query Match 40.7%; Score 969.5; DB 11; Length 393;
Best Local Similarity 52.2%; Pred. No. 1.1e-62;
Matches 214; Conservative 42; Mismatches 85; Indels 69; Gaps 13;

43 LMLTFEGNVLIIVFTSRALAPQNLFLVSLASADIVATLVIPFSLANWGVYTFG 102
9 LILFTIFGNALVLIIVFTSRALAPQNLFLVSLASADIVATLVIPFSLANWGVYTFW 68
103 KAMCEIYALDVLCFTSSIVHLCALISDRYMSITQAIENYLNKRRIRKATIIITWYISA 162
69 RTWCENVYALDVLCFTSSIVHLCALISDRYMSITQAIENYLNKRRIRKATIIITWYISLA 128
163 VISPLPILIEKKGGGGPOP AEPCEINDQKWYISSCIGSFAPCLIMILVYVRIQ 221
129 VISPLPILIEKKGGGGPOP AEPCEINDQKWYISSCIGSFAPCLIMILVYVRIQ 184
222 IAKRRTRVPSRRGPDVAAPPGSTRBRPGGLGPEKSGAGAE---PLPQNG-- 275
185 IAKR-----SNRGRAGAGGEGGSKSRPL-----PGGASAKAVPLASPLSTG 232
276 -APGEPAPAGPRDTALDLESSSSDHAERPPRRRPERGPGKARASQVPR----- 328
233 EANGHPKPTGKE-----EGETSEDPGARLTPSMALPTSGOGOKKAVYLAPEEBAE 286
329 -----GDSL-PRRGP-----ANGICPPAGPGEERGAKAASRMR 363
287 EEEEGDCECEQOAPGLPASCSPSLDQPGSRVLTATLRQVLLGRG---VGAVDGQWMR 343
364 GR--QNRKRRTEFLAVVIGFVVCMPFFFTYTLAV---GCSVPRTLF 408
344 RRTQTRKRRTEFLAVVIGFVVCMPFFFTYSLGAIQPHCKVPHGLF 393

RESULT 10
095N90 PRELIMINARY; PRT; 392 AA.
AC 095N90;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Alpha adrenergic receptor 2B (Fragment).
GN AAR2B.
OS Tadarida brasiliensis (Brazilian free-tailed bat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Molossidae; Tadarida.
OX NCBI_TaxID=9438;

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 12:02:49 ; Search time 15.5 Seconds

(without alignments)
854,214 Million cell updates/sec

Title: US-09-636-259b-4

Perfect score: 2380

Sequence: 1 MGSLQPDAGNMSMGTEAPG.....HDFRRFRKILRCGRKRIV 450

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database : Issued Patents AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2205	92.6	450	1 US-08-444-734A-8	Sequence 8, Appl1
2	2164	90.9	450	1 US-08-194-338-5	Sequence 5, Appl1
3	1665	70.0	358	2 US-08-465-971B-4	Sequence 4, Appl1
4	1537	64.6	330	1 US-08-118-270-21	Sequence 21, Appl1
5	1537	64.6	330	5 PCT-US93-08528-21	Sequence 21, Appl1
6	1523	64.0	334	1 US-08-118-270-22	Sequence 22, Appl1
7	1523	64.0	334	5 PCT-US93-08528-22	Sequence 22, Appl1
8	1465	61.6	450	1 US-08-196-989B-11	Sequence 11, Appl1
9	1465	61.6	450	2 US-08-760-936-11	Sequence 11, Appl1
10	1140.5	47.9	461	1 US-08-194-338-4	Sequence 4, Appl1
11	1046.5	44.0	330	1 PCT-US93-08528-19	Sequence 19, Appl1
12	1046.5	44.0	330	5 PCT-US93-08528-19	Sequence 19, Appl1
13	1029	43.2	330	1 US-08-118-270-20	Sequence 20, Appl1
14	1029	43.2	330	5 PCT-US93-08528-20	Sequence 20, Appl1
15	649	27.3	601	1 US-07-676-174A-2	Sequence 2, Appl1
16	623.5	26.2	443	1 US-07-626-618A-18	Sequence 18, Appl1
17	623.5	26.2	443	1 US-08-333-977-18	Sequence 18, Appl1
18	617.5	25.9	444	1 US-08-194-338-10	Sequence 10, Appl1
19	615	25.8	444	1 US-07-626-618A-19	Sequence 19, Appl1
20	615	25.8	444	1 US-08-333-977-19	Sequence 19, Appl1
21	613	25.8	444	1 US-07-817-920-3	Sequence 3, Appl1
22	590	24.8	422	1 US-08-370-542-3	Sequence 3, Appl1
23	590	24.8	422	1 US-08-117-006-3	Sequence 3, Appl1
24	590	24.8	422	1 US-08-216-594-3	Sequence 3, Appl1
25	590	24.8	422	1 US-08-542-358-3	Sequence 3, Appl1
26	590	24.8	422	1 US-08-157-185-13	Sequence 13, Appl1
27	590	24.8	422	2 US-08-157-185-13	Sequence 13, Appl1

28	590	24.8	422	3 US-08-281-526B-13	Sequence 13, Appl1
29	590	24.8	422	3 US-09-018-351-3	Sequence 3, Appl1
30	590	24.8	422	4 US-09-332-837-13	Sequence 13, Appl1
31	590	24.8	422	5 PCT-US93-00149-3	Sequence 3, Appl1
32	586.5	24.6	443	1 US-08-444-734A-3	Sequence 3, Appl1
33	585.5	24.6	377	2 US-08-461-812-2	Sequence 2, Appl1
34	585.5	24.6	377	3 US-08-157-185-14	Sequence 14, Appl1
35	585.5	24.6	377	4 US-08-281-526B-14	Sequence 14, Appl1
36	585.5	24.6	377	4 US-09-450-790A-14	Sequence 14, Appl1
37	585.5	24.6	377	4 US-08-332-837-14	Sequence 14, Appl1
38	585	24.6	375	1 US-08-370-542-5	Sequence 5, Appl1
39	585	24.6	375	1 US-08-542-358-5	Sequence 5, Appl1
40	585	24.6	375	3 US-09-018-351-5	Sequence 5, Appl1
41	585	24.6	376	1 US-07-817-920-5	Sequence 5, Appl1
42	585	24.6	376	1 US-08-117-006-5	Sequence 5, Appl1
43	585	24.6	376	1 US-08-216-594-5	Sequence 5, Appl1
44	585	24.6	376	5 PCT-US93-00149-5	Sequence 5, Appl1
45	583	24.5	467	1 US-08-056-051-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-08-444-734A-8
Sequence 8, Application US/08444734A

Patent No. 5610282

GENERAL INFORMATION:

APPLICANT: Sibley, David R.

APPLICANT: Monasma, Frederick J.

APPLICANT: Mahan, Lawrence C.

APPLICANT: McVittie, Louis D.

TITLE OF INVENTION: cDNA encoding the rat D1 dopamine receptor linked to adenylyl cyclase activation and

expression of the receptor protein in plasmid-transfected

cells

NUMBER OF INVENTIONS: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson and Bear

STREET: 620 Newport Center Drive, Sixteenth Floor

CITY: Newport Beach

STATE: CA

COUNTRY: USA

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/444,734A

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/029,917

FILING DATE: 03-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/548,714

FILING DATE: 06-JUL-1990

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E.

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER: NIH05.001FW1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (714) 760-0404

TELEFAX: (714) 760-9502

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 450 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: Internal
 US-08-444-734A-8

Query Match 92.6%; Score 2205; DB 1; Length 450;
 Best Local Similarity 93.6%; Pred. No. 7.5e-119;
 Matches 421; Conservative 2; Mismatches 27; Indels 0; Gaps 0;

QY 1 MSLSQPDAGNAGNNGTEAPGGGARRATPYSLOVTLTLVCLAGLMLLTGNGVLIIVAFTR 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1 MSLSQPDAGNAGNNGTEAPGGGARRATPYSLOVTLTLVCLAGLMLLTGNGVLIIVAFTR 60
 QY 61 SRALKAPQNLFLVSLASADILVATLVIPEFLANENWGYWFGKANCEIYALDVLFCISS 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 61 SRALKAPQNLFLVSLASADILVATLVIPEFLANENWGYWFGKANCEIYALDVLFCISS 120
 QY 121 IYHLCALISLDRWYSITQAIENYLNKRPRIKAIITTWVWISAVISPPPLISTEKKGGGGG 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 121 IYHLCALISLDRWYSITQAIENYLNKRPRIKAIITTWVWISAVISPPPLISTEKKGGGGG 180
 QY 181 POPAEPRCEINDQKWYVISCISGFPAPCLIMLVYRIYQIAKRRTRVPPSRGPDAYA 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 181 POPAEPRCEINDQKWYVISCISGFPAPCLIMLVYRIYQIAKRRTRVPPSRGPDAYA 240
 QY 241 APPGGERPRKGLGERSAGPGGAEPPLPTQINGAPGEPAPGPDOTALDLEESSSD 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 241 APPGGERPRKGLGERSAGPGGAEPPLPTQINGAPGEPAPGPDOTALDLEESSSD 300
 QY 301 HARPPGPRRPERGPRGKGARASQYKPGDSLPRRGATGIGTPAAGPEEERVGAAKAS 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 301 HARPPGPRRPERGPRGKGARASQYKPGDSLPRRGATGIGTPAAGPEEERVGAAKAS 360
 QY 361 RMGRONREKRTFVLAVVIGVVCWPFPEFTYTLTAVGCSVPRTLKFFEFWGCNSSLN 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 361 RMGRONREKRTFVLAVVIGVVCWPFPEFTYTLTAVGCSVPRTLKFFEFWGCNSSLN 420
 QY 421 LNPVYITFNHDFRRARFKKILCRGDKRRIV 450
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 421 LNPVYITFNHDFRRARFKKILCRGDKRRIV 450

RESULT 2
 US-08-194-338-5
 ; Sequence 5, Application US/08194338
 ; Patent No. 5474898
 ; GENERAL INFORMATION:
 ; APPLICANT: Venter, John C.
 ; APPLICANT: Fraser, Claire M.
 ; APPLICANT: McCombie, William R.
 ; TITLE OF INVENTION: OCTOPAMINE RECEPTOR
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Knodde, Martens, Olson and Bear
 ; STREET: 620 Newport Center Drive, Sixteenth Floor
 ; CITY: Newport Beach
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92660
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/194,338
 ; FILING DATE: 08-FEB-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/676,174
 ; FILING DATE: 28-MAR-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Israel, Ned A.

REGISTRATION NUMBER: 29,655
 REFERENCE/DOCKET NUMBER: NIH101.001DV1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 235-8550
 TELEFAX: (619) 235-0176
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 450 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: Internal
 US-08-194-338-5

Query Match 90.9%; Score 2164; DB 1; Length 450;
 Best Local Similarity 92.6%; Pred. No. 1.6e-116;
 Matches 415; Conservative 3; Mismatches 30; Indels 0; Gaps 0;

QY 3 SLQPDAGNAGNNGTEAPGGGARRATPYSLOVTLTLVCLAGLMLLTGNGVLIIVAFTR 62
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 3 SLQPDAGNAGNNGTEAPGGGARRATPYSLOVTLTLVCLAGLMLLTGNGVLIIVAFTR 62
 QY 63 ALKAPQNLFLVSLASADILVATLVIPEFLANENWGYWFGKANCEIYALDVLFCISSIV 122
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 63 ALKAPQNLFLVSLASADILVATLVIPEFLANENWGYWFGKANCEIYALDVLFCISSIV 122
 QY 123 HLCALISLDRWYSITQAIENYLNKRPRIKAIITTWVWISAVISPPPLISTEKKGGGGG 182
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 123 HLCALISLDRWYSITQAIENYLNKRPRIKAIITTWVWISAVISPPPLISTEKKGGGGG 182
 QY 183 PAEPCEINDQKWYVISCISGFPAPCLIMLVYRIYQIAKRRTRVPPSRGPDAYAAP 242
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 183 PAEPCEINDQKWYVISCISGFPAPCLIMLVYRIYQIAKRRTRVPPSRGPDAYAAP 242
 QY 243 PGTERPRKGLGERSAGPGGAEPPLPTQINGAPGEPAPGPDOTALDLEESSSDHA 302
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 243 PGTERPRKGLGERSAGPGGAEPPLPTQINGAPGEPAPGPDOTALDLEESSSDHA 302
 QY 303 ERPPGPRRPERGPRGKGARASQYKPGDSLPRRGATGIGTPAAGPEEERVGAAKASRW 362
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 303 ERPPGPRRPERGPRGKGARASQYKPGDSLPRRGATGIGTPAAGPEEERVGAAKASRW 362
 QY 363 RMGRONREKRTFVLAVVIGVVCWPFPEFTYTLTAVGCSVPRTLKFFEFWGCNSSLN 422
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 363 RMGRONREKRTFVLAVVIGVVCWPFPEFTYTLTAVGCSVPRTLKFFEFWGCNSSLN 422
 QY 423 LNPVYITFNHDFRRARFKKILCRGDKRRIV 450
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 423 LNPVYITFNHDFRRARFKKILCRGDKRRIV 450

RESULT 3
 US-08-465-971B-4
 ; Sequence 4, Application US/08465971B
 ; Patent No. 5942414
 ; GENERAL INFORMATION:
 ; APPLICANT: Yi Li and Mark D. Adams
 ; TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Carella, Byrne, Bain, Giffillan,
 ; ADDRESSEE: Cecchi, Stewart & Olstein
 ; STREET: 6 Becker Farm Road
 ; CITY: Roseland
 ; STATE: NJ
 ; COUNTRY: US
 ; ZIP: 07068-1739
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,971B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-465-971B-4

Query Match 70.0%; Score 1665; DB 2; Length 358;
Best Local Similarity 74.0%; Pred. No. 3.4e-88;
Matches 339; Conservative 4; Mismatches 7; Indels 108; Gaps 7;

OY 1 MGSLQPDAGNASWNGTEAPGAGATPYSLOVTLFLVCLAGLMLTLVFGNVLVIATVFT 60
1 MGSLQPDAGNASWNGTEAPGAGATPYSLOVTLFLVCLAGLMLTLVFGNVLVIATVFT 60
DB 1 MGSLQPDAGNASWNGTEAPGAGATPYSLOVTLFLVCLAGLMLTLVFGNVLVIATVFT 60
OY 61 SRLKAPQNFLLV-SLASADILVA--TLVPSLANEWMGYWYFGKAWCEIYLALDVLFC 117
61 SRLKAPQNFLLV-SLASADILVA--TLVPSLANEWMGYWYFGKAWCEIYLALDVLFC 117
DB 61 SRLKAPQNFLLV-SLASADILVA--TLVPSLANEWMGYWYFGKAWCEIYLALDVLFC 120
OY 118 TSSIVHLCAISLDKRYSTQAIENYLNKRPRIKATITITWYSAVISPPPLISIEKKG- 176
118 TSSIVHLCAISLDKRYSTQAIENYLNKRPRIKATITITWYSAVISPPPLISIEKKG- 176
DB 121 TSSIVHLCAISLDKRYSTQAIENYLNKRPRIKATITITWYSAVISPPPLISIEKKG 180
OY 177 -GGGGGQPAEPRIEINDOKWYVSSCIGSFAPCLIMILYVRIYQIAKRRTVPSPSRG 235
177 -GGGGGQPAEPRIEINDOKWYVSSCIGSFAPCLIMILYVRIYQIAKRRTVPSPSRG 235
DB 181 XGGGGQPAEPRIEINDOKWYVSSCIGSFAPCLIMILYVRIYQIAKRRTVPSPSRG 240
OY 236 PDVAAPPGTERPRKGLPERAGGAEPLPTQLNGAGEPAAPGPRDTALDLEE 295
236 PDVAAPPGTERPRKGLPERAGGAEPLPTQLNGAGEPAAPGPRDTALDLEE 295
DB 241 PDVAAPPGGLQ----- 252
OY 296 SSSSDHAERPPGRBERGPRGKARASQVKGDSLPRRPGANGIGTPAAGPGEERYG 355
296 SSSSDHAERPPGRBERGPRGKARASQVKGDSLPRRPGANGIGTPAAGPGEERYG 355
DB 253 -----GGRS-----ASGLPRRAGA----- 268
OY 356 AAKASWRGRONREKRTFLVAVIGVYVWCPPEFFTYTLTAVGCSVPRTLKFFFWMG 415
356 AAKASWRGRONREKRTFLVAVIGVYVWCPPEFFTYTLTAVGCSVPRTLKFFFWMG 415
DB 269 -----GGONREKRTFLVAVIGVYVWCPPEFFTYTLTAVGCSVPRTLKFFFWMG 320
OY 416 YCNSSLNPVIYITFNHDFRRAFKI---LCRGDRKRIY 450
416 YCNSSLNPVIYITFNHDFRRAFKI---LCRGDRKRIY 450
DB 321 YCNSSLNPVIYITFNHDFRRAFKI---LCRGDRKRIY 358

RESULT 4
US-08-118-270-21
Sequence 21, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-21

Query Match 64.6%; Score 1537; DB 1; Length 330;
Best Local Similarity 74.2%; Pred. No. 6.2e-81;
Matches 310; Conservative 7; Mismatches 13; Indels 88; Gaps 6;

OY 33 TLTIVCLAGLMLTLVFGNVLVIATVFTSRLKAPQNFLLV-SLASADILVATLVIPTSLA 92
33 TLTIVCLAGLMLTLVFGNVLVIATVFTSRLKAPQNFLLV-SLASADILVATLVIPTSLA 92
DB 1 TLTIVCLAGLMLTLVFGNVLVIATVFTSRLKAPQNFLLV-SLASADILVATLVIPTSLA 58
OY 93 NEVWGYWYFGKAWCEIYLALDVLFCSTSIIVHLCAISLDKRYSTQAIENYLNKRPRIKA 152
93 NEVWGYWYFGKAWCEIYLALDVLFCSTSIIVHLCAISLDKRYSTQAIENYLNKRPRIKA 152
DB 59 NEVWGYWYFGKAWCEIYLALDVLFCSTSIIVHLCAISLDKRYSTQAIENYLNKRPRIKA 117
OY 153 IITWYSAVISPPPLISIEKKGGGQPAEPRIEINDOKWYVSSCIGSFAPCLIM 212
153 IITWYSAVISPPPLISIEKKGGGQPAEPRIEINDOKWYVSSCIGSFAPCLIM 212
DB 118 IITWYSAVISPPPLISIEKKGGGQPAEPRIEINDOKWYVSSCIGSFAPCLIM 177
OY 213 ILVYVRIYQIAKRRTVPSPSRGPDVAAPPGTERPRKGLPERAGGAEPLPTQ 272
213 ILVYVRIYQIAKRRTVPSPSRGPDVAAPPGTERPRKGLPERAGGAEPLPTQ 272
DB 178 -LVYVRIYQIAKRRTVPSPSRGPDVAAPPGTERPRKGLPERAGGAEPLPTQ 227
OY 273 LMGAGEPAAPGPRDTALDLEE SSSSDHAERPPGRBERGPRGKARASQVKGDSL 332
273 LMGAGEPAAPGPRDTALDLEE SSSSDHAERPPGRBERGPRGKARASQVKGDSL 332
DB 228 -----GGRS-----ASGL 236
OY 333 PRKGATIGTPAAGPGEERYGAAKASWRGRONREKRTFLVAVIGVYVWCPPEFF 392
333 PRKGATIGTPAAGPGEERYGAAKASWRGRONREKRTFLVAVIGVYVWCPPEFF 392
DB 237 PRRAGA-----GGONREKRTFLVAVIGVYVWCPPEFF 272
OY 393 TYTLTAVGCSVPRTLKFFFWMGYCNSSLNPVIYITFNHDFRRAFKIILCRGDRKRIY 450
393 TYTLTAVGCSVPRTLKFFFWMGYCNSSLNPVIYITFNHDFRRAFKIILCRGDRKRIY 450
DB 273 TYTLTAVGCSVPRTLKFFFWMGYCNSSLNPVIYITFNHDFRRAFKIILCRGDRKRIY 330

RESULT 5
PCT-US93-08528-21
Sequence 21, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/08528
 FILING DATE: 09-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/943,236
 FILING DATE: 10-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Townsend, Kevin G.
 REGISTRATION NUMBER: 34,033
 REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 330 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 PCT-US93-08528-21

Query Match 64.6%; Score 1537; DB 5; Length 330;
 Best Local Similarity 74.2%; Pred. No. 6, 2e-81;
 Matches 310; Conservative 7; Mismatches 13; Indels 86; Gaps 6;

33 TLTVCLAGLMLTFVGNVLTIAVFTSRALKAPOMLFVLSASADILVATLVIPFSLA 92
 1 TLTVCLAGLMLTFVGNVLTIAVFTSRALKAPOMLFVLSASADILVATLVIPFSLA 58
 93 NEVNGYWFYFGKAWCEIYLAIDLVLFCSTSIYHLCAISLDRYWSITQAIENYLNKRPRIKA 152
 59 NEVNGYWFYFGKAWCEIYLAIDLVLFCSTSIYHLCAISLDRYWSITQAIENYLNKRPRIKA 117
 153 IITVWVIAVISPPLISIEKKGGGGPOPAEPRCEINDOKWYVSSICISGFAPCLIM 212
 118 IITVWVIAVISPPLISIEKKGGGGPOPAEPRCEINDOKWYVSSICISGFAPCLIM 177
 213 IITVWVIAVISPPLISIEKKGGGGPOPAEPRCEINDOKWYVSSICISGFAPCLIM 272
 178 -LVVYRITQIAKRRTRVPSRGPDAVAAPGGERPRKNGIGPERSAGPGG----- 227
 273 LNGAGPEPAPGPRDTDALDLESSSSSDHARPPGPRRPERGPGKAKARASQYKPGDSL 332
 228 -----GGRGRS-----ASGL 236
 333 PRRGGATGIGTPAAGPEERVGAAKASRMGRGRONREKRTFTFVLAIVYGVVWCFPF 392
 237 PRRRGA-----GGONREKRTFTFVLAIVYGVVWCFPF 272
 393 FTYTLTAVGCVPRTLFKEFFWFGYCNSSLNPIVYITFNHDFRRAFKKILCGDKRRIV 450
 273 FTYTLTAVGCVPRTLFKEFFWFGYCNSSLNPIVYITFNHDFRRAFKKILCGDKRRIV 330

RESULT 6
 US-08-118-270-22
 Sequence 22, Application US/08118270
 Patent No. 5508384
 GENERAL INFORMATION:
 APPLICANT: Murphy, Randall B.

APPLICANT: Schuster, David I.
 TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
 TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
 NUMBER OF SEQUENCES: 348
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/118,270
 FILING DATE: 09-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/943,236
 FILING DATE: 10-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Townsend, Kevin G.
 REGISTRATION NUMBER: 34,033
 REFERENCE/DOCKET NUMBER: MURPHY-2A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 334 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-118-270-22

Query Match 64.0%; Score 1523; DB 1; Length 334;
 Best Local Similarity 71.6%; Pred. No. 3, 9e-80;
 Matches 300; Conservative 10; Mismatches 23; Indels 86; Gaps 3;

33 TLTVCLAGLMLTFVGNVLTIAVFTSRALKAPOMLFVLSASADILVATLVIPFSLA 92
 1 TLTVCLAGLMLTFVGNVLTIAVFTSRALKAPOMLFVLSASADILVATLVIPFSLA 60
 93 NEVNGYWFYFGKAWCEIYLAIDLVLFCSTSIYHLCAISLDRYWSITQAIENYLNKRPRIKA 152
 61 NEVNGYWFYFGKAWCEIYLAIDLVLFCSTSIYHLCAISLDRYWSITQAIENYLNKRPRIKA 119
 153 IITVWVIAVISPPLISIEKKGGGGPOPAEPRCEINDOKWYVSSICISGFAPCLIM 211
 120 IITVWVIAVISPPLISIEKKGGGGPOPAEPRCEINDOKWYVSSICISGFAPCLIM 179
 212 IITVWVIAVISPPLISIEKKGGGGPOPAEPRCEINDOKWYVSSICISGFAPCLIM 271
 180 NNLVYRITQIAKRRTRVPSRGPDAVAAPGGERPRKNGIGPERSAGPGG----- 231
 272 LNGAGPEPAPGPRDTDALDLESSSSSDHARPPGPRRPERGPGKAKARASQYKPGDSL 331
 232 -----GGRGRS-----ASGL 231
 333 PRRGGATGIGTPAAGPEERVGAAKASRMGRGRONREKRTFTFVLAIVYGVVWCFPF 391
 232 -----GGONREKRTFTFVLAIVYGVVWCFPF 275
 392 FTYTLTAVGCVPRTLFKEFFWFGYCNSSLNPIVYITFNHDFRRAFKKILCGDKRRIV 450
 276 FTYTLTAVGCVPRTLFKEFFWFGYCNSSLNPIVYITFNHDFRRAFKKILCGDKRRIV 334

RESULT 7

Db 361 XXXXXXXXREKRTFLAVIVGVCMFPFFFTYTLTAVGCVPTLTKFFFWGYNSS 420
QY 421 LNPVITTFNHDERRAFKKILC 442
Db 421 LNPVITTFNHDERRAFKKILC 442

RESULT 9
US-08-760-936-11
; Sequence 11, Application US/08760936
; Patent No. 5856443
; GENERAL INFORMATION:
; APPLICANT: MacLennan, A. John
; TITLE OF INVENTION: Molecular Cloning and Expression of
; TITLE OF INVENTION: G-Protein Coupled Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,936
; FILING DATE: December 6, 1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Doran R.
; REGISTRATION NUMBER: 38,261
; REFERENCE/DOCKET NUMBER: MAC-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 450 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; US-08-760-936-11

Query Match 61.6%; Score 1465; DB 2; Length 450;
Best local Similarity 68.6%; Pred. No. 1e-76;
Matches 303; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY 1 MGSLOPDAGNAGNMGTEAPGGARATPYSLOVTLTVCLAGLMLTLVFGNVLTIAVFT 60
Db 1 MGSLOPDAGNAGNMGTEAPGGARATPYSLOVTLTVCLAGLMLTLVFGNVLTIAVFT 60

QY 61 SRALKAPQNLFLVSLASADILVATLVLPESLANEVMGWYFGKAMCEIYLAIDVLFCTSS 120
Db 61 SRALKAPQNLFLVSLASADILVATLVLPESLANEVMGWYFGKAMCEIYLAIDVLFCTSS 120

QY 121 IVHCAISLDRTWSTQIAIEYNLKRTPRIKAIITVWVSAVISFPPLISIEKKGSGG 180
Db 121 IVHCAISLDRTWSTQIAIEYNLKRTPRIKAIITVWVSAVISFPPLISIEKKGSGG 180

QY 181 POPAPRCEINDOKWYVTSICISGFAPCLIMILVYRITQIAKRRRVPPSRGPDVA 240
Db 181 POPAPRCEINDOKWYVTSICISGFAPCLIMILVYRITQIAKRRRVPPSRGPDVA 240

QY 241 APGGTERPRGGLPERAGPGAEAPLPQTLNGAGPEPAPGPRTDADLEESSSD 300
Db 241 APGGTERPRGGLPERAGPGAEAPLPQTLNGAGPEPAPGPRTDADLEESSSD 300

QY 301 HAERPGRPRPERGPRGKARASQVKGDSLPRRGPGATGIGTPAAGPGEERVGAAS 360

Db 301 XXX 360
QY 361 RMRGRQNRKRFETFLAVIVGVCMFPFFFTYTLTAVGCVPTLTKFFFWGYNSS 420
Db 361 XXXXXXXXREKRTFLAVIVGVCMFPFFFTYTLTAVGCVPTLTKFFFWGYNSS 420

QY 421 LNPVITTFNHDERRAFKKILC 442
Db 421 LNPVITTFNHDERRAFKKILC 442

RESULT 10
US-08-194-338-4
; Sequence 4, Application US/08194338
; Patent No. 5474898
; GENERAL INFORMATION:
; APPLICANT: Venter, John C.
; APPLICANT: Fraser, Claire M.
; APPLICANT: McCombie, William R.
; TITLE OF INVENTION: OCTOPAMINE RECEPTOR
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,338
; FILING DATE: 08-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,174
; FILING DATE: 28-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Istaelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH101.001DVL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 461 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-194-338-4

Query Match 47.9%; Score 1140.5; DB 1; Length 461;
Best local Similarity 50.7%; Pred. No. 3.1e-58;
Matches 248; Conservative 41; Mismatches 99; Indels 101; Gaps 12;

QY 10 NASMNGTEAPGGARAT-----PYSLOVTLTVCLAGLMLTLVFGNVLTIAVFT 60
Db 19 NAGGAEBSGGVAGNAGSAGWCPRGQYAGAVAGLAAYVGLIYFTVVGNTLVIAVLT 78

QY 61 SRALKAPQNLFLVSLASADILVATLVLPESLANEVMGWYFGKAMCEIYLAIDVLFCTSS 120
Db 79 SRALKAPQNLFLVSLASADILVATLVLPESLANELMAYVFGQVWCGVYLAIDVLFCTSS 138

QY 121 IVHCAISLDRTWSTQIAIEYNLKRTPRIKAIITVWVSAVISFPPLISIEKKGSGG 180

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Db 139 IVHCAISLDRYMSVTGAVENLNKTRPRKATIVAVMIISFPLSLRQPDGA- 197
QY 181 POPAEPCETINDQKWIYSSICISFFAPCLIMILVYRIYQAKRTRVPPSRGPDVA 240
Db 198 ---AYPCGINDETWYLLSSICISFFAPCLIMGLVARIYVAKRRRTLSEKAP---V 251
QY 241 APGCTFRRRKGLGPERGAGPGAE---AEPLTQUNGAGEPAPGPRDTDLDEESS 297
Db 252 GPBGASTTNGLG---AAGAKRTGTARPR-----PTWATR----- 287
QY 298 SSDHAERP---PGRRPERGPGKGKARASQYKPGDSLPRRGATGCTGTPAGGEER 353
Db 288 ---AAGPRGAGPGLR---RGRRRAGAG-----GAGGADGCGAGGAAQ 328
QY 354 VGAAKASRMKG-----RQNRKRTFVLAVNG 381
Db 329 SGALLASRSRSPGGRSLSRASSRVEFFLSRRRRARSSVGRKVAQAREKRTFVLAVNG 388
QY 382 VFVWCFPEFFTYTLTAV---GCSVPRTLKFFPFWFGYCNSSLNPIYTIENHDERARK 438
Db 389 VFVLCNPEFFIYSLVIGICREACQVPLKFFFWIGYCNSLNPIYTVFNODFRASR 448
QY 439 KILCRGDRK 447
Db 449 HILFRRRR 457

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RESULT 11
US-08-118-270-19
; Sequence 19, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118, 270
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943, 236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 330 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-118-270-19

```

```

Query Match 44.0%; Score 1046.5; DB 1; Length 330;
Best Local Similarity 50.7%; Pred. No. 5,2e-53;
Matches 216; Conservative 38; Mismatches 55; Indels 117; Gaps 9;
QY 36 LVCIAGLLMLLVFGVNVITIAVFSRALKAQNLFLVSLASADLVATLVIPESLANEV 95
Db 4 LAAVGFELVFLVGVVAVLVIAVLISLRARQNLFLVSIASADLVATLVIPESLANEI 63
QY 96 MGYWFGKAMCEIYALDLFCTSSIVHLCATSLDRYMSVIOAIEYNLKRPRKATIT 155
Db 64 M-YWFGQVWCQVYLAIDLFCSTSSIVHLCATSLDRYMSVIOAVYENLKRPRKATIV 122
QY 156 TWVVISAVISFPLISIEKGGGPOPAEPCEINDQKWIYSSICISFFAPCLIMILV 215
Db 123 AVMLISAVISFPLVSLVRQPDGA---AYPCGINDETWYLLSSICISFFAPCLITLV 178
QY 216 YVRIYQAKRTRVPPSRGPDVAVAPGCTFRRRKGLGPERGAGCAEAEPLTQUNG 275
Db 179 YARITRVAKRRRTLSEKAP-----VGPDGAS---PTENG 212
QY 276 AEGEPAPGPRDTDLDEESSSDHAERPGRPRPERGPGKGKARASQYKPGDSLPRR 335
Db 213 L----- 213
QY 336 GPGATGIGTPAAGPGEERVGAK--ASRWGR-----QNRKRTFVLAVNGEV 384
Db 214 -----GAAGERTGTARFLSRRRARSSVGRKVAQAREKRTFVLAL---VFV 260
QY 385 VCMPEFFFTYTLTAV---GCSVPRTLKFFPFWFGYCNSSLNPIYTIENHDERARK 441
Db 261 LCMPEFFFTYSLVIGICREACQVPLKFFFWIGYCNSLNPIYTVFNODFRSEKHL 320
QY 442 CRGDRK 447
Db 321 FRRRRR 326

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RESULT 12
PCT-US93-08528-19
; Sequence 19, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08528
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943, 236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 330 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US93-08528-19

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Query Match	44.0%;	Score 1046.5;	DB 5;	Length 330;
Best Local Similarity	50.7%;	Pred. No. 5.2e-53;		
Matches 216;	Conservative 38;	Mismatches 55;	Indels 117;	Gaps 9;

QY 36 LVACGLMLTVEGNVLIIAFTSRALKAPQNLEVLSADILVATLVIPPSLANEV 95
| : | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 4 LAAVVGELIVETVGVNVLVIAVLTSTRALRAPQNLEVLVSADILVATLVMPPSLANEI 63

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QY      96 MGYWFGKAWCEIYLADVLFCTSSIVHLCAISLDRIWSITALEYNLKRTPRKAAIII 15
        |   ||||| : ||| : ||||| : ||||| : ||||| : ||| :
Db      64 M-YWFGQWVCVYLAIDVLEFCTSSIVHLCAISLDRIWSVTQAVEYNLKRTPRKAATIV 12
```

QY 156 TWMVTSAVISFPPLISIEKKGGGQPAPDRCEINDOKWVISSCIGSFAPCLMILV 21
||:|||||: : : | : ||: ||: ||: ||: ||: ||: ||: ||
Db 123 AVWLTSAVISFPPPLVS LRQPDGA---AYPQG LNDETWYIISCSIGSFAPCLLYLLV 17

```

QY      216 YVRIYQIAKRRTTRVPPSSRRGPDAAVAPPGGTERRRPKGIGPERSAGPGGAEEAPLPTQLNG 274
          | |||::||| || | || | || |
Db      179 YARIYVAKRRRTTLEKRAP-----VGPDGAS---PTTENG 211

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QY 276 APGEPAAGPRDTALDLRESSSSDHAERPPRRPERGPRGKARASOVKPGDSLPRR 333
Db 213 L----- 21
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QY      336  GGGATGCTGTPAAGPGCEERVGAAK--ASRWKGR-----QNEKRFTEVLAVLVGVFV 38
          | | | | | : : | | | | | | | | | | | | | | | | | | | | | |
Db      214  -----GAAGAGARTGTARFTLSRRRRRASSVCRKKVAQAAREKRFTEVLAL---VFV 26

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QY      385 VCMPEFFFTYLTAV--GGSVPRLLEKFEFNGYCNSLNPIVITTFNHDPRRAEKIL 444
          :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      261 LCMPEFFFIYSLGICREACQVGPLKEFFMIGYCNSLNPVIATVFENDERPSEKHIL 309
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QY	442	CRGDRK	447
			:
Db	321	FRRRRR	326

RESULT 13
US-08-118-270-20
US-08-118-270-20

Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.

TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.

```

; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
Copyright 1990 PatentIn Data.

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APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
PUBLICATION NUMBER: US 07/043,336

FILED DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:

NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633

```

; INFORMATION FOR SEQ ID NO: 20:
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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 330 amino acids
;   TYPE: amino acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-118-270-20

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Query Match	43.2%	Score 1029;	DB 1;	Length 330;
Best Local Similarity	53.0%	Pred. No. 5.2e-52;		
Matches 221; Conservative	41;	Mismatches 55;	Indels 100;	Gaps 14

Dh QY 33 TLTTCIAGLMLTTEGNNVTIAVFTSRALKAPQNLFVLASADILVATLVTPFSLA 92
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
1 TAAATAATTFLITTFEGNALLIVAVLTRSIRAPQNFVLVSAAADIIVATLIIPFSLA 60

Dh QY 93 NEVMGYWFGKMCETIYLADVLEFCTSSIVHCAISIDRYMSTQAIENYLKRTPRRIKA 15
||:||||| : ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
61 NELIGWYERRTMCEVYLLADVLFECTSSIVHCAISIDRYMAVSRALEYNRSKRTPRIRKC 12

OY 153 IITVWVISAVISFPPLISIEKKGGGGPQ - AEPCEINDQMVISSCIGSFAPCLI 21
||:::||::||||| |||| |:::| ::::| |||||
Db 121 IITVMVIAVAISLPPI-----YKDQGPGPQRGRPOCTINQEAMIISS-IGSFRAPCLI 17

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Oy 212 MILVYVNIQIAKRRTRVPSPSRGPDVAVAAPPGCTERRPKGLGPEBSAGCPGAAEADLPT 2
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Db 176 -LLVYRRLYLIAAR-----SNRGPPA-----KCGGQGESK----- 20

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QY 272 QLNAGPAPAGPRDTALDLEESSSDHAERPPGPRRPERGRGKGARASQVAPGDS 3
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Db 207 -----QPRP-----DH-----GGATASAKLP--- 2

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Oy 332 LPRRGATGCTPAAGPGEERVGAKASRMGRGN--REKRTFVLAVVIGVFVWCMP 30
| : | ||| || : ||||| ||||| |||||
Db 223 -----AIASGRG---VGATGGQMMRRRAHVHREKRFTFVLAVVIGVFVLCMP 2

Oy 390 FFFTYTLTAV--GCSVPRLLEKFEFMEFGYCNSLNPVIYTIIFNHDERRAEKILCR 443
|||::|: | : || :|||::|:|||||::|:|:|:|:|:
Db 268 FFESYSTAICPKCKVPHGLQFPFWIGYCNSLNPIYTIIFENDF-RMFRRIILCR 323

RESULT 14
PCT-US93-08528-20

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; Sequence 20, Application PC/I059306520
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; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
;

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1 TITLE OF INVENTION: RECEPTRANS, AND COMPOSITIONS AND METHODS THEREFOR
2
3 NUMBER OF SEQUENCES: 348
4
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: BROWDY AND NEIMARK
7

STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA

```

;
;      ZIP: 20004
;
;      COMPUTER READABLE FORM:
;
;      MEDIUM TYPE: Floppy disk
;
;      COMPUTER: IBM PC compatible
;

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:
: OPERATING SYSTEM: PC-DOS/ms-DOS
:
: SOFTWARE: PatentIn Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
:
: APPLICATION NUMBER: PCT/US93/08528
:

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: FILING DATE: 09-SEP-1993
:
: PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,003
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ. ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-20

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Query Match          43.2%; Score 1029; DB 5; Length 330;
Best Local Similarity 53.0%; Pred. No. 5,2e-52;
Matches 221; Conservative 41; Mismatches 55; Indels 100; Gaps 14;

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QY 33 TLTLVCLAGLMLTFTGVNLYIAVFTSRALAPQNLFLVSLASADILVATLVIPESLA 92
D 1 TAAIAAIFTLFTFTGNALVITIAVTSRSLAPQNLFLVSLAADIATLVATLVIPESLA 60
QY 93 NEVNGWYFCKANCEIYALDVLCFTSSIVHLCALISDRYWSITQAIENVLTKRTPRRI 152
D 61 NELLGYFRRCEVYALDVLCFTSSIVHLCALISDRYWSITQAIENVLTKRTPRRIK 120
QY 153 IITVWYISAVISPPPLISTEKKGGGGGPOP-AEPRCEINDQWYVYISSCIGSFAPCL 211
D 121 IITVWYISAVISPPPLISTEKKGGGGGPOP-AEPRCEINDQWYVYISSCIGSFAPCL 175
QY 212 MILVYVYIYQAKRRTVPSPSRGPDVAVAPPGTERPRKGLGPESSAGGGAELPLP 271
D 176 -LVYLRIVYIAKR-----SNRGPRA-----KCGGGQESK----- 206
QY 272 QLNAGPEPAPAGPRDLDLDESSSDHAERPPGPRRPERGPRGKARASQVPGDS 331
D 207 -----QPRP-----DH-----GGALSAKLP----- 222
QY 332 LPRRGATGIGTPAAGPEGERYGAKAASWGRQNL-REKRTFLVAVYIGVFWCWP 389
D 223 -----AIASGRG---VGAIGGQWRRRAHVTRERETFLVAVYIGVFWCWP 267
QY 390 FFPTVTLTAV---GCSVPRTLFEFFFGVGNLSNPVYITTFNHFERRAFKILCR 443
D 268 FFPSYSLGALCPKHKCVPHGLTFQFFWIGYCNSSLNPVYITTFNDF-RMFRILCR 323

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RESULT 15
US-07-676-174A-2
Sequence 2, Application US/07676174A
Patent No. 5344776
GENERAL INFORMATION:
APPLICANT: Ventor, J. Craig
TITLE OF INVENTION: Octopamine receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: Eleventh Floor, 1615 L. Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/07/676,174A
FILING DATE: 19910328
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Scott, Watson T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: WTS/5683/79117/KIK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)861-3000
TELEFAX: (202)822-8944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 601 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-676-174A-2

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Query Match          27.3%; Score 649; DB 1; Length 601;
Best Local Similarity 32.7%; Pred. No. 3.8e-30;
Matches 164; Conservative 75; Mismatches 161; Indels 102; Gaps 14;

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D 108 EALLTLVLS-VIYVITIGNILVLSVTTYPLNIVONFTVSLAVADVALLVLPFN 166
QY 91 LANEVWYFCKANCEIYALDVLCFTSSIVHLCALISDRYWSITQAIENVLTKRTPRRI 150
D 167 VAYSILGRWFEIHLKCLTLCVLCFTSSILNLCALISDRYWSITQAIENVLTKRTPRRI 226
QY 151 KAITVWYISAVISPPPLISTEKKGGGGGPOPAP-PRCEINDQWYVYISSCIGSF 206
D 227 LLLISGWLSSLISPLI-----GNDWPDFTSATPCELTQSGYVYSSIGSFF 279
QY 207 ADCLIMILVYRIYQAKRRTVPSPSRGPDVAVAPPGTERPRKGLGPESSAGGGAEL 266
D 280 IPLAINTIYIYIFVATRRRLERARANKLNTIALK-STLEPRANSSPYAASNGSKS 337
QY 267 EFLPQOL-----NGAPGPAPAP----- 285
D 338 RLASMLCCGRDRAQAPATPMIONDESISSETHOPDSSKAGPAGNSDPQOHHVVLVK 397
QY 286 -----BDTDL-----DLESSSDHAER-----PPGRRPRRGRGKAR 323
D 398 SRRATKDSIKHKTGRGKSSSTCEPHGEOULLPAGGDSGSCQPGGSHGGKSDAE 457
QY 324 -----SQAAPGSLPRRGP-GATGIGTPAAGPEGERYGAKA---ASRW 362
D 458 ISTESGDPKGCIGCVTQADBOGSLKLTLPQSSGVAANAVTLPLOKKTSGVNOPIEF 517
QY 363 RGRONREKRTFLVAVYIGVFWCWPFFFTYITLANGCSV--PRTLK-PEFMFGV 419
D 518 KISLSEKERRAARTLGIINGVFCMLPFLMYVLPE-CQCCPPTNKKFNITWLYGINS 576
QY 420 SLNPVYITTFNHFERRAFKIL 441
D 577 GLNPVYITTFNHFERRAFKIL 598

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Search completed: February 14, 2003, 13:48:22
Job time : 17.5 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: February 14, 2003, 12:02:50 : Search time 12.5 Seconds
(Without alignments)
919.760 Million cell updates/sec

Title: US-09-636-259b-4

Perfect score: 2380
Sequence: 1 MGSLQPDAGNASWNGTEAPG.....HDFRAFKKILCRGDKRKRIY 450

Scoring table:

BLASTSUM62

Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 2554876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Public Applications_AA.*
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14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1126.5	47.3	450	US-10-077-870-4	Sequence 4, App11
2	1126.5	47.3	450	US-10-825-923-4	Sequence 4, App11
3	1126	47.3	447	US-10-077-870-2	Sequence 2, App11
4	1126	47.3	447	US-09-825-923-2	Sequence 2, App11
5	649	27.3	601	US-09-782-980-84	Sequence 84, App1
6	649	27.3	601	US-09-884-430-8	Sequence 8, App1
7	590	24.8	422	US-10-166-101-3	Sequence 3, App11
8	585.5	24.6	377	US-10-005-010-2	Sequence 2, App11
9	585	24.6	451	US-10-005-010-2	Sequence 2, App11
10	580	24.4	376	US-09-993-844-6	Sequence 6, App11
11	577.5	24.3	390	US-10-166-101-5	Sequence 5, App11
12	573.5	24.1	517	US-10-005-010-4	Sequence 4, App11
13	573.5	24.1	517	US-09-951-622-10	Sequence 10, App1
14	560	23.8	520	US-10-185-991-4	Sequence 4, App11
15	555	23.5	497	US-10-052-589-2	Sequence 2, App11
16	553.5	23.3	390	US-10-166-101-6	Sequence 6, App11
17	547	23.0	466	US-10-185-991-2	Sequence 2, App11
18	545.5	22.9	466	US-10-185-991-6	Sequence 6, App11
19	542.5	22.8	501	US-09-951-622-11	Sequence 11, App1
			501	US-09-951-622-9	Sequence 9, App11

20	510.5	21.4	370	US-10-109-532A-2	Sequence 2, App11
21	505	21.2	400	US-09-895-211-4	Sequence 4, App11
22	505	21.2	400	US-09-895-211-6	Sequence 6, App11
23	501.5	21.1	445	US-09-349-755-5	Sequence 5, App11
24	501.5	21.1	445	US-09-166-334-5	Sequence 5, App11
25	501.5	21.1	445	US-09-350-206-5	Sequence 5, App11
26	497	20.9	366	US-10-166-101-2	Sequence 2, App11
27	497	20.9	366	US-10-166-101-7	Sequence 2, App11
28	489.5	20.6	408	US-09-895-211-5	Sequence 5, App11
29	489.5	20.6	445	US-09-349-755-2	Sequence 2, App11
30	489.5	20.6	445	US-09-166-334-2	Sequence 2, App11
31	489.5	20.6	445	US-09-350-206-2	Sequence 2, App11
32	486.5	20.4	394	US-09-993-844-7	Sequence 7, App11
33	482.5	20.3	408	US-09-993-844-5	Sequence 5, App11
34	478	20.1	382	US-10-029-009-10	Sequence 10, App1
35	464	19.5	478	US-10-029-009-10	Sequence 10, App1
36	464	19.5	498	US-09-989-861-8	Sequence 8, App11
37	463	19.5	460	US-09-782-980-82	Sequence 82, App1
38	463	19.5	460	US-09-884-430-6	Sequence 6, App11
39	461.5	19.4	279	US-09-864-761-36992	Sequence 36992, A
40	460	19.3	359	US-09-951-622-13	Sequence 13, App1
41	452.5	19.0	445	US-09-989-861-16	Sequence 16, App1
42	444	18.7	388	US-09-989-861-19	Sequence 19, App1
43	441.5	18.6	359	US-09-989-861-19	Sequence 19, App1
44	440	18.5	460	US-10-166-101-4	Sequence 4, App11
45	435	18.3	387	US-09-989-861-2	Sequence 2, App11

ALIGNMENTS

RESULT 1
US-10-077-870-4
Sequence 4, App11
Publication No. US20030003470A1
GENERAL INFORMATION:
APPLICANT: Salomon, Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
FILE REFERENCE: 0993-0183P
CURRENT APPLICATION NUMBER: US/10/077, 870
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: FI 20010323
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 4
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
US-10-077-870-4

Query Match 47.3% Score 1126.5; DB 9; Length 450;
Best Local Similarity 53.2% Pred. No. 2e-63;
Matches 243; Conservative 50; Mismatches 105; Indels 59; Gaps 14;

QY 27 PYSLOVTLTYCLAGLMLTFVFGNVLYITAVFSSRLKAPQNFELVLSASADIVATVY 86
Db PYSVQATATATAATFTLFTIFGNALVILAVLSKLRAPQNFELVLSAAADIVATVLI 65
QY 87 IPFSLANFVWGYWFGKAMCEIYALDVLCTSSIVHCAISIDRWYSITQATEYLNKRT 146
Db IPFSLANFLLGYWFRRTWCDEVYIALDVLCTSSIVHCAISIDRWYAVSRALEYNSKRT 125
QY 147 PRKRIATITVWTSVAISIPPLISIRKKGCGGQPP-APRPEINDQKTYVSSCTGSR 205
Db PRKRIATITVWTSVAISIPPLISIRKKGCGGQPP-APRPEINDQKTYVSSCTGSR 205
QY 126 PRKRIATITVWTSVAISIPPLISIRKKGCGGQPP-APRPEINDQKTYVSSCTGSR 181
Db PRKRIATITVWTSVAISIPPLISIRKKGCGGQPP-APRPEINDQKTYVSSCTGSR 181
QY 206 FAPCLIMILVYRITQAKRTRTPPSRRGPDVAAPGCTERRPKQIGPERSAGCGAE 265
Db FAPCLIMILVYRITQAKRTRTPPSRRGPDVAAPGCTERRPKQIGPERSAGCGAE 265
QY 182 FAPCLIMILVYRITQAKRTRTPPSRRGPDVAAPGCTERRPKQIGPERSAGCGAE 233
Db FAPCLIMILVYRITQAKRTRTPPSRRGPDVAAPGCTERRPKQIGPERSAGCGAE 233
QY 266 AEPPLT-----QNGP-----APGERAPA-GPDDTDALDEES-----SS 298
Db AEPPLT-----QNGP-----APGERAPA-GPDDTDALDEES-----SS 298

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Db 234 LPALASVASAREVNGHSGSTGEKEGETPEDTGTALPPSWAALPNSGOGKEGVCASP 293
OY 299 SDHAERPPGRRPERGPRGKGKARASQYKPGD--SLPRRGP-----ATGIGTPAAGPGE 351
Db 294 EDAEE-----EEDDEEECEBPQAVPVSPASACSPPLQOQGSRYLATLKGQVLLGRG- 348
OY 352 ERVGAAKASRWGRQ--NREKRTFVLAVIGVFWVCFPEFFFTYTLAV---GCSVPRT 406
Db 349 --VGAIGGQWRRRAQLTRKREFTFLAVVIGVFLCMFPFFFSYSLGALCPKHCKVPHG 406
OY 407 LKFEFFWFGYCNSLNPVYITIFNDFRRAFKILCR 443
Db 407 LKFEFFWFGYCNSLNPVYITIFNDFRRAFKILCR 443
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RESULT 2
US-09-825-923-4

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/ Sequence 4, Application US/09825923
/ Patent No. US2001001638A1
/ GENERAL INFORMATION:
/ APPLICANT: Snapir, Amir
/ APPLICANT: Helinonen, Paula
/ APPLICANT: Alhopuro, Pia
/ APPLICANT: Karvonen, Matti
/ APPLICANT: Pesonen, Markku
/ APPLICANT: Koulou, Ullamari
/ APPLICANT: Scheinin, Mika
/ APPLICANT: Salonen, Jukka T
/ APPLICANT: Tuomainen, Tomi-Pekka
/ APPLICANT: Lakka, Timo A
/ APPLICANT: Nyssanen, Kristina
/ APPLICANT: Salonen, Riitta
/ APPLICANT: Kautanen, Jussi
/ APPLICANT: Valkonen, Veli-Pekka
/ TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2b-adrenoceptor
/ FILE REFERENCE: Alpha-2b-AR variant
/ CURRENT APPLICATION NUMBER: US/09/825,923
/ CURRENT FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 09/422,985
/ PRIOR FILING DATE: 2000-05-25
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 450
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-825-923-4
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Query Match 47.3%; Score 1126.5; DB 10; Length 450;
Best Local Similarity 53.2%; Pred. No. 2e-63;
Matches 243; Conservative 50; Mismatches 105; Indels 59; Gaps 14;

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OY 27 PYSLOVTLTVCLAGLMLTVFGNVLTITAVFTSRALKAPQNLFLVSLASADILVATLV 86
Db 6 PYSVQATAIAAATFTLFTFGNALVTLVTSRSLRAPQNLFLVSLAADAIVATLI 65
OY 87 IPESLANEWMGYWYFGKAMCEIYALDVLFCTSSIVHLCAISLDRYWSITQAIENLKRT 146
Db 66 IPESLANELGYWYFRTWCCEVYALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRT 125
OY 147 PRRIKAIITVWISAVISFPLISIEKKGGGGPQAP-APRCEINDQKWYVSSICISGF 205
Db 126 PRRIKCIITVWLIWIAVISLPLI-----YKGDGQPGPRGRPOCKLQNEAWYIILASSIGSF 181
OY 206 FAPCLIMLVVYRIYQIAKKRRTRVPSRRGPDVAAPPGGTERPKGLGPEBSAGPGAG 265
Db 182 FAPCLIMLVYRIYLIYLIAR-----SNRRGPRAGKGGGQESKQPR---PDHGALASAK 233
OY 266 AEPPLT-----QLNG---APGEPAPA-GPRDLDLEES-----SS 298
Db 234 LPALASVASAREVNGHSGSTGEKEGETPEDTGTALPPSWAALPNSGOGKEGVCASP 293
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OY 299 SDHAERPPGRRPERGPRGKGKARASQYKPGD--SLPRRGP-----ATGIGTPAAGPGE 351
Db 294 EDAEE-----EEDDEEECEBPQAVPVSPASACSPPLQOQGSRYLATLKGQVLLGRG- 348
OY 352 ERVGAAKASRWGRQ--NREKRTFVLAVIGVFWVCFPEFFFTYTLAV---GCSVPRT 406
Db 349 --VGAIGGQWRRRAQLTRKREFTFLAVVIGVFLCMFPFFFSYSLGALCPKHCKVPHG 406
OY 407 LKFEFFWFGYCNSLNPVYITIFNDFRRAFKILCR 443
Db 407 LKFEFFWFGYCNSLNPVYITIFNDFRRAFKILCR 443
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RESULT 3
US-10-077-870-2

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/ Sequence 2, Application US/10077870
/ Publication No. US20030003470A1
/ GENERAL INFORMATION:
/ APPLICANT: Salonen, Jukka T
/ TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
/ FILE REFERENCE: 0933-0183P
/ CURRENT APPLICATION NUMBER: US/10/077,870
/ CURRENT FILING DATE: 2002-05-21
/ PRIOR APPLICATION NUMBER: FI 20010323
/ PRIOR FILING DATE: 2001-02-20
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 3.1
/ SEQ ID NO 2
/ LENGTH: 447
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-077-870-2
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Query Match 47.3%; Score 1126; DB 9; Length 447;
Best Local Similarity 53.2%; Pred. No. 2.1e-63;
Matches 243; Conservative 50; Mismatches 102; Indels 62; Gaps 14;

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OY 87 IPESLANEWMGYWYFGKAMCEIYALDVLFCTSSIVHLCAISLDRYWSITQAIENLKRT 146
Db 66 IPESLANELGYWYFRTWCCEVYALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRT 125
OY 147 PRRIKAIITVWISAVISFPLISIEKKGGGGPQAP-APRCEINDQKWYVSSICISGF 205
Db 126 PRRIKCIITVWLIWIAVISLPLI-----YKGDGQPGPRGRPOCKLQNEAWYIILASSIGSF 181
OY 206 FAPCLIMLVVYRIYQIAKKRRTRVPSRRGPDVAAPPGGTERPKGLGPEBSAGPGAG 265
Db 182 FAPCLIMLVYRIYLIYLIAR-----SNRRGPRAGKGGGQESKQPR---PDHGALASAK 233
OY 266 AEPPLT-----QLNG---APGEPAPA-GPRDLDLEES-----SS 298
Db 234 LPALASVASAREVNGHSGSTGEKEGETPEDTGTALPPSWAALPNSGOGKEGVCASP 293
OY 299 SDHAERPPGRRPERGPRGKGKARASQYKPGD--SLPRRGP-----ATGIGTPAAGPGE 351
Db 294 EDAEE-----EEDDEEECEBPQAVPVSPASACSPPLQOQGSRYLATLKGQVLLGRG- 345
OY 352 ERVGAAKASRWGRQ--NREKRTFVLAVIGVFWVCFPEFFFTYTLAV---GCSVPRT 406
Db 346 --VGAIGGQWRRRAQLTRKREFTFLAVVIGVFLCMFPFFFSYSLGALCPKHCKVPHG 403
OY 407 LKFEFFWFGYCNSLNPVYITIFNDFRRAFKILCR 443
Db 404 LKFEFFWFGYCNSLNPVYITIFNDFRRAFKILCR 440
```

RESULT 4
US-09-825-923-2
/ Sequence 2, Application US/09825923

QY	286	---	RDIDAL	-----	DLESSSSDAHER	-----	PPGRARPERGRGKARA	323
Db	398	SRRAKTD	SIHGKTRGGRKSQSSSTPEHEDQULLPAGDGGSCQGGHSGGKDAE	457				
QY	324	-----	-----	-----	-----	-----	-----	-----
Db	458	ISTESGDPKCICQVCTVQADEQTSIKLTPQSSSTGVAANVSVPDLQKTSICVNOFIEKQ	517					
QY	363	RGONREKRFELVAVYGVVCMPEPEFFYTLTAVGCV	-	PRTLFK	-	FFEMFGYCS	419	
Db	518	KISLSKERRAARKTGLTGIVGAVICWLPPEFLMYVILPF	-	CQICCEPTNKKFNITWLGILNS	576			
QY	420	SLNPVITYTIFNHNDFERRAFKIL	441					
Db	577	GLNPVITYTIFNLDYRRARFKRL	598					
RESULT 6								
US-09-884-430-8								
Sequence 8, Application US/09884430								
Patent No. US20020151046A1								
GENERAL INFORMATION:								
APPLICANT: Glucksmann, Maria Alexandra								
APPLICANT: Santiago, Immaculada Sllous								
TITLE OF INVENTION: 528771, A NOVEL HUMAN G PROTEIN COUPLED								
TITLE OF INVENTION: RECEPTOR AND USES THEREOF								
FILE REFERENCE: MNI-165								
CURRENT APPLICATION NUMBER: US/09/884,430								
CURRENT FILING DATE: 2001-06-18								
PRIOR FILING DATE: 2000-06-16								
PRIOR APPLICATION NUMBER: USSN 60/212,331								
PRIOR FILING DATE: 2001-02-16								
NUMBER OF SEQ ID NOS: 8								
SOFTWARE: FastSeq for Windows Version 4.0								
SEQ ID NO 8								
LENGTH: 601								
TYPE: PRT								
ORGANISM: Drosophila melanogaster								
US-09-884-430-8								
Query Match								
Best Local Similarity	32.7%							
Matches 164; Conservative 75; Mismatches 161; Indels 102; Gaps 14;								
QY	31	QYTLTYLCAGLMLTITVFGNVLTIAVTPSRALKAPQNLVFLVSLASADILVATVTPPS	90					
Db	108	EAALLTALVLS-VIYVLTITGNILVILSVTYTKPRIVQPFVYSLAVADLVALLVLPEN	166					
QY	91	LANEVGVYVFGKAWCEIYALDVLEFCTSSIVHLCAISIDRYVSTQALEYMLKTRPRI	150					
Db	167	VAVSIIGRREFGTHLCKLMLTCDVLCCTSSINLCAIALDRYWAIDPINTYAKRTVGRV	226					
QY	151	KAITIVWISANVISPEPLTSTIEKKGGGGPOPAE	---	PROEINDOKMYVVISCGSFF	206			
Db	227	LLILSGVWLISLTISSPLP	-----	GNMDPEFTSAKPCBELTSQREGVYISLSGSF	279			
QY	207	APCLIMILVYVRIYQAKRTRVPSPRRKPDVAAAPDGTERRPKGLGERSAGPEGADA	266					
Db	280	IPLAIMTYIYELFVATRRRLRERARANKLNTALK	-	STELPEMANSSPVASNSGSKS	337			
QY	267	EPLPTQL	-----	NAPPEVPAAPG	-----	285		
Db	338	RLASWMLCCGRDRAQFATPMIQNDQESISSETHQPDSSKAGHGNSDPQOCHVYVLVK	397					
QY	286	-----RPTDAL	-----	DLESSSSDAHER	-----	PPGRARPERGRGKARA	323	
Db	398	SRRAKTKDSIKHGKTRGGRKSQSSSTCEPHGEQULLPAGDGGSCQPGGHSGGKSDAE	457					
QY	324	-----	-----	-----	-----	-----	-----	-----
Db	458	ISTESGDPKCICQVCTVQADEQTSIKLTPQSSSTGVAANVSVPDLQKTSICVNOFIEKQ	517					
QY	363	RGONREKRFELVAVYGVVCMPEPEFFYTLTAVGCV	-	PRTLFK	-	FFEMFGYCS	419	
Db	518	KISLSKERRAARKTGLTGIVGAVICWLPPEFLMYVILPF	-	CQICCEPTNKKFNITWLGILNS	576			
QY	420	SLNPVITYTIFNHNDFERRAFKIL	441					
Db	577	GLNPVITYTIFNLDYRRARFKRL	598					
US-09-884-430-8								
Sequence 8, Application US/09884430								
Patent No. US20020151046A1								
GENERAL INFORMATION:								
APPLICANT: Glucksmann, Maria Alexandra								
APPLICANT: Santiago, Immaculada Sllous								
TITLE OF INVENTION: 528771, A NOVEL HUMAN G PROTEIN COUPLED								
TITLE OF INVENTION: RECEPTOR AND USES THEREOF								
FILE REFERENCE: MNI-165								
CURRENT APPLICATION NUMBER: US/09/884,430								
CURRENT FILING DATE: 2001-06-18								

```

QY 363 RGRNREKRFFVLAIVIGVVCWPPFFFTYTLTAVGCSS--PRTEK-FFEEFGVCS 419
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 518 KISSEKERRARTGIIINGVFIOWLPFLMYLILPF-CQRCPTNKKNFITWLGINS 576
QY 420 SLNPVYITIFNHDFFARFKIL 441
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 577 GLNPVYITIFNLDYRFAFKRL 598

RESULT 7
US-10-166-101-3
: Sequence 3, Application US/10166101
: Publication No. US20030008823a1
: GENERAL INFORMATION:
: APPLICANT: Weinstanek, Richard L.
: APPLICANT: Branchek, Theresa
: APPLICANT: Hatfig, Paul
: TITLE OF INVENTION: DNA Encoding A 5-HT1F Receptor And Uses Thereof
: FILE REFERENCE: 39318-C
: CURRENT APPLICATION NUMBER: US/10/166,101
: CURRENT FILING DATE: 2002-06-10
: PRIOR APPLICATION NUMBER: 09/246,075
: PRIOR FILING DATE: 1999-02-05
: PRIOR APPLICATION NUMBER: 08/483,222
: PRIOR FILING DATE: 1995-06-07
: PRIOR APPLICATION NUMBER: 08/117,006
: PRIOR FILING DATE: 1994-08-22
: PRIOR APPLICATION NUMBER: PCT/US93/00149
: PRIOR FILING DATE: 1993-01-08
: PRIOR APPLICATION NUMBER: 07/817,920
: PRIOR FILING DATE: 1992-01-08
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: Patentln Ver. 2.0 - beta
: SEQ ID NO 3
: LENGTH: 422
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-166-101-3

Query Match 24.8% Score 590; DB 9; Length 422;
Best Local Similarity 34.4%; Pred No. 4.8e-30;
Matches 165; Conservative 60; Mismatches 159; Indels 96; Gaps 20;

QY 1 MGSLOPDAGNASWNGTEAP-----GG--GARATPYSLOVTLTLVCLAGLMLLVFGNV 52
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 MDVLSGGGCG--NTTSPAPFETGNTGIDSVTVSYOVITSL--LGLTLFCAVLGNA 55
QY 53 LVIIAFTSRALKAPONLPLVLSASDILVATLVIPFSLANVMGYWYCKMCEYATL 112
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 56 CVVAAALALESLONVANYLIGLSLAVLDLWVSVLVPMALVQVKNWLGQVTCDFIL 115
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 113 DVLEFCTSYHLCALISLDRTWSTIQAIEYNLKRTPRIRAKIITIVWISAVISFPLISI 172
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 116 DVLCCTSSILHLCALIDRKWATLTPIDYNNKTPRRAALISLWLGFLISIPML-- 173
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 173 EKKGGGGGPOP-AEP-RCEINDQMTYVISSCISFPAFLIMLVVRYQIAK---RRT 227
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 174 ----GWTPEDRSDPDACCTISKDHGYTISTFGAFYIPLMLVYLGIRFARERIRKT 229
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 228 RVPSPSRGPD-----VAAAP-----GTERPRPKGLGPERSACPGGAEAEP.LPTOLNGA- 276
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 230 VKRVEKIGADTRHGASBPQPKKSVNGESGRNWRRLGESKA--GGALC-----ANGAV 281
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 277 -PGEPAAGGRDNDALDLE-----SSSDHAERPPGPRPRERPGKRGARASQVKGDS 331
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 282 RQGD-----DGALELVIEVHRVGNKSLPLP-----SEAGP----- 313
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 332 LPRRGCAITGTPAACGGEERYGAAKASWNRGQ-NREKRFFVLAIVIGVVCWMPF 390
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 314 -----TPCASPASEERKNERNAEKRMALAREKTYKTIGIINGFTILCWLPF 361
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 391 FFVYTLTAIV--GGSVPRTLFFKFFFGVGNSSSLNPVIYIENHDFRFAFKIL---CR 443
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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us-09-636-259b-4.rapb

Page 5

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; CURRENT APPLICATION NUMBER: US/09/993,844
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/245,772
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/260,363
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: amino acid sequence of 5HT1AR-V2R chimera
; OTHER INFORMATION: expressed from the pGABT-B-1/5HT1AR vector
US-09-993-844-6

Query Match      24.6%; Score 585; DB 10; Length 451;
Best Local Similarity 34.2%; Pred. No. 1e-29;
Matches 166; Conservative 59; Mismatches 164; Indels 96; Gaps

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OY      53 LVIAVTSRALKAPONLFLVSLASADILVATLVIFSLANEWGVYFPGKACEIYIAL 112
Db      56 CVAVALLESLGNVANYLIGSLAVTDLKAVSLVLPMAALYQVLKWTLDQVTCDFEIAL 115
OY      113 DVLFTSSIVHLCAISLDRYWSTTQAIIEYNLKRTPRIKALITIVWYISAVISFPLISL 172
Db      116 DVLCTSSIIHLCAILDRIWYATDPIDIVYNKRTPRRAALISLTWILIGLISIPML-- 173
OY      173 EKKGGGGGPOP-KEP-RCEINDOKWVYVSSCIGSFACLMILIVYRIYQAK---RRT 227
Db      174 ---GMFTPEDRSDPACTISIKDHGVTYTSFGAFYIPLMLTLYRIPRAARFRIRGT 229
OY      228 RVPSRRKGP---AVAAPP-----GGTERPPGLGPERGAGVGAEAPLPTQNGA- 276
Db      230 VKKVEKGAOTRHGASPARQPKKSVNGSGSRNMRLVESKA--GGALC-----ANGAV 281
OY      277 -PGEPAAGCRDTDALDLE-----SSSDHAERPPGRRPPEGRGKGRASQVYKPGDS 331
Db      282 RQGD-----DGAALVIEVHRVNSKEHPLP-----SEAGP----- 313
OY      332 LPRRGQATGIGPAPGPEERHVGAKSRNRGRQ-NREKRFTVLAVYGVFVCGPFP 390
Db      314 -----TPCAPASFEKERNERNKAKALAREKTYKTGLIIGTFITLCLWPF 361
OY      391 FETYYTLTAV---GCSVPRTLFEKFEWFEGYCNSSINPIYITIFNHDPRRAFKTL---CR 443
Db      362 FIALVILPCESSCHMPTLGAIIIMWLGSNLSINPIYIVAFYFKDKQNAFKIILKCNFCA 421
OY      444 GDKRR 448
Db      422 AARGR 426

RESULT 10
US-10-166-101-5
: Sequence 5, Application US/10166101
: Publication No. US2003008823A1
: GENERAL INFORMATION:
: APPLICANT: Weinsbank, Richard L.
: APPLICANT: Branchek, Theresa
: APPLICANT: Hartig, Paul
: TITLE OF INVENTION: DNA Encoding A 5- HT1F Receptor And Uses Thereof
: FILE REFERENCE: 39318-C
: CURRENT APPLICATION NUMBER: US/10/166,101
: CURRENT FILING DATE: 2002-06-10
: PRIOR APPLICATION NUMBER: 09/246,075
: PRIOR FILING DATE: 1999-02-05
: PRIOR APP. NO.: 09/246,075

```

PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/117,006
PRIOR FILING DATE: 1994-08-22
PRIOR APPLICATION NUMBER: PCT/US93/00149
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: 07/817,920
PRIOR FILING DATE: 1992-01-08
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0 - beta
SEQ ID NO 5
LENGTH: 376
TYPE: PRT
ORGANISM: Homo sapiens
US-10-166-101-5

Query Match 24.4%; Score 580; DB 9; Length 376;
Best Local Similarity 31.2%; Pred. No. 1.8e-29;
Matches 138; Conservative 66; Mismatches 152; Indels 86; Gaps 9;

QY 4 LQPDGNAWNGTEAPGGGATPYSLQVTLTVCLAGLMLTVFGNVLVIIVFTSRA 63
DB 11 LQGEASNRSLNTESEANDPRTQAKISLAVV--LSVTLAVLSNAFVLTILLTRK 68
QY 64 LKAPQNLFLVSLASADIVLVIPSLANEVWGYWYFGKAMCEIYALDVLFCTSSIVH 123
DB 69 LHPANVYLGISLATDILVLSILMPISMAYTTHTWNGQILCDIMSSDITCTASILDH 128
QY 124 LCAISIDRWSTQAEVYKRPRIKAITVWVISAVISFPLISIEKKGGGGGQHP 183
DB 129 LCVIALDRKWTALTDALFYKRRTAGHATMAIWAISICISIPLEFWQANA-----QE 183
QY 184 AEPREIN-DQKWYVSSICISGFAPCLIMLVYVRIYIAKRRVRPPSRGPAAVAP 242
DB 184 EMDSCVNTSQTSTYTSYTCGAFYIPSVLLIILYGRYRAANRILNPSLIGKFFTTA- 242
QY 243 PGCTERRPKGLPERSAGDAEPLPQLNGAPGEPAPAPRPDADLESSSDHA 302
DB 243 -----HLITGSG-----SSLSLMSLHEGHS 264
QY 303 ERPPGRPRPERGPRGKARASQVKGDSLPRRPGATGIGPPAGPGEERYGAKASRW 362
DB 265 HSAGSPL-----FNNHVKIKLADSALER-----KRISAA----- 293
QY 363 RGNQNEKRTFVLAVVIGFVVCWPEFFTYTLAV---GGSVPRLTKFFFWGECYNS 419
DB 294 -----RRKATKILGIIIGAFIICWLPFEVVSILVDICRDSCHWHPGLDFFTWLGYS 348
QY 420 SLNPVITTFNHDERRAFKIL 441
DB 349 LNPITVTEFEFRQAFQKIV 370

RESULT 11
US-10-005-010-4
Sequence 4, Application US/10005010
Patent No. US20020115149A1

GENERAL INFORMATION:
APPLICANT: Weinstanek et al, Richard L.
TITLE OF INVENTION: Method of Obtaining A Composition Comprising A 5-HT1D
FILE REFERENCE: 36536-BA
CURRENT APPLICATION NUMBER: US/10/005,010
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/371,705
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-10-005-010-4

Query Match 24.3%; Score 577.5; DB 12; Length 390;
Best Local Similarity 30.6%; Pred. No. 2.7e-29;
Matches 140; Conservative 60; Mismatches 152; Indels 105; Gaps 11;

QY 6 PDAGNANW-----NGTEAPGGGATPY-----SLQVTLTVCLAGLMLTVFGNVLVI 55
DB 12 PPAGESEWVQANLSSAPSONCSAKDIYQDSISLPMKVLVWLALITLATTLSNAFYI 71
QY 56 IAVFTSRALKAPQNLFLVSLASADIVLVIPSLANEVWGYWYFGKAMCEIYALDV 115
DB 72 ATVYRTKRLHTPANVYLSLAVTDLLVLSILVMPISMTYTGKWTGQVYVCDWSSDIT 131
QY 116 FCTSSIVHLCASIDRWSTQAEVYKRPRIKAITVWVISAVISFPLISIEKK 175
DB 132 CCTASILHLCYIALDRKWTALTDALVEYSAKTTPRAVMAIWAISISIPLEFWQANA 191
QY 176 GGGGQPPAPREIN-DQKWYVSSICISGFAPCLIMLVYVRIYQIAKR-TRPPSR 233
DB 192 A-----DEEVESECVNTHILTYSTVGAFFYPTLLILALYGRYVEANSRILKQTPN 246
QY 234 RG-----PDVAAPPGCTERRPKGLPERSAGCGAEEPLPQLNG-APGEPAPGPRD 287
DB 247 TGRKLRRAQLITDPSGSTS-----VTSINRVPDVESEG--- 282
QY 288 TDALDLESSSDHAERPPGPRPERGPRGKARASQVKGDSLPRRPGATGIGTPAA 347
DB 283 -----SPVYVQVK----- 291
QY 348 GPGEEYGAAKASRWGRONREKRTFVLAVVIGFVVCWPEFFTYTLAV---GGSVP 404
DB 292 -----VRVSDALLEKKKMAAREKATRTLGIIIGAFIICWLPFEIISLVMPICKDCWFW 347
QY 405 RTLRFEPFWGECYNSLNPVITTFNHDERRAFKIL 441
DB 348 LAIFDFFTWLGYSLNPITVTEFEFRQAFKIL 384

RESULT 12
US-09-951-622-10
Sequence 10, Application US/09951622
Patent No. US20020106734A1

GENERAL INFORMATION:
APPLICANT: Daniel R. Soppet et al.
TITLE OF INVENTION: ADRENERGIC RECEPTOR
FILE REFERENCE: PFI28D2C1
CURRENT APPLICATION NUMBER: US/09/951,622
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 09/339,244
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 09/030,582
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 08/467,568
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: PCT/US94/09051
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 517
TYPE: PRT
ORGANISM: human
US-09-951-622-10

Query Match 24.1%; Score 573.5; DB 10; Length 517;
Best Local Similarity 29.3%; Pred. No. 6.2e-29;
Matches 131; Conservative 82; Mismatches 131; Indels 103; Gaps 8;

QY 10 NASWNGTEAPGGGATPYSLQVTLTVCLAGLMLTVFGNVLVIIVFTSRALKAPON 69
DB 22 NAFTEGPNQNTSSNSTLPQDITRAISVGLVLCATFLPAIVGHIIVLTVACNRHARTPTN 81
QY 70 LFLVSLASADIVLVIPSLANEVWGYWYFGKAMCEIYALDVLFCTSSIVHLCASL 129
DB 70 LFLVSLASADIVLVIPSLANEVWGYWYFGKAMCEIYALDVLFCTSSIVHLCASL 129

Db 82 YFVNLAMADLLSFTVLPFSALVLGWIAGRIFCDIWAADVLCCTASISLCAISI 141
 QY 130 DRYMSITQAIIEVNLKRPRIKAIITVWVSAVISFPLISIKKGGGQPA---EP 186
 Db 142 DRYGVRISLQYPTLVTRKRAIALSLVWVLSVLSIGPL-----GWKEPAPNDK 193
 QY 187 RCEINDQWYVSSICISFPAFLIMLVYRIYQIAKRRTRVPPSRGPDVAAPPGGT 246
 Db 194 ECGVTEEPYALFSSLSGFYIPLAVILVMYCRVYIAKRTK----- 235
 QY 247 ERRKGLGPERSAFGGAFAEPLPTQUNGABEPAPAGPRTDALDESSSSDHAERPP 306
 Db 236 -NLEAGVMKEMS-----NSKELTLRIHSKNFHED--- 263
 QY 307 GRRRPERGPRGKARASQVKGDSLPRRGATGIGTPAAGPGEERVGAAKASRMGRQ 366
 Db 264 -----TLSTKAKGHNRSSIAVAKLFK----- 286
 QY 367 NREKRTFVLAVVIGVVCWPFPEFTYTLTAVGCSV--PRTLKFFPFGYCNSSLNPV 424
 Db 287 SREKKAAKTIGIVGMFILLWLPFFIALPLGSLFSTLKPPDAVFVFWLGFNSCLNPI 346
 QY 425 IYTFNHDFRRAFKIL---CRGDRKR 448
 Db 347 IYPCSSKEFKRAFYRILGCGCRGRRR 373

RESULT 13

US-10-185-991-4
 ; Sequence 4, Application US/10185991
 ; Publication No. US20030022900A1
 ; GENERAL INFORMATION:

APPLICANT: Charles Gluchowski, et al.
 TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
 TREAT BENIGN PROSTATIC HYPERPLASIA

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: COOPER & DUNHAM LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/185,991

FILING DATE: 28-Jun-2002

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/444,783

FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 41878-AA-PCT-US/JPW

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525

TELEX: <unknown>

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 520 amino acids

TYPE: amino acid

TOPOLOGY: 1:linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-185-991-4

Query Match 23.8%; Score 566.5; DB 9; Length 520;

Best Local Similarity 29.1%; Pred. No. 1.7e-28; Matches 130; Conservative 82; Mismatches 132; Indels 103; Gaps 8;

QY 10 NASMNGTEAPGGGARATPYSLQVTLTVCLAGLIMLVGQVNLVIAVTSRAKAPQN 69
 Db 22 NANFTGPNQSSSTLPOLDITFAISVGLVLAFFILFAIVGNLVLSVACNRHLLPTPN 81
 QY 70 LFLVSLASADILVATLVIPPSLANEVMGYFGKANCEIYALDVLCFTSSIVHLCAISL 129
 Db 82 YFVNLAMADLLSFTVLPFSALVLGWIAGRIFCDIWAADVLCCTASISLCAISI 141
 QY 130 DRYMSITQAIIEVNLKRPRIKAIITVWVSAVISFPLISIKKGGGQPA---EP 186
 Db 142 DRYGVRISLQYPTLVTRKRAIALSLVWVLSVLSIGPL-----GWKEPAPNDK 193
 QY 187 RCEINDQWYVSSICISFPAFLIMLVYRIYQIAKRRTRVPPSRGPDVAAPPGGT 246
 Db 194 ECGVTEEPYALFSSLSGFYIPLAVILVMYCRVYIAKRTK----- 235
 QY 247 ERRKGLGPERSAFGGAFAEPLPTQUNGABEPAPAGPRTDALDESSSSDHAERPP 306
 Db 236 -NLEAGVMKEMS-----NSKELTLRIHSKNFHED--- 263
 QY 307 GRRRPERGPRGKARASQVKGDSLPRRGATGIGTPAAGPGEERVGAAKASRMGRQ 366
 Db 264 -----TLSTKAKGHNRSSIAVAKLFK----- 286
 QY 367 NREKRTFVLAVVIGVVCWPFPEFTYTLTAVGCSV--PRTLKFFPFGYCNSSLNPV 424
 Db 287 SREKKAAKTIGIVGMFILLWLPFFIALPLGSLFSTLKPPDAVFVFWLGFNSCLNPI 346
 QY 425 IYTFNHDFRRAFKIL---CRGDRKR 448
 Db 347 IYPCSSKEFKRAFYRILGCGCRGRRR 373

RESULT 14

US-10-052-589-2

; Sequence 2, Application US/10052589

; Patent No. US2002013832A1

; GENERAL INFORMATION:

APPLICANT: Perez, Dianne

APPLICANT: Zuscik, Michael

TITLE OF INVENTION: Model systems for neurodegenerative and cardiovascular disease

FILE REFERENCE: 26473/04200

CURRENT APPLICATION NUMBER: US/10/052,589

PRIOR FILING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: US 09/568,255

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 497

TYPE: PRT

ORGANISM: Mesocricetus sp.

US-10-052-589-2

Query Match 23.5%; Score 560; DB 12; Length 497;

Best Local Similarity 29.1%; Pred. No. 4.1e-28; Matches 136; Conservative 82; Mismatches 132; Indels 118; Gaps 11;

QY 4 LQPD-----AGNASW-----NGTEAPGGGARATPYSLQVTLTVCLAGLIMLV 48
 Db 1 MNPDLDTGHNTPAQNGLKLDANFTGPNQSSSTLPOLDVTRAIISVGLVLAFFILFAI 60
 QY 49 FGNVLVIAVTSRAKAPQNLFLVSLASADILVATLVIPPSLANEVMGYFGKANCEI 108
 Db 61 VGNILVLSVACNRHLLPTVNYFIWNLADIADLLSFTVLPFSALVLGWIAGRIFCDI 120
 QY 109 YLADVLCFTSSIVHLCAISIDRYMSITQAIIEVNLKRPRIKAIITVWVSAVISFPP 168
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BASE COUNT      213 a      461 c      446 g      260 t
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Best Local Similarity 88.1%; Pred. No. 2e-127;
Matches 1190; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

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QY  61  GGGCGCGCGGGGCGACCCCTTACTCCCTGACAGGTGACGCTGAGCTGTGTGCTGGCC 120
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QY  121  GGCCTGCTATGCTGCTACCGGTGTGGGCAAGCTGCTCGTCATCATCGCCGTGTACG 180
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QY  121  GGCCTGCTATGCTGCTACCGGTGTGGGCAAGCTGCTCGTCATCATCGCCGTGTACG 180
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Db   121  GGCCTGCTATGCTGCTACCGGTGTGGGCAAGCTGCTCGTCATCATCGCCGTGTACG 180
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QY  181  AGCCGCGGCGTCAAGGGGCGCCCAAAACCTTTCGCGGTGCTGCGCTGCGCGGACATC 240
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QY  181  AGCCGCGGCGTCAAGGGGCGCCCAAAACCTTTCGCGGTGCTGCGCTGCGCGGACATC 240
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QY  241  CTGGTGGCCAGCGTCGTATCCCTTCTCGCTGGCCCAAGAGTCATGCGCTACTGGTAC 300
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Db   421  TACAACTGTAAGCGCAGCGCGCGCGCATCAAGGCCATCATCATCTGCTGGGTATC 480
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QY  481  TCGGCGCTCATCTCTTCCCGCGCGCTCATTCATCATGAGAAAGAGGGCGGCGCGGC 540
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QY  961  GCGCGAGCGAGCGAGTGAAGCGCGCGCGCAGCAGCTGCGCGCGCGCGCGCGCGCGCG 1020
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Db   961  ACCAAGCGAGCGAGTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
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Db   1261  CTGAACCTCTTATCTTACACATTTTCAACAGAGATTTCCGCGCGCGCTTCAAGAAAGATC 1320
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QY  1321  CTCTGTGCGGGGAGAGAGAGCGGATCGTG 1350
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LOCUS
DEFINITION   Bos taurus alpha2D adrenergic receptor gene, complete cds.
ACCESSION   U79030
VERSION      U79030.1 GI:3282232
KEYWORDS
SOURCE
ORGANISM
    Bos taurus.
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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    Bovidae; Bovinae; Bos.
REFERENCE
    1 (bases 1 to 2923)
    Venkataraman,V., Duda,T. and Sharma,R.K.
    The bovine alpha 2D-adrenergic receptor gene: structure, expression
    in retina, and pharmacological characterization of the encoded
    receptor
    JOURNAL   Mol. Cell. Biochem. 177 (1-2), 113-123 (1997)
    MEDLINE   9811113
    PUBMED   9450652
REFERENCE
    2 (bases 1 to 2923)
    Venkataraman,V., Duda,T.M. and Sharma,R.K.
    Direct Submission
    Submitted (20-NOV-1996) Cell Biology, UMDNJ-SOM, 2 Medical Ctr Dr,
    Stratford, NJ 08084, USA
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Query Match 81.9%; Score 1105.2; DB 10; Length 1552;
Best Local Similarity 88.7%; Pred. No. 7.8e-129;
Matches 1197; Conservative 0; Mismatches 153; Indels 0; Gaps 0;
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DB 1 ATGGGCTCCCTGCGACGCCGCGAGTACGAGTGAAGCGGACCGAGCGCGCGGA 60
OY 61 GCGCGCGCGCGCGACCCCTTACTCCCTGAGGTGACGCTGACGCTGGTGGCTGGCC 120
DB 61 GCGCGCGACCGCGCGACCCCTTACTCCCTGAGGTGACGCTGAGCGCTGGTGGCT 120
OY 121 GGCCTGCTCATGCTCTACACGCTTTCGCGACAGTGTCTGATCATCTGCGCTGTCACG 180
DB 121 GGCCTGCTCATGCTCTACACGCTTTCGCGACAGTGTGTATTTACGAGTTCACG 180
OY 181 AGCGCGCGCGTCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
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OY 721 GCG 780
DB 721 GCG 780
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DB 781 ACCG 840
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DEFINITION Rat alpha-2-adrenergic receptor protein (RG20) gene, complete cds.
VERSION M62372.1 GI:206615
KEYWORDS alpha-2-adrenergic receptor; transmembrane protein.
SOURCE Rattus norvegicus (strain Sprague-Dawley) adult liver DNA.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 1380)
AUTHORS Lanier,S.M., Downing,S., Duzic,E. and Homcy,C.J.
TITLE Isolation of rat genomic clones encoding subtypes of the alpha
2-adrenergic receptor. Identification of a unique receptor subtype
JOURNAL J. Biol. Chem. 266 (16), 10470-10478 (1991)
MEDLINE 91244823
PUBMED 1645350
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Matches 1230;	Conservative	0;	Mismatches 117;	Indels 6; Gaps 2;

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QY	61	GGCGCGCCCGGGGCGCCCTTACTCCCTCGAGGTAGCGCTGACGCTGGTGTCTGGCC	120
Db	109	GGCGGACACCGGGGACCCCTTACTCCCTCGAGGTAGCGGTGACGCTGGTGTCTGGTC	168
QY	121	GACCTGTCATGCTGCTACCGGTGTTGGCAACGTGCTGCTCATATGCGCGTGTTCACG	180
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QY	181	AGCGCGGGGCTCAAGGCGGCCCAAAACGCTCTCGTGTGCTGTGGCTCGGCGCAATC	240
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QY	241	CTGTGGCCACAGCTGTCATCCCTTCTTCGCTGGCCACGAGGTATGGGTACTGTAC	300
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QY	301	TTCGGCAAGGCTTGGTGGAGATCTACCTGGGGGCTGCAGCTGCTTTCGCAAGTCGTC	360
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QY	361	ATCGTGCAACCTTGGGCGCATTCAGCTGGAGCGCCTACTGTGCATCACAGGCGCATCGAG	420
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QY	481	TGCGCGCTCATCTCTTCCCGCGCGTCATCTCATCTGAAAGAAAGGGGGGGCGCGCGG	540
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QY	601	TGCATCGGCTCTTCTTGCCTCCCTGCTCATCATGATCCTGGTCTAGTGGCGATTCAC	660
Db	646	AGCATCGGCTCTTCTTGCCTCCCTGCTCATCATGATCCTGGTGTAGTGGCGATTCAC	705
QY	661	CAGATCGCCAAAGCTGTGGACCGCGCTGGCAACCGCGCGCGGGGTCCGAGACG---CGTC	717
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QY	1078	TCCGGCTGGGCGCGGGCGCGCAGAACCGGAGAAAGGCTTCAGGTCGHTGGCCGTGCTC	1137
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RESULT	13
RNU79031	
LOCUS	RNU79031 1552 bp mRNA linear
DEFINITION	Rattus norvegicus alpha2d adrenergic receptor mRNA, complete cds.
ACCESSION	U79031
VERSION	U79031.1 GI:3282234
KEYWORDS	
SOURCE	Rattus norvegicus.

ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 1552)

AUHOSS
Chalberg, S.C., Duda, T., Rine, J.A. and Sharma, R.N.
TITLE
Molecular cloning, sequencing and expression of an alpha
2-adrenergic receptor complementary DNA from rat brain
JOURNAL
Mol. Cell. Biochem. 97 (2), 161-172 (1990)

REFERENCE	2 (bases 1 to 1552)
MEDLINE	91125329
PUBMED	2177834

AUTHORS WYBIELEWSKI, K., DUDA, T. and SHARMA, R.A.
TITLE Structural, genetic and pharmacological identity of the rat alpha 2-adrenergic receptor subtype CA2-47 and its molecular characterization in rat adrenal, adrenocortical carcinoma and bovine retina
JOURNAL Mol. Cell. Biochem. 144 (2), 181-190 (1995)

MEDLINE 95349560
PUBMED 7623790

REFERENCE	AUTHORS
3 (bases 1 to 1552)	Venkataraman, V., Duda, T.M. and Sharma, R.K

TITLE Direct Submission
JOURNAL Submitted (20-NOV-1996) Cell Biology, UMDN^Y-SOM, 2 Medical Ctr.

Dr., Stratford, NJ 08084, USA

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Query Match      85.2%; Score 1150; DB 4; Length 1728;
Best Local Similarity 90.7%; Pred. No. 2e-134;
Matches 1225; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

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QY 61 GGGCGGCGCGGGGCAACCCCTTACTCCCTGAGGTGAGCGCTGAGCGCTGCTGCGC 120
DB 190 GGGCGGCGCGGGGCAACCCCTTACTCCCTGAGGTGAGCGCTGAGCGCTGCTGCGC 249
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DEFINITION   Cavia porcellus alpha-2a adrenoceptor gene, complete cds.
ACCESSION    U25722
VERSION      U25722.1 GI:818874
KEYWORDS
SOURCE
ORGANISM     Cavia porcellus.
              Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE    1 (bases 1 to 2291)
              Svensson,S.P., Bailey,T.J., Porter,A.C., Richman,J.G. and
              Regan,J.W.
              Heterologous expression of the cloned guinea pig alpha 2A, alpha
              2B, and alpha 2C adrenoceptor subtypes. Radioligand binding and
              functional coupling to a CAMP-responsive reporter gene
              Biochem. Pharmacol. 51 (3), 291-300 (1996)
PUBMED      8573196
JOURNAL      2 (bases 1 to 2291)
MEDLINE     Richman,J.G.
AUTHORS     Direct Submission
TITLE       Submitted (26-APR-1995) Jeremy G. Richman, University of Arizona,
              Pharmacology and Toxicology, College of Pharmacy, Room 235, Tucson,
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RESULT 11

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LOCUS Porcine alpha2A-adrenergic receptor (PORA2AR) gene, complete cds.

DEFINITION J05652

ACCESSION J05652.1 GI:164303

VERSION alpha-2A-adrenergic receptor.

KEYWORDS Porcine liver DNA.

SOURCE ORGANISM

Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE

1 (bases 1 to 1728)

1. Guyer, C.A., Horstman, D.A., Wilson, A.L., Clark, J.D., Kragoe, E.J. Jr. and Limbird, L.E. Unpublished (1990)

2 (bases 70 to 1582)

2. Guyer, C.A., Horstman, D.A., Wilson, A.L., Clark, J.D., Cragoe, E.J. Jr. and Limbird, L.E. Cloning, sequencing, and expression of the gene encoding the porcine alpha 2-adrenergic receptor. Allosteric modulation by Na+, H+, and amiloride analogs (1990)

JOURNAL J. Biol. Chem. 265 (28), 17307-17317 (1990)

MEDLINE 91009167

PUBMED 2170371

COMMENT Draft entry and computer-readable sequence for [J. Biol. Chem. (1990) in press] kindly submitted by C.A. Guyer, 02-AUG-1990.

FEATURES

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location/Qualifiers

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153

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DEFINITION Human platelet alpha-2-adrenergic receptor gene, complete cds.
ACCESSION M18415
VERSION M18415.1 GI:178191
KEYWORDS alpha-2-adrenergic receptor; alpha-adrenergic receptor.
SOURCE Human (lambda-EMBL 3 library) DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1521)
AUTHORS Koblika,B.K., Matsui,H., Koblika,T.S., Yang-Feng,T.L., Francke,U.,
Caron,M.G., Lefkowitz,R.J. and Regan,J.W.
Cloning, sequencing, and expression of the gene coding for the
human platelet alpha 2-adrenergic receptor
JOURNAL Science 238 (4827), 650-656 (1987)
MEDLINE 88042789
PUBMED 2823383
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 204908)
 DIRECT SUBMISSION
 Submitted (13-DEC-2001) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
 On Dec 5, 2001 this sequence version replaced g1:16944857.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em.; EMBL; SW;
 SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP
 database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 10, constructed by the Sanger Centre Chromosome 10
 Mapping Group. Further information can be found at
 http://www.sanger.ac.uk/HGP/Chr10
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COMMENT
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

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ACCESSION      AF284095
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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AUTHORS      Mao,Z.-M., Tang,K., Li,B.-M. and Jing,N.-H.
TITLE      Cloning and expression of human alpha-2A adrenergic receptor in
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JOURNAL      Unpublished
REFERENCE
AUTHORS      Mao,Z.-M., Tang,K., Li,B.-M. and Jing,N.-H.
TITLE      Direct Submission
JOURNAL      Submitted (01-JUN-2000) Shanghai Institute of Physiology, Chinese
Academy of Sciences, 320 Yue Yang Road, Shanghai 200031, P.R. China
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 SOURCE
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
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 AUTHORS Liu, L. and Yuan, L.
 TITLE Human alpha-2A adrenergic receptor gene and the genotype of -1296
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 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 3612)
 AUTHORS Liu, L. and Yuan, L.
 TITLE Direct Submission
 JOURNAL Submitted (17-Apr-2001) Key Laboratory of Molecular Biology,
 General Hospital of Airforce, Fucheng Road No. 30, Beijing 100036,
 China

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VERSION AF262016.2 GI:9864781
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ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Castellano,M., Giacche',M., Rossi,F., Rivasdossi,F., Perani,C.,
Beschl,M. and Agabiti Rosel,E.
TITLE A search for genetic variability in the human alpha-2 adrenergic
receptor on chromosome 10
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1941)
AUTHORS Castellano,M., Giacche',M., Rossi,F., Rivasdossi,F., Perani,C.,
Beschl,M. and Agabiti Rosel,E.
TITLE Direct Submission
JOURNAL Submitted (29-Apr-2000) Medical and Surgical Sciences, University
of Brescia, Spedali Civilli di Brescia, Brescia I-25100, Italy
3 (bases 1 to 1941)
AUTHORS Castellano,M., Giacche',M., Rossi,F., Rivasdossi,F., Perani,C.,
Beschl,M. and Agabiti Rosel,E.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Medical and Surgical Sciences, University
of Brescia, Spedali Civilli di Brescia, Brescia I-25100, Italy
REMARK Sequence update by submitter
COMMENT On Aug 22, 2000 this sequence version replaced gi:9837145.
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AUTHORS		Small,K.M.; Forbes,S.L.; Brown,K.M. and Liggett,S.B.	
TITLE		An asn to lys polymorphism in the third intracellular loop of the human alpha 2A-adrenergic receptor impairs enhanced agonist-promoted G _i coupling	
JOURNAL		J Biol Chem. 275 (49), 38518-38523 (2000)	
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AUTHORS		Small,K.M., Forbes,S.L., Bridges,K.M. and Liggett,S.B.	
TITLE		Direct Submission	
JOURNAL		Submitted (22-JUN-2000) Internal Medicine, University of Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA	
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AUTHORS	Liggett, S. B. and Small, K. M.		
TITLE	Alpha-2 adrenergic receptor polymorphisms		
JOURNAL	Patent: WO 0179561-A 24 25-OCT-2001;		
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 Small,K.M., Forbes,S.L., Brown,K.M. and Ligett,S.B.
 An asn to lys polymorphism in the third intracellular loop of the human alpha 2A adrenergic receptor imparts enhanced agonist-promoted GI coupling
 J. Biol. Chem. 275 (49), 38518-38523 (2000)
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GenCore version 5.1.3
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28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rtd:*
36: em_hcg_mam:*
37: em_hcg_vrl:*
38: em_sy:*
39: em_hcg_hum:*
40: em_hcg_mus:*
41: em_hcg_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1350	100.0	1350	6	AX350513
2	1350	100.0	1350	6	AF316894
3	1348.4	99.9	1353	6	AX350512
4	1348.4	99.9	1353	9	AF281308
5	1348.4	99.9	1353	9	AF262016
6	1348.4	99.9	1353	9	AF262016
7	1348.4	99.9	1353	9	AF284095
8	1348.4	99.9	1353	9	AF284095
9	1325.4	98.2	1353	9	AF284095
10	1317.4	97.6	1521	9	HUMADRA
11	1150	85.2	1728	4	P1G2AR
12	1133.8	84.0	2291	10	CPU25722
13	1105.2	81.9	1552	10	RRU79031
14	1094	81.0	1380	10	RATRG20
15	1093.4	81.0	2923	4	BTU79030
16	1082.8	80.2	1454	10	MUSALP2ADB
17	1082.8	80.2	204317	2	AC113491
18	915.4	67.8	7353	6	AX344975
19	915.4	67.8	7353	6	AX344974
20	836.4	62.0	7353	6	AX344974
21	836.4	62.0	7353	6	AX344974
22	528	39.1	1386	6	AX350528
23	527.4	39.1	1491	9	HUMADRA2C
24	527.4	39.1	14850	9	HSU72648
25	524.8	38.9	1389	9	AF280399
26	517.8	38.4	1995	10	CPU25724
27	517.2	38.3	1374	6	AX350530
28	514	38.1	1377	9	AF280400
29	512.4	38.0	1382	6	E07358
30	512.4	38.0	1382	9	HUMADRA2C
31	505.2	37.4	3461	5	TRU345040
32	464.4	34.4	1503	10	MUSALP2ADA
33	464.4	34.4	1745	10	RATRG10
34	463.6	34.3	1380	10	RNAC24
35	462	34.2	2991	10	MUSADRA
36	462	34.2	5221	10	RATRG20
37	460.4	34.1	1704	10	RATRG20
38	447.6	33.2	22842	9	AC092603
39	446	33.0	1344	6	AX350490
40	446	33.0	1344	9	AF316895
41	443	32.8	1353	6	AX350489
42	443	32.8	9842	9	AF005900
43	439.8	32.6	2072	9	HUMADRA2RA
44	426.6	31.6	1149	4	CVI315935
45	413	30.6	1492	4	DVU04310

ALIGNMENTS

RESULT 1
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LOCUS AX350513 1350 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 25 from Patent WO0179561.
ACCESSION AX350513
VERSION AX350513.1 GI:18616108
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 Liggett, S.B. and Small, K.M.
Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 25 25-OCT-2001;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 204317)
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 Mus musculus, clone RP23-358H2
 Unpublished
 2 (bases 1 to 204317)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N.,

Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collamore,A., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fero,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Garg,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hages,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Lacroque,K., Lamazeres,R., Landers,T., Lenocksky,J., Levine,R., Liu,G., Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Menes,L., Mihova,T., Mienga,Y., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,C., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Roman,J., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schnupack,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trifoglio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
 Submitted (01-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 204317)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N.,

Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collamore,A., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fero,S., Ferreira,P., Fitzgerald,M., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hages,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Lacroque,K., Lamazeres,R., Landers,T., Lenocksky,J., Levine,R., Lindblad-Tch,K., Liu,G., Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Menes,L., Mihova,T., Mienga,Y., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,C., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Roman,J., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schnupack,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trifoglio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
 Submitted (06-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Jun 6, 2002 this sequence version replaced gi:21313866.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WtBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: I23807
 Center clone name: 358.H.2
 ----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads

FEATURES

source

Assembly program: Phrap; version 0.960731
 Consensus quality: 197709 bases at least Q40
 Consensus quality: 200412 bases at least Q30
 Consensus quality: 201149 bases at least Q20
 Insert size: 210000; agarose-fp
 Insert size: 202017; sum-of-contigs
 Quality coverage: 6.3 in Q20 bases; agarose-fp
 Quality coverage: 6.6 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 24 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submittor.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 1 7387: contig of 7387 bp in length
 7388 7487: gap of 100 bp
 7488 7956: contig of 469 bp in length
 7957 8056: gap of 100 bp
 8057 9200: contig of 1144 bp in length
 9201 9300: gap of 100 bp
 9301 10747: contig of 1447 bp in length
 10748 10847: gap of 100 bp
 10848 12877: contig of 2030 bp in length
 12878 12977: gap of 100 bp
 12978 15172: contig of 2195 bp in length
 15173 15272: gap of 100 bp
 15273 18061: contig of 2789 bp in length
 18062 18161: gap of 100 bp
 18162 21071: contig of 2910 bp in length
 21072 21171: gap of 100 bp
 21172 24003: contig of 2832 bp in length
 24004 24103: gap of 100 bp
 24104 27175: contig of 3072 bp in length
 27176 27275: gap of 100 bp
 27276 30561: contig of 3286 bp in length
 30562 30661: gap of 100 bp
 30662 66767: contig of 36106 bp in length
 66768 66867: gap of 100 bp
 66868 73300: contig of 6633 bp in length
 73301 73400: gap of 100 bp
 73401 78880: contig of 5480 bp in length
 78881 78980: gap of 100 bp
 78981 89075: contig of 10095 bp in length
 89076 89175: gap of 100 bp
 89176 98581: contig of 9406 bp in length
 98582 98681: gap of 100 bp
 98682 105311: contig of 6630 bp in length
 105312 105411: gap of 100 bp
 105412 122788: contig of 17377 bp in length
 122789 122888: gap of 100 bp
 122889 132289: contig of 9401 bp in length
 132290 132389: gap of 100 bp
 132390 144818: contig of 12429 bp in length
 144819 144918: gap of 100 bp
 144919 159101: contig of 14183 bp in length
 159102 159201: gap of 100 bp
 159202 177288: contig of 18087 bp in length
 177289 177388: gap of 100 bp
 177389 201231: contig of 23843 bp in length
 201232 201331: gap of 100 bp
 201332 204317: contig of 2986 bp in length.
 Location/Qualifiers
 1. 204317
 /organism="Mus musculus"
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 /clone="RP23-358H2"
 /clone_lib="RPC1-23 Female Mouse BAC"
 1. 7387
 /note="assembly_fragment"

misc_feature

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 KAMEITLADLVLEFCTSTYISLDRWISTQALEIBNKRIPRKRATIVTWT
 SAVSEIPPLISIEKKAGCGGQOAPPEKPRINDQAVYISCTGSEAPCLMLIVAAV
 IYQIAKRRTIRPPSRKRGPDAAALPGAERRINDQVIGRGVGAAPLVLVLRNA
 PGGEAPAGPDADGLDEESSHAHRPPDRSESGPRAKSRASVYFVPCGSLPR
 RGPAPGAPADTAGEEERGGSVAASWRGKONKEKREFTVLAVIVFVVCWCPPEFF
 TYTLTAGCVSPPLTLFKFPFWGFCNSLNDPIYTLINHDFRRAFKILICGDRKRIY
 "

	Query Match	84.4%	Score 34.6;	DB 4;	Length 1728;
	Best Local Similarity	90.2%;	Pred.	No. 0.84;	Mismatches
	Matches	37;	Conservative	0;	Indels 0; Gaps 0;
Oy	1 GGGGCCACCGAGGCGCACGGGTCTGSGCCCCGCAGC	41			
Db	859 GGGGGGCCCGACGCGCAATGTCCTTACCCTCCCAGC	899			

RESULT 12			
MUSALP2ADB			
LOCUS	1454 bp	DNA	linear
DEFINITION	Mouse alpha-2 adrenergic receptor,		ROD 27-APR-1993
ACCESSION	complete cds.		
M94377			

KEYWORDS	alpha-2 adrenergic receptor.
SOURCE	Mus musculus (strain 129/Sv) DNA.
ORGANISM	Mus musculus

REFERENCE
AUTHORS
TITLE

Link, R., Daunt, D., Barsh, G., Chruscinski, A., and Kobilka, B.
Cloning of two mouse genes encoding alpha 2-adrenergic receptor

alpha 2-C10 homolog responsible for an interspecies variation in
antagonist binding
Mol. Pharmacol. 42 (1), 16-27 (1992)
JOURNAL
MEDLINE
PUBMED
92342131
1353249

FEATURES	location/Qualifiers
source	1..1454
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	/strain="129/Sv"
	/db.xref="taxon:10090"
CDS	51..1403

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 KWACEITLADLVFCTSSIVHLCAISLDRTWSTQIALEYNIKRRPRTIKATITVWYVY
 SAISEPPLISIEIKKGGGGOOPAEPCIKNDOKWYISSISGFPACILIMLYVY
 IYQIAKRRTRVPPSRRGDADACAPGGADRRPNCIGERRAGCPGAEDLPVLQNA
 PGEPAPGPRDGDALDEESSSEHARPPGPRPDGPFTKATRSVQKPGDGLSR
 RCGCAAGPRASSGSGHCEKRGGAASWRRORNEKKEFTVLAVIVFVWCMPPEFF
 TYLIAAGCPVPSQLNEFFEFWFGCNSLNPVITYTTFNHDFRRAFKKILCRGDKRIRIV
 "

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Query Match%      80.5%   Score 33;   DB 10;   Length 1434;
Best Local Similarity 87.8%   Pred. No. 2.6;
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0.

QY      1 GGGGGCAGCAGCCAGCCAGCCAGGCGTGTGGGCCCCCAGCGC 41
      |||||  |||||  |||||  |||||  |||||  |||||
DB      780 GGGGGCGCGATGCGAGGCCCCAACGCGGCTGGGCCCCGAGCG 820

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RESULT 13

LOCUS	RRU79031	1552 bp	mRNA	linear	ROD 14-JUN-2000
DEFINITION	Rattus norvegicus alpha2d adrenergic receptor mRNA, complete cds.				
ACCESSION	U79031				
VERSION	U79031.1	GI:3282234			
KEYWORDS					
SOURCE	Rattus norvegicus.				
ORGANISM	Rattus norvegicus				

REFERENCE
1 (bases 1 to 1552)
AUTHORS Chabberg,S.C., Duda,T., Rhine,J.A. and Sharma,R.K.
TITLE Molecular cloning, sequencing and expression of an alpha
2-adrenergic receptor complementary DNA from rat brain
JOURNAL Mol. Cell. Biochem. 97 (2), 161-172 (1990)
MEDLINE 91125329

REFERENCE

TITLE

TITLE	ABSTRACT	KEYWORDS
Structural, genetic and pharmacological identity of the rat alpha 2-adrenergic receptor subtype CA2-47 and its molecular characterization in rat adrenal, adrenocortical carcinoma and bovine retina	Abstract text...	Keywords...

JOURNAL
MOL. CELL. Biochem. 144 (2), 181-190 (1995)
MEDLINE 95349560

PUBMED 7623790

AUTHOR

VENKATARAMAN, V., DUDA, T. M. and SHARMA, R. K.

Submitted (20-NOV-1996) Cell Biology, UMDNJ-SOM, 2 Medical Ctr.
Dr., Stratford, NJ 08084, USA

source

CDS

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/strain="Sprague-Dawley"
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LFTVGNVLVIIAVETSRALKAPONFLVLSAADIILVTLVLPESLAIEWNGYYP
KWCYIETLADLVETCKSSIVHLASLDRWSTIOALENLRTPRIKRLIIVTVV
SAVISEPPLISLEKKGAGGGGQOAPAESCKINDOKWVISSSGSPAPCLIIIVNG
IYOAKRRTRVPSPSRGPDACSAIPGCGADRPNGLDEPGACGAGAEAPLITQLVG
PEPAPTRPDGSDALDESSSSSEHARPPGPKPRGPRAGKTAASVYKGSJLP
RCPGAGGAGSGCGGERAGACASRWRRQRREKRTFLVAVYGVVCMPEFFPEF
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"
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BASE COUNT	244 a	504 c	498 g	306 t
ORIGIN				
Query Match		80.5%;	Score 33;	DB 10;
Best Local Similarity		87.8%;	Pred. No. 2.6;	
Matches	36;	Conservative	0;	Mismatches 5;
QY	1	GGGGGACCGAGGCGAGGCCAAGGCTGTGGGCCCCGAGCG	41	
Db	730	GGGGGCCCCGANTGCGACAGGCCCAACGGGCTGTGGCCCCGAGCG	770	

RESULT 14	AC113491/c	LOCUS	DEFINITION
	AC113491	204317 bp	DNA
			1linear HMG 06-JUN-2002
			Mus musculus clone RP23-358H2, WORKING DRAFT SEQUENCE, 24 ordered
			pieces.
ACCESSION	AC113491		
VERSION	AC113491.3	GI:21327601	

SOURCE	house mouse.
ORGANISM	Mus musculus

REFERENCE 1 (bases 1 to 3653)
 AUTHORS Mao, Z.-M., Tang, K., Li, B.-M. and Jing, N.-H.
 TITLE Cloning and expression of human alpha-2A adrenergic receptor in
 3T3 cells
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 3653)
 AUTHORS Mao, Z.-M., Tang, K., Li, B.-M. and Jing, N.-H.
 TITLE Direct Submission
 JOURNAL Submitted (01-JUL-2000) Shanghai Institute of Physiology, Chinese
 Academy of Sciences, 320 Yue Yang Road, Shanghai 200031, P.R. China

FEATURES
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 SAVISFPLISIEKGGGGGPOPAEPCIEINDKWYVSSICGSFPAFLMILVYR
 IYQIAKRTVPVPSRRGPDVAAPPGCTGEPGLGERSAGGGAADPLTOLNGA
 PGEPAPAGPRDTPALDLEESSSDHAERPPGPRGPRGSKARASQVKKPQDSLPR
 RCGPATGICGPACGPEERYGAKASRWGRQREKRFETVLAVVIGVAVCVCFPEEF
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BASE COUNT 681 a 1168 c 1028 g 776 t

ORIGIN

Query Match 96.1%; Score 39.4; DB 9; Length 3653;
 Best Local Similarity 97.6%; Pred. No. 0.027; 1; Indels 0; Gaps 0;
 Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGGGGCAGCGAGCGAGCGCCAGGCTGTGGGCCCCGAGCG 41
 ||||||||||||||||||||||||||||||||||||||||
 DB 1609 GGGGGCAGCGAGCGAGCGCCAGGCTGTGGGCCCCGAGCG 1649

RESULT 10
 AL158163 204908 bp DNA linear PRI 13-DEC-2001
 LOCUS Human DNA sequence from clone RP11-348N5 on chromosome 10, complete
 DEFINITION sequence.
 ACCESSION AL158163
 VERSION AL158163.11 GI:17384427
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 204908)
 AUTHORS Johnson, C.
 TITLE Direct Submission
 JOURNAL Submitted (13-DEC-2001) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humgeny@sanger.ac.uk
 On Dec 5, 2001 this sequence version replaced gi:16944857.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em, EMBL, Sw, SWISSPROT; Tr, TrEMBL; Wp, WormPEP; Information on the WormPEP
 database can be found at
 http://www.sanger.ac.uk/projects/c_elegans/wormpep
 This sequence was generated from part of bacterial clone contigs of human
 chromosome 10, constructed by the Sanger Centre Chromosome 10
 Mapping Group. Further information can be found at
 http://www.sanger.ac.uk/HGP/Chr10
 RP11-348N5 is from the library RPCI-11.2 constructed by the group
 of Pieter de Jong. For further details see
 http://www.Chori.org/bacpac/home.htm
 VECTOR: pPACe3.6
 This sequence is the entire insert of clone RP11-348N5 The true
 left end of clone RP11-479A21 is at 179266 in this sequence. The
 true right end of clone RP11-313D6 is at 44800 in this sequence.

FEATURES
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 /db_xref="taxon:9606"
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 /clone_1lb="RPCI-11.2"
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BASE COUNT 62115 a 36724 c 39536 g 66533 t

ORIGIN

Query Match 96.1%; Score 39.4; DB 9; Length 204908;
 Best Local Similarity 97.6%; Pred. No. 0.013;
 Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGGGGCAGCGAGCGAGCGCCAGGCTGTGGGCCCCGAGCG 41
 ||||||||||||||||||||||||||||||||||||||||
 DB 196299 GGGGGCAGCGAGCGAGCGCCAGGCTGTGGGCCCCGAGCG 196339

RESULT 11
 PIGA2AR 1728 bp DNA linear MAM 27-APR-1993
 LOCUS Porcine alpha2A-adrenergic receptor (PIGA2AR) gene, complete cds.
 DEFINITION J05652
 ACCESSION J05652.1 GI:164303
 VERSION alpha-2A-adrenergic receptor.
 KEYWORDS Porcine liver DNA.
 SOURCE Sus scrofa
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 REFERENCE 1 (bases 1 to 1728)
 AUTHORS Guyer, C.A., Horstman, D.A., Wilson, A.L., Clark, J.D., Kragee, E.J., Jr.
 and Limbird, L.E.
 TITLE Unpublished (1990)
 JOURNAL 2 (bases 70 to 1582)
 AUTHORS Guyer, C.A., Horstman, D.A., Wilson, A.L., Clark, J.D., Cragoe, E.J., Jr.
 and Limbird, L.E.
 TITLE Cloning, sequencing, and expression of the gene encoding the
 porcine alpha 2-adrenergic receptor. Allosteric modulation by Na⁺,
 H⁺, and amiloride analogs
 J. Biol. Chem. 265 (28), 17307-17317 (1990)
 MEDLINE 91009167
 PUBMED 2170371
 COMMENT Draft entry and computer-readable sequence for [J. Biol. Chem.
 (1990) In press] kindly submitted
 by C.A.Guyer, 02-AUG-1990.

FEATURES
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 130..1482
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 /db_xref="GI:164304"

ORIGIN

Query Match 96.1%; Score 39.4; DB 9; Length 1941;
Best Local Similarity 97.6%; Pred. No. 0.03;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGGCACCAGCGAGCCCAAGGCTCTGGCCCCGAGCG 41
|||||
Db 1248 GGGGGCACCAGCGAGCCCAAGGCTCTGGCCCCGAGCG 1288

RESULT 7

HUMADRA2R 3604 bp DNA linear PRI 30-OCT-1994
LOCUS
DEFINITION Human alpha 2 adrenergic receptor gene, complete cds.
ACCESSION M23533.1 GI:178195
VERSION
KEYWORDS adrenergic receptor; alpha-2 adrenergic receptor.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
Cloning, sequence analysis, and permanent expression of a human alpha 2-adrenergic receptor in Chinese hamster ovary cells.
Evidence for independent pathways of receptor coupling to adenylylate cyclase attenuation and activation
J. Biol. Chem. 264 (20), 11754-11761 (1989)

JOURNAL
MEDLINE
PUBMED
89308571
2568356

COMMENT
Draft entry and computer-readable sequence for [1] kindly submitted by W.R.McCombie, 30-MAR-1989.

FEATURES

source
1..3604
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="10q23-q25"
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1707..1712
/note="glucocorticoid response element"
1723..1728
/note="GRE related sequence"
2078..3430
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/db_xref="GI:178195"
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KAMCEIYLAIDVFCSSIVHLCALSIDRWYSITQAIYNNKRPRIKATITTVVI
SAVISPEPLISIEKKGGGGQPAPEPCINDDKQWYVSSCGSEFACILNITLYVR
IYOIAKRRTRVPSRRGPDVAVAPPGCTERRNGGPERSGAGAEAPLPTOLNGA
RGEPAAGPRDLDLDESSSDHAERPPGRRPGRPGKGRASQVPRGSLPR
AGRRKSGRRLLGRGHSASGLPRRAGAGQRRKRTFVLAVVIGVVCWCPFFP
TYTLTAVGCSVPRTLKFFFWFGYCNSSINPIYITIFNHDFRAFKIILCRGDRKRIY

BASE COUNT 555 a 1272 c 1134 g 643 t
ORIGIN

Query Match 96.1%; Score 39.4; DB 9; Length 3604;
Best Local Similarity 97.6%; Pred. No. 0.027;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGGCACCAGCGAGCCCAAGGCTCTGGCCCCGAGCG 41
|||||
Db 2807 GGGGGCACCAGCGAGCCCAAGGCTCTGGCCCCGAGCG 2847

RESULT 8

AY032736 3612 bp DNA linear PRI 12-MAY-2001
LOCUS
DEFINITION Homo sapiens alpha-2A adrenergic receptor (ADRA2A) gene, complete cds.

ACCESSION AY032736
VERSION
KEYWORDS
SOURCE
Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 3612)
Human alpha-2A adrenergic receptor gene and the genotype of -1296 nucleotide and motlonsickness
Unpublished
2 (bases 1 to 3612)
Liu, L. and Yuan, L.
Direct Submission
Submitted (17-APR-2001) Key Laboratory of Molecular Biology,
General Hospital of Airforce, Fucheng Road No. 30, Beijing 100036,
China

JOURNAL
AUTHORS
TITLE

FEATURES

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RPGATGCTPAAGGGEERVGAASRMGRQNRKRTFVLAVVIGVVCWCPFFP
TYTLTAVGCSVPRTLKFFFWFGYCNSSINPIYITIFNHDFRAFKIILCRGDRKRIY

BASE COUNT 555 a 1278 c 1136 g 643 t
ORIGIN

Query Match 96.1%; Score 39.4; DB 9; Length 3612;
Best Local Similarity 97.6%; Pred. No. 0.027;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGGCACCAGCGAGCCCAAGGCTCTGGCCCCGAGCG 41
|||||
Db 2814 GGGGGCACCAGCGAGCCCAAGGCTCTGGCCCCGAGCG 2854

RESULT 9

AF284095 3653 bp mRNA linear PRI 27-MAR-2001
LOCUS
DEFINITION Homo sapiens alpha-2A adrenergic receptor mRNA, complete cds.

ACCESSION AF284095
VERSION
KEYWORDS
SOURCE
Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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/db_xref="taxon:9606"
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/gene="ADRA2A"
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/feature="G-protein coupled receptor"
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/protein_id="AAF91441.1"
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PGPAPAGPRDIDLDESSSDHAERPGRRERGRGKARASQVRCGDSLPR
RGPGATGCTPAGPGEERVGAAKASRMGRQNRKREFTFVLAVVIGVYVVCWPEFFF
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BASE COUNT      200 a      490 c      442 g      221 t
ORIGIN
Query Match      96.1%; Score 39.4; DB 9; Length 1353;
Best Local Similarity 97.6%; Pred. No. 0.032;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1 GGGGGCACCAGCGCGAGCCCAAGGCTGTGGCCCCGAGCG 41
          |||||
Db      730 GGGGGCACCAGCGCGAGCCCAAGGCTGTGGCCCCGAGCG 770
          |||||

RESULT 5
HUMADRA      1521 bp      DNA      linear      PRI 30-OCT-1994
DEFINITION   Human platelet alpha-2-adrenergic receptor gene, complete cds.
ACCESSION    M18415
VERSION      M18415.1 GI:178191
KEYWORDS     alpha-2-adrenergic receptor; alpha-adrenergic receptor.
SOURCE       Human (lambda-EMBL 3 library) DNA.
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 1521)
AUTHORS     Koblika,B.K., Matsui,H., Koblika,T.S., Yang-Peng,T.L., Francke,U.,
            Caron,M.G., Lefkowitz,R.J. and Regan,J.W.
TITLE        Cloning, sequencing, and expression of the gene coding for the
            human platelet alpha 2-adrenergic receptor
JOURNAL      Science 238 (4827), 650-656 (1987)
MEDLINE      88042789
PUBMED
FEATURES     source
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            /db_xref="taxon:9606"
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            PGPAPAGPRDIDLDESSSDHAERPGRRERGRGKARASQVRCGDSLPR
            RGPGATGCTPAGPGEERVGAAKASRMGRQNRKREFTFVLAVVIGVYVVCWPEFFF
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            CDS
            305 a      676 c      624 g      336 t
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ORIGIN      Chromosome 10q23-q25.
Query Match      96.1%; Score 39.4; DB 9; Length 1521;
Best Local Similarity 97.6%; Pred. No. 0.032;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1 GGGGGCACCAGCGCGAGCCCAAGGCTGTGGCCCCGAGCG 41
          |||||
Db      788 GGGGGCACCAGCGCGAGCCCAAGGCTGTGGCCCCGAGCG 828
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RESULT 6
LOCUS      AF262016      1941 bp      DNA      linear      PRI 22-AUG-2000
DEFINITION   Homo sapiens adrenergic receptor alpha-2A gene, complete cds.
ACCESSION    AF262016
VERSION      AF262016.2 GI:9864781
KEYWORDS
SOURCE       Homo sapiens.
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 1941)
AUTHORS     Beschli,M., and Agabiti Rosel,E.
TITLE        Direct Submission
JOURNAL      Submitted (29-APR-2000) Medical and Surgical Sciences, University
            of Brescia, Spedali Civilli di Brescia, Brescia I-25100, Italy
            3 (bases 1 to 1941)
            Castellano,M., Giacche',M., Rossi,F., Rivasdossi,F., Perani,C.,
            Beschli,M., and Agabiti Rosel,E.
            Direct Submission
            Submitted (22-AUG-2000) Medical and Surgical Sciences, University
            of Brescia, Spedali Civilli di Brescia, Brescia I-25100, Italy
            Sequence update by submitter
            On Aug 22, 2000 this sequence version replaced gi:9837145.
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            /db_xref="taxon:9606"
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            261
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            Geography 10:151-160, 1996"
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            RGPGATGCTPAGPGEERVGAAKASRMGRQNRKREFTFVLAVVIGVYVVCWPEFFF
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            "
            CDS
            305 a      676 c      624 g      336 t
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FEATURES Liggett, Stephen B. (US) ; Small, Kersten M. (US)
Location/Qualifiers
SOURCE 1.1350
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 199 a 489 c 442 g 220 t

ORIGIN

Query Match 100.0%; Score 41; DB 6; Length 1350;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGGCAGCGAGCGAGCGAGCGGCTGTGGCCCGAGCG 41
|||||

Db 730 GGGGGCAGCGAGCGAGCGAGCGGCTGTGGCCCGAGCG 770

RESULT 2
AF316894 1353 bp DNA linear PRI 07-FEB-2001
LOCUS Homo sapiens alpha 2A adrenergic receptor (ADRA2A) gene, complete
DEFINITION cds.
ACCESSION AF316894.1 GI:12698667
VERSION AF316894.1
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Small, K.M., Forbes, S.L., Brown, K.M. and Liggett, S.B.
TITLE 1 (bases 1 to 1353)
An asn to lys polymorphism in the third intracellular loop of the
human alpha 2A-adrenergic receptor imparts enhanced
agonist-promoted G1 coupling
J. Biol. Chem. 275 (49), 38518-38523 (2000)

JOURNAL MEDLINE 20556293
PUBMED 10948191

REFERENCE 2 (bases 1 to 1353)
Small, K.M., Forbes, S.L., Brown, K.M. and Liggett, S.B.
Direct Submission
Submitted (26-OCT-2000) Internal Medicine, University of
Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA

FEATURES Location/Qualifiers
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/organism="Homo sapiens"
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/note="compared to wild type sequence presented in GenBank
Accession Number AF281308; polymorphic sequence encodes
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BASE COUNT 200 a 489 c 443 g 221 t

ORIGIN

Query Match 100.0%; Score 41; DB 9; Length 1353;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGGCAGCGAGCGAGCGAGCGGCTGTGGCCCGAGCG 41
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Db 730 GGGGGCAGCGAGCGAGCGAGCGGCTGTGGCCCGAGCG 770

RESULT 3
AX350512 1350 bp DNA linear PAT 06-FEB-2002
LOCUS Sequence 24 from Patent WO0179561.
DEFINITION AX350512
ACCESSION AX350512
VERSION AX350512.1 GI:18616107
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Liggett, S.B. and Small, K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
Patent: WO 0179561-A 24 25-OCT-2001;
Liggett, Stephen B. (US) ; Small, Kersten M. (US)

FEATURES Location/Qualifiers
source 1.1350
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 199 a 490 c 441 g 220 t

ORIGIN

Query Match 96.1%; Score 39.4; DB 6; Length 1350;
Best Local Similarity 97.6%; Pred. No. 0.032; 1; Indels 0; Gaps 0;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGGGGCAGCGAGCGAGCGAGCGGCTGTGGCCCGAGCG 41
|||||

Db 730 GGGGGCAGCGAGCGAGCGAGCGGCTGTGGCCCGAGCG 770

RESULT 4
AF281308 1353 bp DNA linear PRI 05-DEC-2000
LOCUS Homo sapiens alpha 2A adrenergic receptor (ADRA2A) gene, complete
DEFINITION cds.
ACCESSION AF281308
VERSION AF281308.1 GI:9652209
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Small, K.M., Forbes, S.L., Brown, K.M. and Liggett, S.B.
TITLE 1 (bases 1 to 1353)
An asn to lys polymorphism in the third intracellular loop of the
human alpha 2A-adrenergic receptor imparts enhanced
agonist-promoted G1 coupling
J. Biol. Chem. 275 (49), 38518-38523 (2000)

JOURNAL MEDLINE 20556293
PUBMED 10948191

REFERENCE 2 (bases 1 to 1353)
Small, K.M., Forbes, S.L., Bridges, K.M. and Liggett, S.B.
Direct Submission
Submitted (22-JUN-2000) Internal Medicine, University of
Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA

FEATURES Location/Qualifiers
source 1.1353

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 12:29:07 : Search time 121.55 Seconds
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9816.632 Million cell updates/sec

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Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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5: gb_ov: *
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12: gb_sy: *
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14: gb_vt: *
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18: em_in: *
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25: em_ro: *
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27: em_un: *
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31: em_hcg_inv: *
32: em_hcg_other: *
33: em_hcg_mus: *
34: em_hcg_pln: *
35: em_hcg_rtd: *
36: em_hcg_mam: *
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	41	100.0	1350	6	AX350513	AX350513 Sequence
2	41	100.0	1353	6	AF316894	AF316894 Homo sapi
3	39.4	96.1	1350	6	AX350512	AX350512 Sequence
4	39.4	96.1	1353	9	AF281308	AF281308 Homo sapi
5	39.4	96.1	1351	9	HUMADRA	M18415 Human plate
6	39.4	96.1	1941	9	AF262016	AF262016 Homo sapi
7	39.4	96.1	3604	9	HUMADRA2R	M25333 Human alpha
8	39.4	96.1	3612	9	AY032736	AY032736 Homo sapi
9	39.4	96.1	3653	9	AF284095	AF284095 Homo sapi
10	39.4	96.1	204908	9	AL158163	AL158163 Human DNA
11	34.6	84.4	1728	4	P1GA2AR	J05652 Porcine alp
12	33	80.5	1454	10	MUSARP2ADB	M99377 Mouse alpha
13	33	80.5	1552	10	RNU79031	U79031 Rattus norv
14	33	80.5	204317	2	AC113491	AC113491 Mus muscu
15	31.4	76.6	2291	2	CEU25722	U25722 Cavia porce
16	31.4	76.6	2923	4	BTU79030	U79030 Bos taurus
17	29.8	72.7	1380	10	RATRG20	M62372 Rat alpha-2
18	25.8	62.9	163156	2	AP004085	AP004085 Oryza sat
19	25	61.0	1263	9	HSCA1	X65140 H. sapiens A
20	25	61.0	26621	2	AC020878	AC020878 Mus muscu
21	25	61.0	39407	2	AC010648	AC010648 Homo sapi
22	25	61.0	51146	2	AC090342	AC090342 Homo sapi
23	25	61.0	64711	2	AC114552	AC114552 Mus muscu
24	25	61.0	65069	2	AC112706	AC112706 Homo sapi
25	25	61.0	100000	9	AP000498	AP000498 Homo sapi
26	25	61.0	144494	9	AC099534	AC099534 Homo sapi
27	25	61.0	176291	2	AC023583	AC023583 Homo sapi
28	25	61.0	182224	9	AC093116	AC093116 Homo sapi
29	25	61.0	203230	2	AC026346	AC026346 Homo sapi
30	25	61.0	270000	2	AB026898	AB026898 Homo sapi
31	24.8	60.5	10543	1	AE007241	AE007241 Sinorhizo
32	24.8	60.5	315000	1	RME03644	AL603644 Rhizobium
33	24	58.5	8113	14	HSPB1CP4A	L14320 Bovine herp
34	24	58.5	13301	14	BHY1CGEN	AJ004801 Bovine he
35	24	58.5	135301	14	BHY1CGEN	AJ004801 Bovine he
36	24	58.5	147425	2	AC094576	AC094576 Rattus no
37	23.6	57.6	3036	6	AX056468	AX056468 Sequence
38	23.6	57.6	3514	9	AF100318	AF100318 Homo sapi
39	23.6	57.6	81740	9	AL663123	AL663123 Human DNA
40	23.4	57.1	4734	10	MNG1JR	X66367 M. musculus
41	23.4	57.1	5579	1	AH7276030	AJ276030 Aeromonas
42	23.4	57.1	7353	6	AX344974	AX344974 Sequence
43	23.4	57.1	7353	6	AX348495	AX348495 Sequence
44	23.4	57.1	82195	2	AC121221	AC121221 Rattus no
45	23.4	57.1	178418	2	AC013243	AC013243 Homo sapi

ALIGNMENTS

RESULT 1
AX350513
LOCUS AX350513 1350 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 25 from Patent WO0179561.
ACCESSION AX350513
VERSION AX350513.1 GI:18616108
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Liggett, S.B. and Small, K.M.
Alpha-2 adrenergic receptor polymorphisms
Patent: WO 0179561-A 25 25-OCT-2001;
JOURNAL

; PRIOR FILING DATE: 2000-02-29
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 3018
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-802-127-6

Query Match 53.2%; Score 21.8; DB 10; Length 3018;
 Best Local Similarity 78.8%; Pred. No. 62;
 Matches 26; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CGGCTCCAGGCCCCCGCAGACCGGCGGT 33
 ||| ||||| ||||| ||| ||| |||
 Db 1339 CGGCTCCAGGCCCCCGCAGAGCGCGCATAGT 1307

RESULT 14
 US-09-802-127-4/C
 ; Sequence 4, Application US/09802127
 ; Patent No. US20020045212A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Glucksmann, Maria Alexandra
 ; APPLICANT: Meyers, Rachel
 ; TITLE OF INVENTION: No. US20020045212A1 Human GTPase Activator Proteins
 ; FILE REFERENCE: 035800/158994
 ; CURRENT APPLICATION NUMBER: US/09/802,127
 ; CURRENT FILING DATE: 2001-02-23
 ; PRIOR APPLICATION NUMBER: 60/185,611
 ; PRIOR FILING DATE: 2000-02-29
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 3391
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (78)...(3095)
 US-09-802-127-4

Query Match 53.2%; Score 21.8; DB 10; Length 3391;
 Best Local Similarity 78.8%; Pred. No. 61;
 Matches 26; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CGGCTCCAGGCCCCCGCAGACCGGCGGT 33
 ||| ||||| ||||| ||| ||| |||
 Db 1416 CGGCTCCAGGCCCCCGCAGAGCGCGCATAGT 1384

RESULT 15
 US-09-764-868-1501/C
 ; Sequence 1501, Application US/09764868
 ; Patent No. US20020168711A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PT232
 ; CURRENT APPLICATION NUMBER: US/09/764,868
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - refer to PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 1510
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 1501
 ; LENGTH: 5968
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-764-868-1501

Query Match 53.2%; Score 21.8; DB 9; Length 5968;
 Best Local Similarity 78.8%; Pred. No. 58;
 Matches 26; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CGGCTCCAGGCCCCCGCAGACCGGCGGT 33
 ||| ||||| ||||| ||| ||| |||
 Db 225 CGGCTCCAGGCCCCCGCAGAGCGCGCATAGT 193

Search completed: February 13, 2003, 07:50:17
 Job time : 9.82052 secs

LENGTH: 1675
TYPE: DNA
ORGANISM: Homo sapiens
US-09-808-387-21

Query Match 53.2%; Score 21.8; DB 10; Length 1675;
Best Local Similarity 70.7%; Pred. No. 66;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 CGGCTCTCAGGCGCCGAGACCGGCGTCCCGGGG 41
Db 1427 CGGCGCCGAGCTCCCGCTGAGACCCCGGCTCCCGGTG 1467

RESULT 11
US-09-793-306-162/c
Sequence 162, Application US/09793306
Patent No. US20020098200A1
GENERAL INFORMATION:
APPLICANT: Campos-Neto, Antonio
APPLICANT: Skelky, Yasir
APPLICANT: Owendale, Pamela
APPLICANT: Jen, Shyian
APPLICANT: Lodes, Michael
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
FILE REFERENCE: 014058-008740US
CURRENT APPLICATION NUMBER: US/09/793,306
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/185,037
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 60/223,828
PRIOR FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 164
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 162
LENGTH: 1863
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: MO-2 (aspartokinase)
NAME/KEY: CDS
LOCATION: (1)..(1266)
OTHER INFORMATION: MO-2
US-09-793-306-162

Query Match 53.2%; Score 21.8; DB 10; Length 1863;
Best Local Similarity 70.7%; Pred. No. 65;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 CGGCTCTCAGGCGCCGAGACCGGCGGTCGCGGGG 41
Db 1111 CGGCGCCGAGCTCCCGCTGAGACCCCGGGG 1071

RESULT 12
US-09-796-753-31
Sequence 31, Application US/09796753
Publication No. US20030027998A1
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean A.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-227-999
CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 09/223,094
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/224,246

PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/259,388
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/122,458
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 09/312,359
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/236,536
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 09/342,687
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 09/345,464
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/365,164
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 09/399,723
PRIOR FILING DATE: 1999-09-20
PRIOR APPLICATION NUMBER: 09/409,634
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 09/471,179
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 09/474,071
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/474,072
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/514,010
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: 09/516,745
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/572,002
PRIOR FILING DATE: 2000-05-14
PRIOR APPLICATION NUMBER: 09/597,993
PRIOR FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 09/599,596
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/630,334
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 09/606,565
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/606,317
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/665,666
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 09/677,751
PRIOR FILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 31
LENGTH: 2576
TYPE: DNA
ORGANISM: Homo sapiens
US-09-796-753-31

Query Match 53.2%; Score 21.8; DB 9; Length 2576;
Best Local Similarity 70.7%; Pred. No. 63;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 CGGCTCTCAGGCGCCGAGACCGGCGGTCGCGGGG 41
Db 154 CGGCTCTGTTGTCGCGCGCCCGGCGGCTCCCGCGG 194

RESULT 13
US-09-802-127-6/c
Sequence 6, Application US/09802127
Patent No. US20020045212A1
GENERAL INFORMATION:
APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: NO. 20020045212A1 Human GTPase Activator Proteins
FILE REFERENCE: 035800/158994
CURRENT APPLICATION NUMBER: US/09/802,127
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185,611

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, RESULT 10
, US-09-808-387-21
, Sequence 21, Application US/09808387
, Patent No. US20020132293A1
, GENERAL INFORMATION:
, APPLICANT: Kaia Palm
, APPLICANT: Toniis Timmusk
, APPLICANT: Cemlines Research
, TITLE OF INVENTION: MAMMALIAN NEURALIZED FAMILY OF
, TITLE OF INVENTION: TRANSCRIPTION REGULATORS AND USES THEREFOR
, FILE REFERENCE: CEMNES.001A
, CURRENT APPLICATION NUMBER: US/09/808.387
, CURRENT FILING DATE: 2001-03-14
, NUMBER OF SEQ ID NOS: 48
, SOFTWARE: FastSeq for Windows Version 4.0
, SEQ ID NO 21

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;; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
;; FILE REFERENCE: Bb116 US CIP
;; CURRENT APPLICATION NUMBER: US/09/931,457A
;; CURRENT FILING DATE: 2002-02-22
;; PRIOR APPLICATION NUMBER: 09/424,976
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: 60/065,385
;; PRIOR FILING DATE: 1997-11-12
;; PRIOR APPLICATION NUMBER: 60/049,406
;; PRIOR FILING DATE: 1997-06-12
;; NUMBER OF SEQ ID NOS: 72
;; SOFTWARE: Microsoft Office 97
;; SEQ ID NO 44
;; LENGTH: 1402
;; TYPE: DNA
;; ORGANISM: Oryza sativa
US-09-931-457A-44

Query Match 53.7%; Score 22; DB 9; Length 1402;
Best Local Similarity 73.7%; Pred. No. 58;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 4 CCTCCAGGCCCCGAGACCCGAGCGGTCCCGGGG 41
| | | | | | | | | | | | | | | | | | | | | |
Db 303 CCTCCAGGACCTCGCCGCGCGCGCGCTTCGACGGG 340

RESULT 3
US-09-815-242-7695/c
; Sequence 7695, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELTRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7695
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; NAME/KEY: CDS
; LOCATION: (1)...(1998)
US-09-815-242-7695

Query Match 53.7%; Score 22; DB 10; Length 1998;
Best Local Similarity 73.7%; Pred. No. 56;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 GCGTCCAGGCCCCGAGACCCGAGCGGTCCCGGG 40
| | | | | | | | | | | | | | | | | | | | | |
Db 1513 GCGTCCAGGCGACCGCGACTGACCGGTGCGCGGG 1476

RESULT 4
US-10-044-090-592
; Sequence 592, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 592
; LENGTH: 3006
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 1683849CB1
US-10-044-090-592

Query Match 53.7%; Score 22; DB 12; Length 3006;
Best Local Similarity 73.7%; Pred. No. 54;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 4 CCTCCAGGCCCCGAGACCCGAGCGGTCCCGGGG 41
| | | | | | | | | | | | | | | | | | | | | |
Db 1418 CCTCCAGGACCCCGCACTGCGAGCGCGCGCGGAG 1455

RESULT 5
US-09-764-877-3220/c
; Sequence 3220, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3220
; LENGTH: 19616
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3220

Query Match 53.7%; Score 22; DB 10; Length 19616;
Best Local Similarity 73.7%; Pred. No. 44;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 CGGCTTCAGGCGCGCGAGACCCGAGCGGTCCCGG 38
| | | | | | | | | | | | | | | | | | | | | |
Db 13958 CGGCTTCAGGCGCGCGAGACCTATTGGCGCGCTTCGG 13921

RESULT 6
US-09-854-133-304
; Sequence 304, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.

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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 424239 seqs, 25461826 residues

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Minimum DB seq length: 0

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Maximum Match 100%
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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the chance being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25.2	61.5	7011	12 US-10-033-026-9	Sequence 9, Appl1
2	22	53.7	1402	9 US-09-931-457A-44	Sequence 44, Appl1
3	22	53.7	1998	10 US-09-815-242-7695	Sequence 7695, Ap
4	22	53.7	3006	12 US-10-044-090-592	Sequence 592, App
5	22	53.7	13616	10 US-09-764-877-3220	Sequence 3220, Ap
6	21.8	53.2	441	9 US-09-854-133-504	Sequence 304, App
7	21.8	53.2	441	10 US-09-738-973-304	Sequence 304, App
8	21.8	53.2	955	10 US-09-808-387-25	Sequence 25, Appl1
9	21.8	53.2	1129	10 US-09-808-387-23	Sequence 23, Appl1
10	21.8	53.2	1675	10 US-09-808-387-21	Sequence 21, Appl1
11	21.8	53.2	1863	10 US-09-793-306-162	Sequence 162, App
12	21.8	53.2	2576	9 US-09-796-753-31	Sequence 31, Appl1
13	21.8	53.2	3018	10 US-09-802-127-6	Sequence 6, Appl1
14	21.8	53.2	3391	10 US-09-802-127-4	Sequence 4, Appl1
15	21.8	53.2	5968	9 US-09-764-868-1501	Sequence 1501, Appl1
16	21.6	52.7	5222	10 US-09-416-384A-1	Sequence 1, Appl1
17	21.6	52.7	5566	10 US-09-416-384A-4	Sequence 4, Appl1
18	21.4	52.2	64	9 US-10-057-940-10	Sequence 10, Appl1
19	21.4	52.2	865	10 US-09-804-615-1	Sequence 1, Appl1

c 20	21.4	52.2	1274	10 US-09-919-172-93	Sequence 93, Appl1
c 21	21.2	51.7	1667	9 US-10-078-770-81	Sequence 81, Appl1
c 22	21.2	51.7	2048	9 US-10-174-590-533	Sequence 533, App
c 23	21.2	51.7	2048	9 US-10-176-758-533	Sequence 533, App
c 24	21.2	51.7	2048	9 US-10-175-737-533	Sequence 533, App
c 25	21.2	51.7	2048	9 US-10-173-706-533	Sequence 533, App
c 26	21.2	51.7	2048	9 US-10-176-728-533	Sequence 533, App
c 27	21.2	51.7	2048	9 US-10-175-732-533	Sequence 533, App
c 28	21.2	51.7	2048	9 US-10-176-482-533	Sequence 533, App
c 29	21.2	51.7	2048	9 US-10-176-757-533	Sequence 533, App
c 30	21.2	51.7	2048	9 US-10-176-913-533	Sequence 533, App
c 31	21.2	51.7	2048	9 US-10-180-552-533	Sequence 533, App
c 32	21.2	51.7	2048	9 US-10-180-557-533	Sequence 533, App
c 33	21.2	51.7	2048	9 US-10-173-700-533	Sequence 533, App
c 34	21.2	51.7	2048	9 US-10-174-572-533	Sequence 533, App
c 35	21.2	51.7	2048	9 US-10-174-579-533	Sequence 533, App
c 36	21.2	51.7	2048	9 US-10-174-582-533	Sequence 533, App
c 37	21.2	51.7	2048	9 US-10-174-588-533	Sequence 533, App
c 38	21.2	51.7	2048	9 US-10-175-739-533	Sequence 533, App
c 39	21.2	51.7	2048	9 US-10-175-740-533	Sequence 533, App
c 40	21.2	51.7	2048	9 US-10-175-743-533	Sequence 533, App
c 41	21.2	51.7	2048	9 US-10-176-488-533	Sequence 533, App
c 42	21.2	51.7	2048	9 US-10-176-492-533	Sequence 533, App
c 43	21.2	51.7	2048	9 US-10-176-747-533	Sequence 533, App
c 44	21.2	51.7	2048	9 US-10-176-750-533	Sequence 533, App
c 45	21.2	51.7	2048	9 US-10-176-985-533	Sequence 533, App

ALIGNMENTS

```

RESULT 1
US-10-033-026-9/c
; Sequence 9, Application US/10033026
; Patent No. US20020147309A1
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/10/033,026
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/268,163
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: US 60/077,901
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 7011
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..7008
; US-10-033-026-9

Query Match      61.5%; Score 25.2; DB 12; Length 7011;
Best Local Similarity 78.9%; Pred. No. 5.1;
Matches 30; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CGGCTCCAGAGCCCGCCGACACCCGAGCGGCTCCCG 38
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Db      88 CGGCGCCCGCGCGCCCGCCGCGGACCCGCTCCCGG 51

RESULT 2
US-09-931-457A-44
; Sequence 44, Application US/09931457A
; Patent No. US20020157132A1
; GENERAL INFORMATION:
; APPLICANT: Falco, S. Carl
; APPLICANT: Allen, Stephen M.

```

CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07784
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: THIES, J. ERIC
REGISTRATION NUMBER: 35,382
REFERENCE/DOCKET NUMBER: 19132
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3904
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1150 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US95-07784-10

Query Match 53.7%; Score 22; DB 5; Length 1150;
Best Local Similarity 73.7%; Pred. No. 74;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGGCTCCAGAGGCCCGAGACCCGAGCGGTCGCCG 38
DB 340 CGGCATCTCGGGCCGGGTGGACACTGCGGCTCCG 377

RESULT 14
US-09-382-106-1/c
Sequence 1, Application US/09382106
Patent No. 6221631
GENERAL INFORMATION:
APPLICANT: Huang, Jiansheng
APPLICANT: Jiang, Xianhe
APPLICANT: McDevitt, Damien
APPLICANT: Van Horn, Stephanie
TITLE OF INVENTION: kTSA
FILE REFERENCE: GM10236
CURRENT APPLICATION NUMBER: US/09/382,106
CURRENT FILING DATE: 1999-08-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1998
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-382-106-1

Query Match 53.7%; Score 22; DB 4; Length 1998;
Best Local Similarity 73.7%; Pred. No. 70;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTTCAGAGGCCCGAGACCCGAGCGGTCGCCG 40
DB 1513 GCTTCAGAGCCCGCGAGCTCGACCGCTCGCGCGG 1476

RESULT 15
US-08-592-126-102
Sequence 102, Application US/08592126

Patent No. 5821091
GENERAL INFORMATION:
APPLICANT: Gregory Doljanov
TITLE OF INVENTION: Transcripts Encoding Immunomodulatory
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dellinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,126
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 2200 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: G89con.seq
US-08-592-126-102

Query Match 53.2%; Score 21.8; DB 1; Length 2200;
Best Local Similarity 70.7%; Pred. No. 79;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 CGGCTTCAGAGGCCCGAGACCCGAGCGGTCGCCG 41
DB 144 CAGCTTCGGGCGGCCCGAGCCCGCGACGCGAGTCGCGCGG 184

Search completed: February 13, 2003, 07:47:18
Job time : 22.1902 secs

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; NAME: THIES, J. ERIC
; REGISTRATION NUMBER: 35,382
; REFERENCE/DOCKET NUMBER: 19132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3904
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 783 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-08-264-861A-11

Query Match          53.7%; Score 22; DB 1; Length 783;
Best Local Similarity 73.7%; Pred. No. 78;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGGCTCCAGGGCCCCGAGACCGGCGGTCCCG 38
Db 279 CGGCATCTCGGGCGGGTGACAGTGGCGGTCTCCG 316

RESULT 11
PCT-US95-07784-11
; Sequence 11, Application PC/TUS9507784
; GENERAL INFORMATION:
; APPLICANT: MOTAMEDI, HAIDEH
; APPLICANT: SHAITEE, ALI
; TITLE OF INVENTION: EXPRESSION CASSETTES USEFUL IN
; TITLE OF INVENTION: CONSTRUCTION OF INTEGRATIVE AND REPLICATIVE EXPRESSION
; TITLE OF INVENTION: VECTORS FOR STREPTOMYCES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: J. ERIC THIES
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07784
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: THIES, J. ERIC
; REGISTRATION NUMBER: 35,382
; REFERENCE/DOCKET NUMBER: 19132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3904
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 783 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
PCT-US95-07784-11

Query Match          53.7%; Score 22; DB 5; Length 783;
Best Local Similarity 73.7%; Pred. No. 78;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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QY 1 CGGCTCCAGGGCCCCGAGACCGGCGGTCCCG 38
Db 279 CGGCATCTCGGGCGGGTGACAGTGGCGGTCTCCG 316

RESULT 12
US-08-264-861A-10
; Sequence 10, Application US/08264861A
; Patent No. 5622866
; GENERAL INFORMATION:
; APPLICANT: MOTAMEDI, HAIDEH
; APPLICANT: SHAITEE, ALI
; TITLE OF INVENTION: EXPRESSION CASSETTES USEFUL IN
; TITLE OF INVENTION: CONSTRUCTION OF INTEGRATIVE AND REPLICATIVE EXPRESSION
; TITLE OF INVENTION: VECTORS FOR STREPTOMYCES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: J. ERIC THIES
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,861A
; FILING DATE: 23-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: THIES, J. ERIC
; REGISTRATION NUMBER: 35,382
; REFERENCE/DOCKET NUMBER: 19132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3904
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1150 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-08-264-861A-10

Query Match          53.7%; Score 22; DB 1; Length 1150;
Best Local Similarity 73.7%; Pred. No. 74;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGGCTCCAGGGCCCCGAGACCGGCGGTCCCG 38
Db 340 CGGCATCTCGGGCGGGTGACAGTGGCGGTCTCCG 377

RESULT 13
PCT-US95-07784-10
; Sequence 10, Application PC/TUS9507784
; GENERAL INFORMATION:
; APPLICANT: MOTAMEDI, HAIDEH
; APPLICANT: SHAITEE, ALI
; TITLE OF INVENTION: EXPRESSION CASSETTES USEFUL IN
; TITLE OF INVENTION: CONSTRUCTION OF INTEGRATIVE AND REPLICATIVE EXPRESSION
; TITLE OF INVENTION: VECTORS FOR STREPTOMYCES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: J. ERIC THIES
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
```


Query Match 56.1%; Score 23; DB 2; Length 4692;
Best Local Similarity 74.4%; Pred. No. 32;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 GCCTCCAGGGCCCGCAGACCGGCGGTCCCGGGG 41
DB 2146 GGCACCCGGCCCTGCAGAGCTGGGCGCCCGCCTGGG 2184

RESULT 8
US-09-225-170-1
Sequence 1, Application US/09225170
Patent No. 6017763
GENERAL INFORMATION:
APPLICANT: Stephens, Len
APPLICANT: Hawkins, Phillip Thomas
APPLICANT: Braedelmann, Sylvia
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,170
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,917
FILING DATE: 15-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8549-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4692 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-225-170-1

Query Match 56.1%; Score 23; DB 3; Length 4692;
Best Local Similarity 74.4%; Pred. No. 32;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 GCCTCCAGGGCCCGCAGACCGGCGGTCCCGGGG 41
DB 2146 GGCACCCGGCCCTGCAGAGCTGGGCGCCCGCCTGGG 2184

RESULT 9
US-09-247-155-148/c
Sequence 148, Application US/09247155A
Patent No. 6312922
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclet, Aymeric
APPLICANT: Bougueleret, Lydie

TITLE OF INVENTION: Complementary DNAs
FILE REFERENCE: GENSET.021A
CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
SEQ ID NO 148
LENGTH: 949
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 100..351
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 100..207
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 4.1999980926514
OTHER INFORMATION: seq CLAVSWAAGCHG/AG
FEATURE:
NAME/KEY: polyA_site
LOCATION: 940..949
FEATURE:
NAME/KEY: misc_feature
LOCATION: 745
OTHER INFORMATION: n=a, g, c or t
US-09-247-155-148

Query Match 54.6%; Score 22.4; DB 4; Length 949;
Best Local Similarity 72.5%; Pred. No. 58;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 2 GGCCTCCAGGGCCCGCAGACCGGCGGTCCCGGGG 41
DB 254 GGCCTCCAGGGCCCTGCACACCTAGCGGCGCTGCTGTG 215

RESULT 10
US-08-264-861A-11
Sequence 11, Application US/08264861A
Patent No. 5622866
GENERAL INFORMATION:
APPLICANT: MOTAMED, HAIDEN
APPLICANT: SHAFIE, ALI
TITLE OF INVENTION: EXPRESSION CASSETTES USEFUL IN
TITLE OF INVENTION: CONSTRUCTION OF INTEGRATIVE AND REPLICATIVE EXPRESSION
NUMBER OF SEQUENCES: 13
VECTORS FOR STREPTOMYCES
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. ERIC THIES
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,861A
FILING DATE: 23-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

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; Patent No. 5859201
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,629
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/672,211
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Halliuh, Albert P.
; REGISTRATION NUMBER: 25,277
; REFERENCE/DOCKET NUMBER: 8549-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-3660
; TELEFAX: (415)854-3694
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
; US-08-972-629-1

Query Match          56.1%; Score 23; DB 2; Length 4692;
Best Local Similarity 74.4%; Pred. No. 32;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy 3 GCCTCCAGGGCCCCGACGCCGCGGTCCCGGGG 41
Db 2146 GGCACCCGGGCGCTGCGAGAGCTGGCGCGCCCTGSG 2184

RESULT 6
US-08-972-630-1
; Sequence 1, Application US/08972630
; Patent No. 5869271
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip T.
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,630
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/672,211
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Halliuh, Albert P.
; REGISTRATION NUMBER: 25,277
; REFERENCE/DOCKET NUMBER: 8549-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-3660
; TELEFAX: (415)854-3694
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
; US-08-972-630-1

Query Match          56.1%; Score 23; DB 2; Length 4692;
Best Local Similarity 74.4%; Pred. No. 32;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy 3 GCCTCCAGGGCCCCGACGCCGCGGTCCCGGGG 41
Db 2146 GGCACCCGGGCGCTGCGAGAGCTGGCGCGCCCTGSG 2184

RESULT 7
US-08-672-211-1
; Sequence 1, Application US/08672211
; Patent No. 5874273
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip T.
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,211
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Halliuh, Albert P.
; REGISTRATION NUMBER: 25,277
; REFERENCE/DOCKET NUMBER: 8549-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-3660
; TELEFAX: (415)854-3694
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
; US-08-672-211-1
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/153,599A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: FER2159P0041US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2299 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-153-599A-1

Query Match
Best Local Similarity 61.0%; Score 25; DB 4; Length 2299;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGGCTCCAGAGCGCCGCGAGCCGCGCGTCCCGCGGG 41
Db 1601 GCGCTCCAGCTTCGAGAGAGACTGTCGCGGTCTCGGGG 1641

RESULT 3
US-08-916-917-1
; Sequence 1, Application US/08916917
; Patent No. 5856132
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip Thomas
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,917
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/672,211
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel B
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 8549-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
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```

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-916-917-1

Query Match
Best Local Similarity 56.1%; Score 23; DB 2; Length 4692;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCGTCAGGCGCCCGCAGACCGGCGGTCGCCGGGG 41
Db 2146 GCGACCGGGGCGCTCGAGAGCTGGGCGCGCCCGCTGGG 2184

RESULT 4
US-08-972-631-1
; Sequence 1, Application US/08972631
; Patent No. 5856133
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip T.
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,631
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/672,211
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,277
; REFERENCE/DOCKET NUMBER: 8549-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-3660
; TELEFAX: (415)854-3694
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; US-08-972-631-1

Query Match
Best Local Similarity 56.1%; Score 23; DB 2; Length 4692;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCGTCAGGCGCCCGCAGACCGGCGGTCGCCGGGG 41
Db 2146 GCGACCGGGGCGCTCGAGAGCTGGGCGCGCCCGCTGGG 2184

RESULT 5
US-08-972-629-1
; Sequence 1, Application US/08972629
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2003, 06:16:02 ; Search time 2.19024 Seconds
(without alignments)
5740.812 Million cell updates/sec

Title: US-09-636-259b-1_COPY_730_770

Perfect score: 1 cggcctccagggcccgccag.....cccgagcgctcccgagg 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	25.2	61.5	7011	4	US-09-268-163-9	Sequence 9, Appl1
2	25	61.0	2299	4	US-09-153-599A-1	Sequence 1, Appl1
3	23	56.1	4692	2	US-08-916-917-1	Sequence 1, Appl1
4	23	56.1	4692	2	US-08-972-631-1	Sequence 1, Appl1
5	23	56.1	4692	2	US-08-972-629-1	Sequence 1, Appl1
6	23	56.1	4692	2	US-08-972-630-1	Sequence 1, Appl1
7	23	56.1	4692	2	US-08-672-211-1	Sequence 1, Appl1
8	23	56.1	4692	2	US-09-225-170-1	Sequence 1, Appl1
C 9	22.4	54.6	949	4	US-09-247-155-148	Sequence 148, Appl1
10	22	53.7	783	5	US-08-264-861A-11	Sequence 11, Appl1
11	22	53.7	783	5	PCT-US95-07784-11	Sequence 11, Appl1
12	22	53.7	1150	1	US-08-264-861A-10	Sequence 10, Appl1
13	22	53.7	1150	5	PCT-US95-07784-10	Sequence 10, Appl1
C 14	22	53.7	1150	5	US-09-382-106-1	Sequence 10, Appl1
15	21.8	53.2	2200	1	US-08-592-126-102	Sequence 102, Appl1
16	21.8	53.2	4403765	4	US-09-103-840A-2	Sequence 2, Appl1
17	21.4	52.2	1866	4	US-09-224-048A-1	Sequence 1, Appl1
C 18	21.4	52.2	3411	4	US-08-890-865A-3	Sequence 3, Appl1
19	21.4	52.2	4403765	4	US-09-103-840A-2	Sequence 2, Appl1
C 20	21.2	51.7	4771	3	US-08-840-062-3	Sequence 3, Appl1
21	20.8	50.7	436	4	US-09-397-787-257	Sequence 257, Appl1
22	20.8	50.7	835	6	5223425-7	Patent No. 5223425
C 23	20.8	50.7	1120	4	US-08-586-165-1	Sequence 1, Appl1
24	20.8	50.7	1290	4	US-09-149-476-81	Sequence 81, Appl1
C 25	20.8	50.7	2537	6	5168051-1	Patent No. 5168051
26	20.8	50.7	2745	4	US-09-661-753-28	Sequence 28, Appl1
C 27	20.8	50.7	2745	5	PCT-US94-03705-3	Sequence 3, Appl1

28	20.8	50.7	2838	4	US-08-246-489-1 Sequence 1, Appl 1
29	20.8	50.7	3937	3	US-08-586-165-8 Sequence 8, Appl 1
30	20.8	50.7	4040	2	US-08-685-118-1 Sequence 1, Appl 1
31	20.8	50.7	4040	2	US-08-915-495-1 Sequence 1, Appl 1
32	20.8	50.7	4040	2	US-08-914-520-1 Sequence 1, Appl 1
33	20.8	50.7	4411529	4	US-09-103-840A-1 Sequence 36, Appl 1
34	20.6	50.2	336	2	US-08-577-492-36 Sequence 36, Appl 1
35	20.6	50.2	336	4	US-09-079-630-36 Sequence 27, Appl 1
36	20.6	50.2	4233	4	US-09-056-105-27 Sequence 14, Appl 1
37	20.4	49.8	2470	1	US-07-745-206A-14 Sequence 12, Appl 1
38	20.4	49.8	2470	1	US-08-311-363-14 Sequence 12, Appl 1
39	20.4	49.8	5467	2	US-07-745-206A-12 Sequence 7, Appl 1
40	20.4	49.8	5467	2	US-08-311-363-12 Sequence 7, Appl 1
41	20.4	49.8	6854	4	US-08-194-905-7 Sequence 8, Appl 1
42	20.4	49.8	7175	1	US-08-455-543A-8 Sequence 8, Appl 1
43	20.4	49.8	7175	2	US-08-193-078B-8 Sequence 8, Appl 1
44	20.4	49.8	7175	2	US-08-223-305C-8 Sequence 8, Appl 1
45	20.4	49.8	7175	2	US-08-149-097D-8 Sequence 8, Appl 1

ALIGNMENTS

RESULT 1
US-09-268-163-9/c
Sequence 9, Application US/09268163B
Patent No. 6353091
GENERAL INFORMATION:
APPLICANT: Lipscombe, Diane
FILE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
FILE REFERENCE: B1055/7000
CURRENT APPLICATION NUMBER: US/09/268,163B
EARLIER APPLICATION NUMBER: US 60/077,901
EARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 7011
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: CDS
LOCATION: 1..7008
US-09-268-163-9

Query Match 61.5% Score 25.2; DB 4; Length 7011;
Best Local Similarity 78.9% Pred. No. 7;
Matches 30; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CGGCCTCCAGGCGCCGCGAGACCGGCGGTCGCCG 38
DB 88 CGGCGCCGCGCGCCGCGCCGCGCGAGCCGCGTCGCCG 51

RESULT 2
US-09-153-599A-1
Sequence 1, Application US/09153599A
Patent No. 6420177
GENERAL INFORMATION:
APPLICANT: Weber, J. Mark
FILE OF INVENTION: Method for Strain Improvement of
TITLE OF INVENTION: Erythromycin Producing Bacterium
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Rockey, Milanow & Katz, Ltd.
STREET: 180 N. Stetson Avenue, 2 Prudential Plaza
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601

ORIGIN

Query Match 63.9% Score 26.2; DB 12; Length 765;
Best Local Similarity 90.3%; Pred. No. 5e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGCCTCCAGGGCCCCGAGACCCGAGCGCG 32
|||||
Db 74 GGCCTCCAGGGCCCCGAGACCCGAGCGCG 44

RESULT 14
BF343380 779 bp mRNA linear EST 22-NOV-2000
LOCUS 602014679F1 NCI_CGAP_Brn64 Homo sapiens CDNA clone IMAGE:4150483
DEFINITION 5', mRNA sequence.
ACCESSION BF343380
VERSION BF343380.1 GI:11290651
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 779)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@b-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM9413 row: n column: 20
High quality sequence stop: 643.
Location/Qualifiers
1. 779
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="4150483"
/clone_lib="NCI_CGAP_Brn64"
/tissue_type="g1oblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site: 1; NotI;
Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 166 a 180 c 258 g 174 t
ORIGIN

Query Match 63.9% Score 26.2; DB 12; Length 779;
Best Local Similarity 90.3%; Pred. No. 5e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGCCTCCAGGGCCCCGAGACCCGAGCGCG 32
|||||
Db 63 GGCCTCCAGGGCCCCGAGACCCGAGCGCG 33

RESULT 15
BM083862 780 bp mRNA linear EST 16-NOV-2001
LOCUS imagec6_2000/sj0343bdf42.x2 NIH-MGC_20 Homo sapiens CDNA clone
DEFINITION IMAGE:3543837 5', mRNA sequence.
ACCESSION BM083862
VERSION BM083862.1 GI:16972621
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 780)
AUTHORS Kale,P.I., Harsch,T.J., Folta,P.A., Nelson,D.O., Sanders,C.G. and Prange,C.K.
TITLE The I.M.A.G.E. Consortium quality control effort: clone
JOURNAL resequencing for verification
COMMENT Unpublished (2001)
Contact: Prange CK
The I.M.A.G.E. Consortium
Lawrence Livermore National Laboratory
Livermore, CA, USA
Email: help@image.llnl.gov
This read has been produced as part of the I.M.A.G.E. Consortium
quality control effort. High quality sequence is defined as having
100 or more base pairs with a phred quality value of 20 or greater,
where a sliding window of 4 base pairs with a phred quality value
of 15 or greater marks the beginning and end of the sequence. For
information on obtaining this clone, please contact
info@image.llnl.gov.
Plate: LDCM238 row: a column: 22
Seq primer: -21m13
High quality sequence stop: 780.
Location/Qualifiers
1. 780
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="3543837"
/clone_lib="NIH-MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site: 1; XhoI; Site: 2;
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(g). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 173 a 167 c 264 g 172 t
ORIGIN

Query Match 63.9% Score 26.2; DB 13; Length 780;
Best Local Similarity 90.3%; Pred. No. 5e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGCCTCCAGGGCCCCGAGACCCGAGCGCG 32
|||||
Db 93 GGCCTCCAGGGCCCCGAGACCCGAGCGCG 63

Search completed: February 15, 2003, 18:02:50
Job time : 85.5273 secs

SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 687)
AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM8452 row: f column: 11
High quality sequence start: 2
High quality sequence stop: 614.
Location/Qualifiers
1..687

FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:486891"
/clone_lib="NIH-MGC_49"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pORF7; Site.1: XhoI; Site.2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(6). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH-MGC
Library."

BASE COUNT 181 a 162 c 255 g 159 t
ORIGIN

Query Match 63.9%; Score 26.2; DB 12; Length 757;
Best Local Similarity 90.3%; Pred. No. 5e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGCTCCAGGGCCCGCAGACCCGAGCCGG 32
|||||
Db 58 GGCTCCAGGGCCCGCAGACCCGAGCCGG 28

RESULT 13
LOCUS BG716838 765 bp mRNA linear EST 08-MAY-2001
DEFINITION 602677955F1 NIH_MGC_96 Homo sapiens CDNA clone IMAGE:4801333 5',
mRNA sequence.
ACCESSION BG716838
VERSION BG716838.1 GI:13996025
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 757)
AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM10693 row: m column: 14
High quality sequence stop: 755.
Location/Qualifiers
1..765

FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4801333"
/clone_lib="NIH-MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescriptPR (modified
pBluescript KS+); Site.1: BamHI; Site.2: SalI-XhoI (gtcag
); Oligo-dT primed using primer 5'-TTTCTTTTCTTTTCTT-3',
size-selected for average insert size 2.3 kb and
normalized to R0T 5. This is a primary library enriched
for full-length clones and constructed using the
cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT 168 a 169 c 261 g 167 t

SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 687)
AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM1739 row: p column: 16
High quality sequence stop: 615.
Location/Qualifiers
1..757

FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4801333"
/clone_lib="NIH-MGC_49"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pORF7; Site.1: XhoI; Site.2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(6). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH-MGC
Library."

BASE COUNT 181 a 162 c 255 g 159 t
ORIGIN

Query Match 63.9%; Score 26.2; DB 12; Length 757;
Best Local Similarity 90.3%; Pred. No. 5e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGCTCCAGGGCCCGCAGACCCGAGCCGG 32
|||||
Db 58 GGCTCCAGGGCCCGCAGACCCGAGCCGG 28

RESULT 13
LOCUS BG716838 765 bp mRNA linear EST 08-MAY-2001
DEFINITION 602677955F1 NIH_MGC_96 Homo sapiens CDNA clone IMAGE:4801333 5',
mRNA sequence.
ACCESSION BG716838
VERSION BG716838.1 GI:13996025
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 757)
AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM10693 row: m column: 14
High quality sequence stop: 755.
Location/Qualifiers
1..765

FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4801333"
/clone_lib="NIH-MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescriptPR (modified
pBluescript KS+); Site.1: BamHI; Site.2: SalI-XhoI (gtcag
); Oligo-dT primed using primer 5'-TTTCTTTTCTTTTCTT-3',
size-selected for average insert size 2.3 kb and
normalized to R0T 5. This is a primary library enriched
for full-length clones and constructed using the
cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT 168 a 169 c 261 g 167 t

plate: LLCM198 row: f column: 16
High quality sequence stop: 607.
Location/Qualifiers
1. .634

FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3528591"
/clone_lib="NIH_MGC_17"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: pORF7; Site:1: EcoRI;
Site:2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT
151 a 130 c 219 g 133 t 1 others

ORIGIN

Query Match 63.9%; Score 26.2; DB 10; Length 634;
Best Local Similarity 90.3%; Pred. No. 5e+02; 3; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GGCTTCAGGGCGCCGACAGCCGAGCGCG 32
|||||
Db 34 GGCTTCAGGGCGCCGACAGCCGAGCGCG 4

RESULT 9
BE389699/c 660 bp mRNA linear EST 21-JUL-2000
LOCUS 60128194.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603731 5',
DEFINITION mRNA sequence.
ACCESSION BE389699
VERSION BE389699.1 GI:9335064
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 660)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM249 row: a column: 12
High quality sequence stop: 610.
Location/Qualifiers
1. .660

FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3603731"
/clone_lib="NIH_MGC_44"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pORF7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT
153 a 140 c 223 g 144 t

ORIGIN

Query Match 63.9%; Score 26.2; DB 10; Length 660;
Best Local Similarity 90.3%; Pred. No. 5e+02; 3; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GGCTTCAGGGCGCCGACAGCCGAGCGCG 32
|||||
Db 49 GGCTTCAGGGCGCCGACAGCCGAGCGCG 19

RESULT 10
BE391389/c 670 bp mRNA linear EST 21-JUL-2000
LOCUS 601284042.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605723 5',
DEFINITION mRNA sequence.
ACCESSION BE391389
VERSION BE391389.1 GI:9336754
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 670)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM254 row: d column: 12
High quality sequence stop: 615.
Location/Qualifiers
1. .670

FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3605723"
/clone_lib="NIH_MGC_44"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pORF7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT
156 a 140 c 226 g 148 t

ORIGIN

Query Match 63.9%; Score 26.2; DB 10; Length 670;
Best Local Similarity 90.3%; Pred. No. 5e+02; 3; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GGCTTCAGGGCGCCGACAGCCGAGCGCG 32
|||||
Db 49 GGCTTCAGGGCGCCGACAGCCGAGCGCG 19

RESULT 11
BE547791/c 687 bp mRNA linear EST 09-AUG-2000
LOCUS 601073643.F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3459466 5',
DEFINITION mRNA sequence.
ACCESSION BE547791
VERSION BE547791.1 GI:9776436
KEYWORDS EST.


```
/tissue_type="brain"
/dev_stage="fetal"
/lab_host="X1-2blue"
/note="Vector: PAMPl; Site_1: NotI; Site_2: SalI"

BASE COUNT      101 a 101 c 162 g 86 t
ORIGIN

Query Match      63.9%; Score 26.2; DB 9; Length 450;
Best Local Similarity 90.3%; Pred. No. 5.1e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 GGCCTCAGGCGCCCGCAGACCCGACGCGG 32
    |||||||
Db 112 GGCCTCAGGCGCCCGCAGACCCGACGCGG 82

RESULT 6
BE408607/c      610 bp      mRNA      linear      EST 21-JUL-2000
DEFINITION      601304118F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638356 5',
ACCESSION      BE408607
VERSION      BE408607
KEYWORDS      GI:9345057
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 610)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: L10M339 row: d column: 05
High quality sequence stop: 610.
Location/Qualifiers
1..610
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="3638356"
/clone_id="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pORF7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```
BASE COUNT      145 a 127 c 208 g 130 t
ORIGIN

Query Match      63.9%; Score 26.2; DB 10; Length 610;
Best Local Similarity 90.3%; Pred. No. 5e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 GGCCTCAGGCGCCCGCAGACCCGACGCGG 32
    |||||||
Db 46 GGCCTCAGGCGCCCGCAGACCCGACGCGG 16

RESULT 7
BG287661/c      627 bp      mRNA      linear      EST 21-FEB-2001
LOCUS      BG287661
```

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DEFINITION      602384488F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4513772 5',
ACCESSION      BG287661
VERSION      BG287661.1 GI:13041716
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 627)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L10M10400 row: o column: 21
High quality sequence stop: 627.
Location/Qualifiers
1..627
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="4513772"
/clone_id="NIH_MGC_93"
/tissue_type="transitional cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: bladder; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
```

```
BASE COUNT      149 a 130 c 217 g 131 t
ORIGIN

Query Match      63.9%; Score 26.2; DB 12; Length 627;
Best Local Similarity 90.3%; Pred. No. 5e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 GGCCTCAGGCGCCCGCAGACCCGACGCGG 32
    |||||||
Db 66 GGCCTCAGGCGCCCGCAGACCCGACGCGG 36

RESULT 8
BE294050/c      634 bp      mRNA      linear      EST 20-JUL-2000
DEFINITION      601173259F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528591 5',
ACCESSION      BE294050
VERSION      BE294050.1 GI:9177580
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 634)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
```

Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center for information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gdbco
High quality sequence stop: 445.

FEATURES

Source

1. 561
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6136374"
/clone_lib="Melton Normalized Human Islet 4 NA-HIS 1"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pSPORT1, Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an EcoT of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

BASE COUNT 63 a 215 c 210 g 73 t
ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 561;
Best Local Similarity 100.0%; Pred. No. 0.044;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGTCCAGGGCGCCGACCGAGCGGTCCCGGGG 41
|||||

Db 261 CGGCTCCAGGGCGCCGACCGAGCGGTCCCGGGG 221
|||||

RESULT 4
AA341747/c 219 bp mRNA linear EST 21-APR-1997
LOCUS AA341747
DEFINITION EST747148 Fetal kidney II Homo sapiens cDNA 5' end, mRNA sequence.
ACCESSION AA341747
VERSION AA341747.1 GI:1993984
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 219)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulner,R.A., Bult
C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,
Clute,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A.,
Gnethm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,
Kellely,J.C., Liu,L.-I., Marrairos,S.M., Merrick,J.M.,
Moreno-Palanges,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bedarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dime,D., Feng,D.-F., Fertie,A., Fischer,C., Hastings,G.A., He,W.W.,
Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L.,
Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon

TITLE
JOURNAL
MEDLINE
COMMENT
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13-21.

FEATURES

source

1. 219
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="ATCC (ihost):143413"
/db_xref="taxon:9606"
/clone_lib="Fetal Kidney II"
/dev_stage="fetus"
/note="Organ: kidney; Vector: pBluescript KS-; Site_1:
XhoI; Site_2: EcoRI"

BASE COUNT 41 a 47 c 82 g 49 t

Query Match 63.9%; Score 26.2; DB 9; Length 219;
Best Local Similarity 90.3%; Pred. No. 5.3e+02;

Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGCCTCAGGGCGCCGACCGAGCGGTCCCGGG 32
|||||

Db 48 GGCCTCAGGGCGCCGACCGAGCGGTCCCGGG 18
|||||

RESULT 5
AL036562/c 450 bp mRNA linear EST 29-FEB-2000
LOCUS AL036562
DEFINITION DKFZ564K1262.F1 564 (synonym: hfr2) Homo sapiens cDNA clone
ACCESSION DKFZ564K1262.5, mRNA sequence.
VERSION AL036562
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 450)
Blum,H., Bauersachs,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Blum, et al.)
Unpublished (1999)
Contact: Blum H
MIPS
Am Klopferstr. 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;
Sequenced by LMU (Ludwig Maximilians University,
Munich/Germany) within the cDNA sequencing consortium of the German
Genome Project.
s1 sequence also available.
This clone (DKFZ564K1262) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: cloneerzpd.de.
Location/Qualifiers

FEATURES

source

1. 450
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZ564K1262"
/clone_lib="564 (synonym: hfr2)"

Fax: 617-495-8557
Email: dmeltone@iobp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center This clone is
available royalty-free through WUGS; please contact the IMAGE
consortium (info@image.lln.gov) for further information
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco.
Location/Qualifiers
1. 453

FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="6136736"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

BASE COUNT 41 a 189 c 164 g 59 t
ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 453;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGCTCCAGGGCCCGCAGACCGCGGTCGCCGGG 41
|||||
Db 261 CGGCTCCAGGGCCCGCAGACCGCGGTCGCCGGG 221

RESULT 2
BM967243/c 492 bp mRNA linear EST 29-APR-2002
LOCUS 133209.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
DEFINITION ALPHA-2A ADRENERGIC RECEPTOR ;, mRNA sequence.
ACCESSION BM967243
VERSION BM967243.1 GI:19561038
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 492)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Weising,B., Rittler,E., Ronko,I., Bennett,J., Cardenas
, M., Gibbons,M., McCann,R., Cole,R., Tsagarashvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: 133209.x1

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812

Fax: 617-495-8557
Email: dmeltone@iobp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 455.
Location/Qualifiers
1. 492

FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="6136336"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

BASE COUNT 44 a 202 c 182 g 64 t
ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 492;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGCTCCAGGGCCCGCAGACCGCGGTCGCCGGG 41
|||||
Db 261 CGGCTCCAGGGCCCGCAGACCGCGGTCGCCGGG 221

RESULT 3
BM967248/c 561 bp mRNA linear EST 29-APR-2002
LOCUS 133204.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
DEFINITION ALPHA-2A ADRENERGIC RECEPTOR ;, mRNA sequence.
ACCESSION BM967248
VERSION BM967248.1 GI:19561047
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 561)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Weising,B., Rittler,E., Ronko,I., Bennett,J., Cardenas
, M., Gibbons,M., McCann,R., Cole,R., Tsagarashvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: 133204.x1

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138

Db 220 CCCAGGGCCCCGGACCCCGCCAGCCCC 188

RESULT 15
AAAF21895/c
ID AAAF21895 standard; DNA; 1093 BP.

XX AC AAAF21895;

XX DT 27-MAR-2001 (first entry)

XX DE Human breast and ovarian cancer associated antigen gene SEQ ID 282.

XX KW Human: breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW neutrotropic; neutrotrophic; antiviral; antiallergic; hepatotropic;
KW antidiabetic; antineoplastic; antitumor; antiparasitic; cardiant; immune disorder;
KW Addison's disease; allergy; autoimmune haemolytic anaemia;
KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW cardiovascular disorder; wound healing; neurological disease; ds.

XX OS Homo sapiens.

XX PN WO200055173-A1.

XX PD 21-SEP-2000.

XX PF 08-MAR-2000; 2000WO-US05881.

XX PR 12-MAR-1999; 99US-0124270.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ruben SM;

XX DR WPI: 2000-611515/58.

XX DR P-PSDB; AAB58992.

XX PT New human breast and ovarian cancer associated gene sequences and the
XX PT polypeptides encoded by these genes, useful in the prevention,
XX PT treatment and diagnosis of cancer, immune disorders, cardiovascular
XX PT disorders and neurological diseases -

XX PS Claim 1; Page 698; 1299pp; English.

XX CC Sequences AAAF21614 - AAAF22031 represent DNA sequences encoding human
XX CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
XX CC associated with breast and ovarian cancer. Included in the invention are
XX CC sequences AAAF22032 - AAAF22040 and AAB59129 which are used in the
XX CC isolation and characterisation of the DNA and protein sequences of the
XX CC invention. The breast and ovarian cancer associated DNA, protein, agonist
XX CC or antagonist sequences exhibit cytostatic; immunosuppressive;
XX CC neutrotropic; neutrotrophic; antiviral; antiallergic; hepatotropic;
XX CC antidiabetic; antineoplastic; antitumor; antiparasitic; cardiant; immune
XX CC antibacterial; antifungal; antiparasitic and cardiant activity. The
XX CC polynucleotide and protein sequences are used in the diagnosis of cancer,
XX CC particularly breast and ovarian cancer. The nucleic acid sequences,
XX CC proteins, agonists and antagonists may also be used in the diagnosis,
XX CC prevention and treatment of immune disorders e.g. Addison's disease,
XX CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
XX CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
XX CC arthritis and ulcerative colitis; cardiovascular disorders such as
XX CC myocardial ischaemias; wound healing; neurological diseases such as
XX CC cerebral anoxia and epilepsy; and infectious diseases.

XX SO Sequence 1093 BP; 208 A; 362 C; 308 G; 209 T; 6 other;

Query Match 56.1%; Score 23; DB 21; Length 1093;
Best Local Similarity 74.4%; Pred. No. 2.3e+02;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2 GGCCTCCAGGGCCCCGACAGCCCGAGCGGTCCTCCCGG 40
II IIII IIII IIII IIII IIII IIII IIII IIII
Db 130 GGGACCCAGTGGCCCGAAGACCCGAGCACTTCATGGG 92

Search completed: February 15, 2003, 14:29:34
Job time : 68.0206 secs

PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226682.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227182.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 12-SEP-2000; 2000US-0232081.
 PR 14-SEP-2000; 2000US-0233397.
 PR 14-SEP-2000; 2000US-0233398.
 PR 14-SEP-2000; 2000US-0233399.
 PR 14-SEP-2000; 2000US-0233399.
 PR 14-SEP-2000; 2000US-0234401.
 PR 14-SEP-2000; 2000US-0234401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.

PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI; 2001-483426/52.
 DR Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 XX
 PS Disclosure; SEQ ID NO 38594; 3071pp + Sequence Listing; English.
 XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 61710 BP; 11560 A; 18542 C; 18148 G; 13460 T; 0 other;
 Query Match 57.1%; Score 23.4; DB 22; Length 61710;
 Best Local Similarity 81.8%; Pred. No. 1.1e+02;
 Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 5 CTCGAGGCCCGCCGACGCCGAGCGGTCGCC 37


```
XX 07-JUL-2000; 2000EP-0114089.
PF 08-JUL-1999; 99JP-0194486.
XX 11-JAN-2000; 2000JP-0118774.
PR 02-MAY-2000; 2000JP-0183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
DR WPI: 2001-524255/58.
XX P-PSDB: AAM93659.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their
XX use in genetic manipulation -
XX
PS Claim 8; SEQ ID NO 3531; 1380bp + sequence listing; English.
XX
CC The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesizing the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesized by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is a full length
CC human cDNA of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ Sequence 2239 BP; 362 A; 734 C; 712 G; 431 T; 0 other;

Query Match 57.1%; Score 23.4; DB 22; Length 2239;
Best Local Similarity 73.2%; Pred. No. 1.6e+02;
Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 1 CGGCTCCAGGCGCCGACGCCGAGCGCGTCCCGGGG 41
Db 1386 CTGCATGCACTGCCCGACGACGACGAGCGTCCCGGGG 1346

RESULT 13
AAK83781/c
ID AAK83781 standard; DNA; 37664 BP.
XX
AC AAK83781;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38593.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytosolic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN NC020157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001MO-US01354.
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PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0203515.
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PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226881.
PR 22-AUG-2000; 2000US-0226881.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
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Db 72903 CGGCATCCGGCGGAGCGAGCAGTGGCGGTCTCCG 72940

RESULT 10

AAH21860/C
ID AAH21860 standard; cDNA; 7185 BP.

XX
AC AAH21860;

DT 16-AUG-2001 (first entry)

DE Mouse N-calcium channel alpha 1B subunit encoding cDNA SEQ ID NO:1.

XX Mouse; N-calcium channel alpha 1B subunit; blood pressure control;

KW N-calcium channel knockout animal; blood glucose level control;

KW pain transfer; hypotensive; analgesic; ss.

XX Mus musculus.

XX Key Location/Qualifiers

FH 121..6987

FT CDS /tag= a

FT /product= "N-calcium channel alpha 1B subunit"

XX MO200130137-A1.

XX 03-MAY-2001.

XX 26-OCT-2000; 2000MO-JP07503.

XX 26-OCT-1999; 99JP-0303809.

XX 16-FEB-2000; 2000JP-0037839.

XX 31-AUG-2000; 2000JP-0261979.

XX (EISA) EISAI CO LTD.

XX Ito M, Miyamoto N, Takahashi E, Oki T, Yoshinaga T, Hatakeyama S;

XX Nildome T, Sawada K, Nishizawa Y, Tanaka I;

XX WPI: 2001-300406/31.

XX P-PSDB; AAB98073.

XX N-type calcium channel deficient non-human animals useful for screening

XX for new drugs -

XX Claim 5; Page 39-49; 64pp; Japanese.

XX The present invention describes an N-type calcium channel deficient

XX non-human animal whose gene for the calcium channel has been disrupted.

XX The gene that is disrupted encodes the N-type calcium channel alpha 1B

XX subunit. Also described are: (1) a method for assaying usefulness of

XX substances using the animal; (2) a method for screening for substances

XX with potential pharmacological use; (3) useful substances found by the

XX method; and (4) a method for producing pharmaceuticals using this method

XX (specifically methods for producing a hypotensive drug, a pain killer

XX and a drug for lowering blood sugar and the substances themselves). The

XX N-type calcium channel deficient non-human animal can be used for

XX screening substances for pharmaceutical use. Active substances include

XX a hypotensive drug, a pain killer and a drug for lowering blood sugar.

XX The present sequence encodes the mouse N-calcium channel alpha 1B

XX subunit from the present invention.

XX Sequence 7185 BP; 1588 A; 2045 C; 1967 G; 1585 T; 0 other;

XX Query Match 57.6%; Score 23.6; DB 22; Length 7185;

XX Best Local Similarity 76.3%; Pred. No. 1.2e+02;

XX Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CGGCTCCAGGGCGCCGAGACCGGCGGTCCCG 38

DB 208 CCGCCCGCGGCGCCCGCGCGCGAGCCGCTCCCG 171

RESULT 11

AAT13279
ID AAT13279 standard; cDNA; 9444 BP.

XX
AC AAT13279;

DT 20-SEP-1996 (first entry)

DE cDNA to genomic hepatitis C virus RNA.

XX hepatitis C virus; antibody; detection; diagnosis; vaccine;

KW classify; subtype; ss.

XX Hepatitis C virus.

XX Key Location/Qualifiers

FH complement (34..9105)

FT CDS /tag= a

XX JP08056672-A.

XX 05-MAR-1996.

XX 26-AUG-1994; 94JP-0223933.

XX 26-AUG-1994; 94JP-0223933.

XX (SAYAMA/) SAYAMA K.

XX WPI: 1996-182301/19.

XX P-PSDB; AAR94462.

XX Claim 2; Page 9-12; 25pp; Japanese.

XX The present sequence represents cDNA to a hepatitis C virus (HCV)

XX genomic RNA. The sequence encodes a polypeptide cont. a 3023 amino

XX acid sequence (see AAR94462) which can be easily detected by antibodies

XX in an assay for the detection of HCV. The DNA and the protein are

XX useful for classifying the subtype of HCV. At least a part of the

XX protein may be used as a vaccine against HCV.

XX Sequence 9444 BP; 2079 A; 2608 C; 2682 G; 2075 T; 0 other;

XX Query Match 57.6%; Score 23.6; DB 17; Length 9444;

XX Best Local Similarity 76.3%; Pred. No. 1.2e+02;

XX Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 GGCCTCCAGGGCGCCGAGACCGGCGGTCCCGG 39

DB 3487 GGCCTCCAGGGCGCCGAGACCGGCGGTCCCGG 3524

RESULT 12

AAK94594/C
ID AAK94594 standard; cDNA; 2239 BP.

XX
AC AAK94594;

DT 06-NOV-2001 (first entry)

DE Human full-length cDNA, SEQ ID NO: 3531.

XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

XX Homo sapiens.

XX EP1130094-A2.

XX 05-SEP-2001.

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Query Match      61.5%: Score 25.2; DB 21; Length 77536;
Best Local Similarity 78.9%: Pred. No. 33;
Matches 30; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
OY      1 CGGCTCCAGGCCCCCGAGACCGAGCGGTCGCCG 38
      ||||| ||| ||||| || ||||| || ||||| |||

```

mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.

Sequence 206 BP; 35 A; 45 C; 85 G; 40 T; 1 other;

Query Match 63.9%; Score 26.2; DB 21; Length 206;
Best Local Similarity 90.3%; Pred. No. 32;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GGCCTCAGGGCCCCGACGCCGAGCGG 32
|||||
Db 80 GGCCTCAGGGCCGCGCAGACCCGACGCCG 50

RESULT 8

AAH52225/C
ID AAH52225 standard; cDNA; 576 BP.

AAH52225;

10-SEP-2001 (first entry)

Human AFP protein encoding cDNA sequence SEQ ID NO:265.

Human; secreted protein; secretion; bacterial cell; fungal cell;
eukaryotic cell; fusion protein; maltose binding protein;
immunoglobulin constant region; polyhistidine tag; ss.

Homo sapiens.

MO200129221-A2.

26-APR-2001.

20-OCT-2000; 2000WO-US29052.

20-OCT-1999; 99US-0160712.

(ZYMO) ZYMOGENETICS INC.

Conklin DC, Yee DP;

WPI; 2001-300340/31.

P-PSDB; AAG81374.

Isolated polypeptide for directing secretion of proteins of interest from a host cell including, e.g. bacteria, includes contiguous amino acid residues of polypeptide with specified amino acids

Claim 9; Page 459-460; 617pp; English.

AAH52093 to AAH52303 encode the human secreted proteins given in AAG81242 to AAG81453. The secreted proteins can be used for directing the secretion of proteins of interest from a host cell including bacteria, fungal cells, and cultured higher eukaryotic cells. The present invention also describes fusion proteins, where a secreted protein of the invention is operably linked via a peptide bond or peptide linker to a second protein selected from the group consisting of maltose binding protein, an immunoglobulin constant region, a polyhistidine tag and a peptide given in AAG81453.

Sequence 576 BP; 140 A; 124 C; 199 G; 113 T; 0 other;

Query Match 63.9%; Score 26.2; DB 22; Length 576;
Best Local Similarity 90.3%; Pred. No. 28;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GGCCTCAGGGCCCCGACGCCGAGCGG 32
|||||
Db 66 GGCCTCAGGGCCGCGCAGACCCGACGCCG 36

RESULT 9

AAH14651
ID AAH14651 standard; DNA; 77536 BP.

AAH14651;

08-AUG-2000 (first entry)

Nucleotide sequence of the FK-520 biosynthetic gene cluster.

FK-520; polyketide synthase; PKS; gene cluster; immunosuppressant;
Streptomyces hygroscopicus var. ascomyceticus; immunophilin;
FK-506 binding protein; polyketide compound; transplant rejection;
graft-versus-host disease; uveitis; alopecia universalis;
autoimmune chronic active hepatitis; inflammatory bowel disease;
multiple sclerosis; primary biliary cirrhosis; scleroderma;
neurile outgrowth; nerve regrowth; Parkinson's disease;
Alzheimer's disease; stroke; traumatic spinal cord; brain injury;
peripheral neuropathy; ss.

Streptomyces hygroscopicus.

OS

XX

XX

XX

XX

XX

XX

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KW	gene; ds.
OS	Homo sapiens.
PN	WO200200928-A2.
XX	
PD	03-JAN-2002.
PF	02-JUL-2001; 2001WO-EP07537.
XX	
PR	30-JUN-2000; 2000DE-1032529.
XX	
PA	01-SEP-2000; 2000DE-1043826.
XX	
PI	(EPIG-) EPIGENOMICS AG.
DR	Olek A, Piepenbrock C, Berlin K;
XX	WPI; 2002-130909/17.
PT	Nucleic acid comprising fragment of chemically modified gene, useful
PT	for diagnosis and treatment of diseases associated with abnormal
PS	cytosine methylation -
XX	
CC	Claim 1; SEQ ID NO 46; 32pp + Sequence Listing; German.
CC	The present invention provides a number of human immune system associated
CC	genes which are modified by the methylation of cytosines. The sequences
CC	can be used in the diagnosis and treatment of immune system disorders,
CC	including eye diseases such as retinopathy, neovascular glaucoma and
CC	macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC	leukemia, Alzheimer's disease, AIDS, epilepsy, neuroproliferation,
CC	rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
XX	diseases. The present sequence is a gene of the invention.
SQ	Sequence 7353 BP; 1713 A; 384 C; 2140 G; 3116 T; 0 other;
	Query Match 65.4%; Score 26.8; DB 24; Length 7353;
	Best Local Similarity 81.6%; Pred. No. 14;
	Matches 31; Conservative 0; Mismatches 7; Indels 0; Gaps 0
OY	1 CGGCCTCAGGGCGGCCGACACCAGCGCGGTCCCGC 38
DB	1444 GCACCTCCAAACCCCGCAACCCGACCGCATCCCCG 1407
RESULT 6	
AAD28363/c	
ID	AAD28363 standard; DNA; 7353 BP.
XX	
AC	AAD28363;
XX	
DT	22-APR-2002 (first entry)
XX	
DE	Human chemically treated genomic DNA #4.
XX	
KW	Human; cytostatic; antidepressant; neuroleptic; nootropic; antiaddictive;
KW	adrenergic alpha-1C-receptor; cytosine methylation; therapy; alcoholism;
KW	Behavioral disorder; neurological; psychiatric; cancer; schizophrenia;
KW	Tourette's syndrome; smoking; human immunodeficiency virus dementia;
KW	drug abuse; migraine; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200202809-A2.
XX	
PD	10-JAN-2002.
XX	
PF	02-JUL-2001; 2001WO-EP07540.
XX	
PR	30-JUN-2000; 2000DE-1032529.
XX	
PA	01-SEP-2000; 2000DE-1043826.
XX	
PI	(EPIG-) EPIGENOMICS AG.
DR	Olek A, Piepenbrock C, Berlin K;
XX	WPI; 2002-130909/17.
PT	Nucleic acid comprising fragment of chemically modified gene, useful
PT	for diagnosis and treatment of diseases associated with abnormal
PS	cytosine methylation -
XX	
CC	Claim 1; SEQ ID NO 46; 32pp + Sequence Listing; German.
CC	The present invention provides a number of human immune system associated
CC	genes which are modified by the methylation of cytosines. The sequences
CC	can be used in the diagnosis and treatment of immune system disorders,
CC	including eye diseases such as retinopathy, neovascular glaucoma and
CC	macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC	leukemia, Alzheimer's disease, AIDS, epilepsy, neuroproliferation,
CC	rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
XX	diseases. The present sequence is a gene of the invention.

```

XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI: 2002-154759/20.
XX XX
XX PT Novel nucleic acid useful for diagnosis and therapy of behavioral
PT disorder, neurological disorder and cancer, comprises a sequence of a
PT segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
PT gene -
XX PS
XX PS Claim 1: Page 36-40; 190pp; English.
XX CC
XX CC The invention relates to nucleic acids comprising a segment of chemically
CC pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also
CC relates to oligonucleotides or peptide nucleic acid (PNA) oligomers
CC useful for detecting cytosine methylations. The pretreated DNA is useful
CC for the diagnosis or therapy of behavioural disorders, neurological
CC disorders and cancer, in particular major depressive disorder, Tourette's
CC syndrome, schizophrenia, psychiatric and neurological disorders, smoking,
CC drug abuse, alcoholism, personality traits, compulsive gambling, human
CC immunodeficiency virus dementia, migraine, behaviours in schizophrenic
CC and schizoaffective patients, and suicidal behaviour in patients with
CC schizophrenia. The nucleic acid is useful for detecting the methylation
CC state of all CpG dinucleotides and/or single nucleotide polymorphisms
CC (SNPs). The present sequence is human chemically treated genomic DNA.
XX SO
SQ Sequence 7353 BP; 1713 A; 384 C; 2140 G; 3116 T; 0 other;

Query Match 65.4%; Score 26.8; DB 24; Length 7353;
Best Local Similarity 81.6%; Pred. No. 14;
Matches 31; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CGGCCTCCAGGCCCGCACCGACCGCGGGTCCC 38
DB 1444 CGACTCTCAAAACCCTCCGCAACCCGACGCGATCCCCG 1407
||| ||||| ||||| ||||| ||||| |||||
||| ||||| ||||| ||||| ||||| |||||

RESULT 7
AACI0059/c
ID AACI0059 standard; cDNA; 206 BP.
XX AC
XX AC AACI0059;
XX DT 06-OCT-2000 (first entry)
DE Human secreted protein 5' EST, SEQ ID NO: 14134.
XX KW Human secreted protein 5' EST, SEQ ID NO: 14134.
XX KW gene therapy; chromosome mapping; ss.
OS Homo sapiens.
XX PN EP1033401-A2.
XX PD 06-SEP-2000.
XX PF 21-FEB-2000; 2000EP-0200610.
XX PR 26-FEB-1999; 99US-0122487.
XX PA (GEST ) GENSET.
XX PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX DR WPI: 2000-500381/45.
XX CC
XX CC New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX PS
XX PS Claim 1; SEQ ID 14134; 71pp + CD-ROM; English.
XX CC
XX CC The present sequence is one of a large number of 5' ESTs derived from

```

drug; side effect; cancer; central nervous system; cardiovascular;
KM gastrointestinal; respiratory system; single nucleotide polymorphism;
KM SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP10074.
XX
PR 01-SEP-2000; 2000DE-1043826.
XX
PR 05-SEP-2000; 2000DE-1044543.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX
PS Claim 12; 56bp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (1) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (11) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABL013410-AB054121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
SQ Sequence 1733 BP; 271 A; 211 C; 625 G; 626 T; 0 other;
XX
Query Match 65.4%; Score 26.8; DB 24; Length 1733;
Best Local Similarity 81.6%; Pred. No. 17;
Matches 31; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY 1 CGGCTCCAGGCGCCCGCAGACCCGAGCGGTCCCG 38
ID ||||||| ||||||| ||||||| ||||||| |||||||
DB 564 CGACCTCCAAAACCCCGCAACCGCAGCGATCCCG 527
XX
RESULT 4
AB047501
ID AB047501 standard; DNA; 1733 BP.
XX
AC AB047501;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 34092.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.

XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP10074.
XX
PR 01-SEP-2000; 2000DE-1043826.
XX
PR 05-SEP-2000; 2000DE-1044543.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX
PS Claim 12; 56bp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (1) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (11) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABL013410-AB054121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
SQ Sequence 1733 BP; 626 A; 625 C; 211 G; 271 T; 0 other;
XX
Query Match 65.4%; Score 26.8; DB 24; Length 1733;
Best Local Similarity 81.6%; Pred. No. 17;
Matches 31; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY 1 CGGCTCCAGGCGCCCGCAGACCCGAGCGGTCCCG 38
ID ||||||| ||||||| ||||||| ||||||| |||||||
DB 1170 CGACCTCCAAAACCCCGCAACCGCAGCGATCCCG 1207
XX
RESULT 5
ABL32073/C
ID ABL32073 standard; DNA; 7353 BP.
XX
AC ABL32073;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 46.
XX
KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianaemic; cytosatic; noctropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antineumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;

```
XX (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
XX LIGgett SB, Small KM.
PI
XX WPI: 2001-611728/70.
DR P-PSDB; AAM52122.
XX
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
XX Example 7; Page 151; 163pp; English.
PS
XX
XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (III)
CC or a site comprising (A) (ggggcgggcg) or (B) (ggggcgctgag) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfine, idazoxan, tolazoline, phenolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2AAR gene
CC (Genbank Accession AF281308).
XX
XX Sequence 1350 BP; 199 A; 490 C; 441 G; 220 T; 0 other;
SQ
XX
XX Query Match 100.0%; Score 41; DB 23; Length 1350;
XX Best Local Similarity 100.0%; Pred. No. 0.0011;
XX Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CGGCTCCAGGGCCCGCAGACCCGAGCGGTCGCCGGGG 41
XX |||||||||||||||||||||||||||||||||||
DB 910 CGGCTCCAGGGCCCGCAGACCCGAGCGGTCGCCGGGG 950
XX
XX RESULT 2
XX AA199918
XX AA199918 standard; DNA; 1350 BP.
XX
XX AA199918;
AC
XX
XX 18-FEB-2002 (first entry)
DT
XX
XX Human alpha-2AAR variant encoding DNA.
DE
XX
XX Human: genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2AAR; chromosome 10; ds.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX CDS 1..1353
XX FT /*tag= a
XX FT /product= "alpha-2AAR"
XX FT replace(753,C)
XX
XX allele
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FT /*tag= b
XX
XX WO200179561-A2.
PN
XX
XX 25-OCT-2001.
PD
XX
XX 17-APR-2001; 2001WO-US12575.
XX
XX
XX 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
XX
XX (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
XX LIGgett SB, Small KM;
PI
XX
XX WPI: 2001-611728/70.
DR P-PSDB; AAM52123.
XX
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
XX Disclosure; Page 152; 163pp; English.
PS
XX
XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (III)
CC or a site comprising (A) (ggggcgggcg) or (B) (ggggcgctgag) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfine, idazoxan, tolazoline, phenolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2AAR variant
CC gene.
XX
XX Sequence 1350 BP; 199 A; 489 C; 442 G; 220 T; 0 other;
SQ
XX
XX Query Match 100.0%; Score 41; DB 23; Length 1350;
XX Best Local Similarity 100.0%; Pred. No. 0.0011;
XX Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CGGCTCCAGGGCCCGCAGACCCGAGCGGTCGCCGGGG 41
XX |||||||||||||||||||||||||||||||||||
DB 910 CGGCTCCAGGGCCCGCAGACCCGAGCGGTCGCCGGGG 950
XX
XX RESULT 3
XX ABQ47500/C
XX ABQ47500 standard; DNA; 1733 BP.
XX
XX ABQ47500;
AC
XX
XX 12-JUL-2002 (first entry)
DT
XX
XX Oligonucleotide for detecting cytosine methylation SPQ ID NO 34091.
DE
XX
XX Human: cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
```

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OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 11:01:28 ; Search time 11.7706 Seconds
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Title: US-09-636-259b-1_COPY_730_770

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Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	1350	23	AA199917 Human alpha-2AAR e
2	41	100.0	1350	23	AA199918 Human alpha-2AAR v
3	26.8	65.4	1733	24	ABQ47501 Oligonucleotide fo
4	26.8	65.4	1733	24	ABQ47501 Oligonucleotide fo
5	26.8	65.4	7353	24	ABL32073 Human immune syste
6	26.8	65.4	7353	24	ADD28363 Human chemically t
7	26.2	63.9	206	21	AACT10059 Human secreted pro
8	26.2	63.9	576	22	AAH52225 Human AFP protein
9	25.2	61.5	77536	21	AAAI4651 Nucleotide sequenc

C	10	23.6	57.6	7185	22	AAH21860 Mouse N-calcium ch
C	11	23.6	57.6	9444	17	AAAT33279 CDNA to genomic he
C	12	23.4	57.1	2239	22	AAK94594 Human full-length
C	13	23.4	57.1	37664	22	AAK85781 Human immune/haema
C	14	23.4	57.1	61710	22	AAK83782 Human immune/haema
C	15	23.3	56.1	1093	21	AAE21895 Human breast and o
C	16	23.3	56.1	1396	24	ABK84443 Human CDNA differe
C	17	23.3	56.1	1596	22	ABA09009 Human PROVI homolo
C	18	23.3	56.1	1596	22	AAH96678 Human protein enco
C	19	23.3	56.1	4692	19	AAV04633 Porcine phosphino
C	20	23.3	56.1	4692	20	AAV74099 Porcine G-protein
C	21	22.4	54.6	348	21	AAZ86812 Pig p101 regulator
C	22	22.4	54.6	949	20	AAZ40845 Human secreted pro
C	23	22.4	54.6	1232	22	AAV27733 Human transport pr
C	24	22.4	54.6	2033	23	ABV24123 Human prostate exp
C	25	22.4	54.6	2033	23	ABV30001 Human prostate exp
C	26	22.4	54.6	2537	19	AAV52933 Human pre-transfor
C	27	22.4	54.6	7110	22	AAF81361 Quorum sensing con
C	28	22.4	54.6	12638	22	AAK70641 Human immune/haema
C	29	22.4	54.6	295	21	AAA42360 Human secreted exp
C	30	22.2	53.7	783	17	AAAT03651 31-O-desmethyl-Fk5
C	31	22.2	53.7	1150	17	AAAT03650 Pseudomonas aerugi
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C	33	22.2	53.7	1998	22	AAAT03650 Pseudomonas aerugi
C	34	22.2	53.7	1998	22	AAAT03650 Pseudomonas aerugi
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C	38	22.2	53.7	1998	22	AAAT03650 Pseudomonas aerugi
C	39	22.2	53.7	1998	22	AAAT03650 Pseudomonas aerugi
C	40	22.2	53.7	1998	22	AAAT03650 Pseudomonas aerugi
C	41	22.2	53.7	1998	22	AAAT03650 Pseudomonas aerugi
C	42	22.2	53.7	1998	22	AAAT03650 Pseudomonas aerugi
C	43	22.2	53.7	1998	22	AAAT03650 Pseudomonas aerugi
C	44	22.2	53.7	1998	22	AAAT03650 Pseudomonas aerugi
C	45	22.2	53.7	1998	22	AAAT03650 Pseudomonas aerugi

ALIGNMENTS

RESULT 1	AA199917	standard; DNA; 1350 BP.
ID	AA199917	
AC	AA199917	
XX	18-FEB-2002	(first entry)
DT		
XX	Human alpha-2AAR encoding DNA.	
DE		
XX	Human: genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;	
KW	polymorphic site; allelic variant; cardiovascular disease;	
KW	central nervous system disease; adenylyl cyclase; MAP kinase activity;	
KW	phosphorylation; inositol phosphate; alpha-2AAR;	
KW	GenBank Accession AF261308; chromosome 10; ds.	
XX	Homo sapiens.	
OS		
XX		
PH	Key	Location/Qualifiers
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FT		/product= "alpha-2AAR"
XX		
PN	W020019561-A2.	
XX		
PD	25-OCT-2001.	
XX		
PF	17-APR-2001; 2001WO-US12575.	
XX		
PR	17-APR-2000; 2000US-0551744.	
PR	10-AUG-2000; 2000US-0636259.	
PR	19-OCT-2000; 2000US-0692077.	


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177389..201231
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Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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OY 1 CGGCTCCAGGCCCCGACAGCCGAGCGGTCGCCGG 40
Db 130648 CGGCCCCGGGGCGCCGACCGACCGCGGCCCGGAG 130609
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RESULT 15

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LOCUS PIGA2AR 1728 bp DNA linear MAM 27-APR-1993
DEFINITION Porcine alpha2A-adrenergic receptor (PORA2AR) gene, complete cds.
ACCESSION J05652
VERSION J05652.1 GI:164303
KEYWORDS alpha-2A-adrenergic receptor.
SOURCE Porcine liver DNA.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 1728)
AUTHORS Guyer,C.A., Horstman,D.A., Wilson,A.L., Clark,J.D., Kragoe,E.J., Jr.
and Limbird,L.E.
JOURNAL Unpublished (1990)
REFERENCE 2 (bases 70 to 1582)
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AUTHORS Guyer,C.A., Horstman,D.A., Wilson,A.L., Clark,J.D., Kragoe,E.J., Jr.
and Limbird,L.E.
TITLE Cloning, sequencing, and expression of the gene encoding the
porcine alpha 2-adrenergic receptor. Allosteric modulation by Na+,
H+, and amiloride analogs
JOURNAL J. Biol. Chem. 265 (28), 17307-17317 (1990)
MEDLINE 91009167
PUBMED 2170371
COMMENT Draft entry and computer-readable sequence for [J. Biol. Chem.
(1990) In press] kindly submitted
by C.A.Guyer, 02-AUG-1990.
FEATURES
source
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/db_xref="taxon:9823"
130..1482
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KAWCEIYIALDVLEFCTSIYHLCALSLDYSITQAIENLKRTPRRKAIITVWVI
SAVISFPPLISIEKAGGGQOPAEPRCEINDQKMYVISSCIGSFAPCLIMILYVR
IYQIAKRTTRVPPSRGPDAAALPGAGRRPNGIGPERGVGVGAEEPLVQNLGA
PGPPAPAGPRDADGLDLEESSSEHAERPPRGRRSGPRAKSAASQVPCDLPK
RGPAPGAPAPATGAGEEPRGCVAKASRRHGRGRNRKRTFTVLAVITGVVQMPFEF
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BASE COUNT 268 a 590 c 562 g 308 t
ORIGIN
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Best Local Similarity 85.0%; Pred. No. 64;
Matches 34; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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OY 1 CGGCTCCAGGCCCCGACAGCCGAGCGGTCGCCGG 40
Db 1039 CGGCCCCGTGGCCCGCAGAGTCGAGCGGGCCCTCGGG 1078
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Search completed: February 15, 2003, 16:45:22
Job time : 246.55 secs
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ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 204317)

REFERENCE

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

TITLE

Mus musculus, clone RP23-358H2

JOURNAL

Unpublished

AUTHORS

2 (bases 1 to 204317)

REFERENCE

Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B.,

TITLE

Brown, A., Camarata, J., Campiano, A., Chang, J., Chazaro, B.,

JOURNAL

Choepe, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,

AUTHORS

Cooke, P., Deatellano, K., Dewar, K., Diaz, J., Dodge, S., Ferro, S.,

REFERENCE

Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,

TITLE

Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,

JOURNAL

Kamat, A., Karatas, A., Kells, C., Laroque, K., Lamazares, R.,

AUTHORS

Landers, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C.,

REFERENCE

Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,

TITLE

McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, I.,

JOURNAL

Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,

AUTHORS

Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,

REFERENCE

Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,

TITLE

Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,

JOURNAL

Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S.,

AUTHORS

Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,

REFERENCE

Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,

TITLE

Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,

JOURNAL

Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,

AUTHORS

Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

REFERENCE

Direct Submission

TITLE

Submitted (01-MAR-2002) Whitehead Institute/MIT Center for Genome

JOURNAL

Research, 320 Charles Street, Cambridge, MA 02141, USA

AUTHORS

3 (bases 1 to 204317)

REFERENCE

Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N.,

TITLE

Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,

JOURNAL

Boukhgalter, B., Brown, A., Camarata, J., Campiano, A., Chang, J.,

AUTHORS

Chazaro, B., Choepe, Y., Colangelo, M., Collins, S., Collymore, A.,

REFERENCE

Cook, A., Cooke, P., Deatellano, K., Dewar, K., Diaz, J., Dodge, S.,

TITLE

Faro, S., Ferreira, P., Fitzgerald, M., Fitzhugh, W., Gage, D.,

JOURNAL

Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L.,

AUTHORS

Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I.,

REFERENCE

Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Laroque, K.,

TITLE

Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K.,

JOURNAL

Liu, G., Maclean, C., Macdonald, P., Major, J., Marquis, N.,

AUTHORS

Mathews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J.,

REFERENCE

Meneus, L., Mihova, I., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,

TITLE

Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P.,

JOURNAL

O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,

AUTHORS

Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C.,

REFERENCE

Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,

TITLE

Schupack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N.,

JOURNAL

Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testaye, S.,

AUTHORS

Theodore, J., Topham, K., Travers, M., Travis, N., Triggillo, J.,

REFERENCE

Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,

TITLE

Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 197709 bases at least Q40

Consensus quality: 200412 bases at least Q30

Consensus quality: 201149 bases at least Q20

Insert size: 210000; agarose-fp

Insert size: 202017; sum-of-coverage

Quality coverage: 6.3 in Q20 bases; agarose-fp

Quality coverage: 6.6 in Q20 bases; sum-of-coverage

NOTE: This is a 'working draft' sequence. It currently

consists of 24 contigs. Gaps between the contigs

are represented as runs of N. The order of the pieces

is believed to be correct as given, however the sizes

of the gaps between them are based on estimates that have

provided by the submitter.

This sequence will be replaced

by the finished sequence as soon as it is available and

the accession number will be preserved.

1 7387: contig of 7387 bp in length

7388 7487: gap of 100 bp

7488 7956: contig of 469 bp in length

7957 8056: gap of 100 bp

8057 9200: contig of 1144 bp in length

9201 9300: gap of 100 bp

9301 10747: contig of 1447 bp in length

10748 10847: gap of 100 bp

10848 12877: contig of 2030 bp in length

12878 12977: gap of 100 bp

12978 15172: contig of 2195 bp in length

15173 15272: gap of 100 bp

15273 18061: contig of 2789 bp in length

18062 18161: gap of 100 bp

18162 21071: contig of 2910 bp in length

21072 21171: gap of 100 bp

21172 24003: contig of 2832 bp in length

24004 24103: gap of 100 bp

24104 27175: contig of 3072 bp in length

27176 27275: gap of 100 bp

27276 30561: contig of 3286 bp in length

30562 30661: gap of 100 bp

30662 66767: contig of 36106 bp in length

66768 66867: gap of 100 bp

66868 73300: contig of 6433 bp in length

73301 73400: gap of 100 bp

73401 78880: contig of 5480 bp in length

78881 78980: gap of 100 bp

78981 89075: contig of 10095 bp in length

89076 89175: gap of 100 bp

89176 98581: contig of 9406 bp in length

98582 98681: gap of 100 bp

98682 105311: contig of 6630 bp in length

105312 105411: gap of 100 bp

105412 122788: contig of 17377 bp in length

122789 122888: gap of 100 bp

122889 132289: contig of 9401 bp in length

132290 132389: gap of 100 bp

132390 144818: contig of 12429 bp in length

144819 144918: gap of 100 bp

144919 159101: contig of 14183 bp in length

159102 159201: gap of 100 bp

159202 177288: contig of 18087 bp in length

177289 177388: gap of 100 bp

177389 201231: contig of 23843 bp in length

201232 201331: gap of 100 bp

201332 204317: contig of 2966 bp in length.

FEATURES

Source

Center: Whitehead Institute/ MIT Center for Genome Research

Web site: http://www-seq.wi.mit.edu

Contact: sequence.submissions@genome.wi.mit.edu

Project Information

Center project name: L23807

Center clone name: 358_H2

Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

RESULT 14	AC113491/c	204317 bp	DNA	linear	HTG 06-JUN-2002
LOCUS	AC113491				
DEFINITION	mus musculus clone RP23-358H2, WORKING		DRAFT	SEQUENCE, 24	ordered
ACCESSION	AC113491				
VERSION	AC113491.3				
KEYWORDS	HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.				
SOURCE	house mouse.				

REFERENCE 1 (bases 1 to 3653)
 AUTHORS Mao, Z.-M., Tang, K., Li, B.-M. and Jing, N.-H.
 TITLE Cloning and expression of human alpha-2A adrenergic receptor in
 SYS1 cells
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 3653)
 AUTHORS Mao, Z.-M., Tang, K., Li, B.-M. and Jing, N.-H.
 TITLE Direct Submission
 JOURNAL Submitted (01-Jun-2000) Shanghai Institute of Physiology, Chinese
 Academy of Sciences, 320 Yue Yang Road, Shanghai 200031, P.R. China

FEATURES
 source
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 IYQIAKRRTRVPSRRGPDVAAPRGCTERRRNGDGPERSAGPGAGAEPLPTQUNGA
 PGEPAPAGRRDDALDIESSSSDHAERPGRRRNGDGPERSAGPGAGAEPLPTQUNGA
 RGGPAGTGTTPAAGPGEERGAASRRNGRRRNGDGPERSAGPGAGAEPLPTQUNGA
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 PGEPAPAGRRDDALDIESSSSDHAERPGRRRNGDGPERSAGPGAGAEPLPTQUNGA
 RGGPAGTGTTPAAGPGEERGAASRRNGRRRNGDGPERSAGPGAGAEPLPTQUNGA
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BASE COUNT 681 a 1168 c 1028 g 776 t

ORIGIN

Query Match 100.0%; Score 41; DB 9; Length 3653;
 Best Local Similarity 100.0%; Pred. No. 0.078;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCTCCAGGGCCCGACGCCGAGCGGGTCCCGGGG 41
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 Db 1789 CGGCTCCAGGGCCCGACGCCGAGCGGGTCCCGGGG 1829

RESULT 10
 AL158163 204908 bp DNA linear PRI 13-DEC-2001
 LOCUS Human DNA sequence from clone RP11-348N5 on chromosome 10, complete
 DEFINITION
 AL158163
 accession
 AL158163
 version
 AL158163.11 GI:17384427
 keywords
 HTG.
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 204908)
 Johnson, C.
 Direct Submission
 Submitted (13-DEC-2001) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humuery@sanger.ac.uk
 humuery@sanger.ac.uk
 On Dec 5, 2001 this sequence version replaced gi:16944857.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em; EMBL; Sw;
 SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information on the WORMPEP
 database can be found at:
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
 This sequence was generated from part of bacterial clone contigs of human
 chromosome 10, constructed by the Sanger Centre Chromosome 10
 Mapping group. Further information can be found at
<http://www.sanger.ac.uk/Chp/Chr10>
 RP11-348N5 is from the library RP11-11.2 constructed by the group
 of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
 VECTOR: pBAC3.6
 This sequence is the entire insert of clone RP11-348N5. The true
 left end of clone RP11-479A21 is at 179266 in this sequence. The
 true right end of clone RP11-313D6 is at 44800 in this sequence.

FEATURES
 source
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 /db_xref="taxon:9606"
 /chromosome="10"
 /clone="RP11-348N5"
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BASE COUNT 62115 a 36724 c 39536 g 66533 t

ORIGIN

Query Match 100.0%; Score 41; DB 9; Length 204908;
 Best Local Similarity 100.0%; Pred. No. 0.023;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCTCCAGGGCCCGACGCCGAGCGGGTCCCGGGG 41
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 Db 196479 CGGCTCCAGGGCCCGACGCCGAGCGGGTCCCGGGG 196519

RESULT 11
 MUSALP2ADB 1454 bp DNA linear ROD 27-APR-1993
 LOCUS Mouse alpha-2 adrenergic receptor, complete cds.
 DEFINITION
 M99377
 accession
 M99377.1 GI:191882
 version
 M99377.1
 keywords
 alpha-2 adrenergic receptor.
 SOURCE
 Mus musculus (strain 129/Sv) DNA.
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1454)
 Link, R., Daunt, D., Barsh, G., Chruscinski, A. and Koblika, B.
 Cloning of two mouse genes encoding alpha 2-adrenergic receptor
 subtypes and identification of a single amino acid in the mouse
 alpha 2-C10 homolog responsible for an interspecies variation in
 antagonist binding
 antagomist binding
 Mol. Pharmacol. 42 (1), 16-27 (1992)
 MEDLINE
 PUBMED
 92342131
 1353249

FEATURES
 source
 1..1454
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 /strain="129/Sv"
 /db_xref="taxon:10090"
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 /db_xref="GI:191883"
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 IYQIAKRRTRVPSRRGPDVAAPRGCTERRRNGDGPERSAGPGAGAEPLPTQUNGA
 PGEPAPAGRRDDALDIESSSSDHAERPGRRRNGDGPERSAGPGAGAEPLPTQUNGA
 RGGPAGTGTTPAAGPGEERGAASRRNGRRRNGDGPERSAGPGAGAEPLPTQUNGA
 TYTLTAVGCSVPRTLEKFFFGYGCSSLNPIYTLTFNDFRRARKKILCRDGRRIY"

ORIGIN

Query Match 100.0%; Score 41; DB 9; Length 1941;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGCTCCAGAGCCCGCAGACCCGAGCGGTCGCCGGGG 41
|||||
Db 1428 CGGCTCCAGAGCCCGCAGACCCGAGCGGTCGCCGGGG 1468

RESULT 7

LOCUS HUMADRA2R 3604 bp DNA linear PRI 30-OCT-1994
DEFINITION Human alpha 2 adrenergic receptor gene, complete cds.
ACCESSION M23533
VERSION M23533.1 GI:178195
KEYWORDS adrenergic receptor; alpha-2 adrenergic receptor.
SOURCE Human DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 3604)
Fraser, C.M., Arakawa, S., McCombie, W.R. and Venter, J.C.
Cloning, sequence analysis, and permanent expression of a human
alpha 2-adrenergic receptor in Chinese hamster ovary cells.
Evidence for independent pathways of receptor coupling to adenylylate
cyclase attenuation and activation
J. Biol. Chem. 264 (20), 11754-11761 (1989)
2568356
PUBMED
JOURNAL MEDLINE

COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
by W.R. McCombie, 30-MAR-1989.
FEATURES
source Location/Qualifiers
1..3604
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1578..1583
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1723..1728
/note="GRE related sequence"
2078..3430
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/gene="ZNF32"
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/codon_start=1
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/db_xref="GI:178196"
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CDS

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SAVISFPLISIEKGGGGGPOPAERPCREINDOKWYVISCIGSFAPCLIMITYVR
IYQIAKRRTRVPPSRGPDVAAPRGTERPNCIGPERSGSGAEAPLPTQLNGA
GEPAPAGPRDADLDLESSSDHAERPPRRPRGKRGKARASQVAGDSLR
AGRGSGSRRLDGRGRSASGLPRRARGGQNRKRTFVLAVIGVAVGVPWFPEFF
TYTLVAVGCSVPRTLFKFFFWFGYCNSSLNPVIYITFNHDFRAFKILICGRDKRRIY
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BASE COUNT 555 a 1272 c 1134 g 643 t
ORIGIN

Query Match 100.0%; Score 41; DB 9; Length 3604;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGCTCCAGAGCCCGCAGACCCGAGCGGTCGCCGGGG 41
|||||
Db 2987 CGGCTCCAGAGCCCGCAGACCCGAGCGGTCGCCGGGG 3027

RESULT 8

LOCUS AY032736 3612 bp DNA linear PRI 12-MAY-2001
DEFINITION Homo sapiens alpha-2A adrenergic receptor (ADRA2R) gene, complete
cds.
ACCESSION AY032736
VERSION AY032736.1 GI:14029162
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 3612)
Liu, L. and Yuan, L.
Human alpha-2A adrenergic receptor gene and the genotype of -1296
nucleotide and motionsickness
Unpublished
2 (bases 1 to 3612)
Liu, L. and Yuan, L.
Submitted (17-APR-2001) Key Laboratory of Molecular Biology,
General Hospital of Airforce, Fucheng Road No. 30, Beijing 100036,
China

FEATURES

source Location/Qualifiers
1..3612
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/gene="ADRA2R"
/contig=">3437"
/product="alpha-2A adrenergic receptor"
2085..3437
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/product="alpha-2A adrenergic receptor"
/protein_id="AAK51162.1"
/db_xref="GI:14029163"

CDS

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SAVISFPLISIEKGGGGGPOPAERPCREINDOKWYVISCIGSFAPCLIMITYVR
IYQIAKRRTRVPPSRGPDVAAPRGTERPNCIGPERSGSGAEAPLPTQLNGA
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BASE COUNT 555 a 1278 c 1136 g 643 t
ORIGIN

Query Match 100.0%; Score 41; DB 9; Length 3612;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2994 CGGCTCCAGAGCCCGCAGACCCGAGCGGTCGCCGGGG 3034

RESULT 9

LOCUS AF284095 3653 bp mRNA linear PRI 27-MAR-2001
DEFINITION Homo sapiens alpha-2A adrenergic receptor mRNA, complete cds.
ACCESSION AF284095
VERSION AF284095.1 GI:13447750
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

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Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 41; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;
QY      1 CGGCTCCAGGCGCCGACAGCCGAGCGGTCGCCGGGG 41
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Db      910 CGGCTCCAGGCGCCGACAGCCGAGCGGTCGCCGGGG 950
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RESULT 5
HUMADRA      1521 bp      DNA      linear      PRI 30-OCT-1994
LOCATION      Human platelet alpha-2-adrenergic receptor gene, complete cds.
DEFINITION      M18415.1 GI:178191
VERSION      alpha-2-adrenergic receptor; alpha-adrenergic receptor.
KEYWORDS      Homo sapiens
SOURCE      Human (lambda-EMBL 3 library) DNA.
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 1521)
AUTHORS      Koblika,B.K., Matsui,H., Koblika,T.S., Yang-Feng,T.L., Francke,U.,
Caron,M.G., Lefkowitz,R.J. and Regan,J.W.
TITLE      Cloning, sequencing, and expression of the gene coding for the
human platelet alpha 2-adrenergic receptor
JOURNAL      Science 238 (4827), 650-656 (1987)
MEDLINE      88042789
PUBMED      2823383
FEATURES
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Location/Qualifiers
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variation
305 a      676 c      624 g      336 t
BASE COUNT
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Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 41; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;
QY      1 CGGCTCCAGGCGCCGACAGCCGAGCGGTCGCCGGGG 41
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RESULT 6
AF262016      1941 bp      DNA      linear      PRI 22-AUG-2000
LOCUS      Homo sapiens adrenergic receptor alpha-2A gene, complete cds.
DEFINITION      AF262016
VERSION      AF262016.2 GI:9864781
KEYWORDS      Homo sapiens.
SOURCE      Homo sapiens.
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 1941)
AUTHORS      Castellano,M., Giacche,'M., Rossi,F., Rivadossi,F., Perani,C.,
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE      A search for genetic variability in the human alpha-2 adrenergic
receptor on chromosome 10
JOURNAL      Submitted (29-APR-2000) Medical and Surgical Sciences, University
of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy
3 (bases 1 to 1941)
AUTHORS      Castellano,M., Giacche,'M., Rossi,F., Rivadossi,F., Perani,C.,
Beschl,M. and Agabiti Rosel,E.
TITLE      Direct Submission
JOURNAL      Submitted (22-AUG-2000) Medical and Surgical Sciences, University
of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy
REMARK      Sequence update by submitter
COMMENT      On Aug 22, 2000 this sequence version replaced gi:9837145.
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Geography 10:151-160, 1996"
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variation
305 a      676 c      624 g      336 t
BASE COUNT
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Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGCTCCAGGGCCCCCGACGCCGCGTCCCGGGG 41
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DB 910 CGGCTCCAGGGCCCCCGACGCCGCGTCCCGGGG 950

RESULT 2
AX350513
LOCUS AX350513 1350 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 25 from Patent WO0179561.
ACCESSION AX350513
VERSION AX350513.1 GI:18616108
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1
AUTHORS Liggett, S.B. and Small, K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNML Patent: WO 0179561-A 25-25-0CT-2001;
Liggett, Stephen B. (US) ; Small, Kersten M. (US)
FEATURES
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BASE COUNT 199 a 489 c 442 g 220 t

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Query Match 100.0%; Score 41; DB 6; Length 1350;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGCTCCAGGGCCCCCGACGCCGCGTCCCGGGG 41
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DB 910 CGGCTCCAGGGCCCCCGACGCCGCGTCCCGGGG 950

RESULT 3
AF281308
LOCUS AF281308 1353 bp DNA linear PRI 05-DEC-2000
DEFINITION Homo sapiens alpha 2A adrenergic receptor (ADRA2A) gene, complete cds.
ACCESSION AF281308
VERSION AF281308.1 GI:9652209
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 1353)
AUTHORS Small, K.M., Forbes, S.L., Brown, K.M. and Liggett, S.B.
TITLE An asn to lys polymorphism in the third intracellular loop of the human alpha 2A adrenergic receptor impacts enhanced agonist-promoted Gi coupling
JOURNAL J. Biol. Chem. 275 (49), 38518-38523 (2000)
MEDLINE 20556293
PUBMED 10948191

REFERENCE
2 (bases 1 to 1353)
AUTHORS Small, K.M., Forbes, S.L., Bridges, K.M. and Liggett, S.B.
TITLE Direct Submission
JOURNAL Submitted (22-JUN-2000) Internal Medicine, University of

FEATURES
source
Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA
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ADRA2A

MRNA

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BASE COUNT 200 a 490 c 442 g 221 t

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Query Match 100.0%; Score 41; DB 9; Length 1353;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 910 CGGCTCCAGGGCCCCCGACGCCGCGTCCCGGGG 950

RESULT 4
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LOCUS AF316894 1353 bp DNA linear PRI 07-FEB-2001
DEFINITION Homo sapiens alpha 2A adrenergic receptor (ADRA2A) gene, complete cds.
ACCESSION AF316894
VERSION AF316894.1 GI:12698667
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 1353)
AUTHORS Small, K.M., Forbes, S.L., Brown, K.M. and Liggett, S.B.
TITLE An asn to lys polymorphism in the third intracellular loop of the human alpha 2A adrenergic receptor impacts enhanced agonist-promoted Gi coupling
JOURNAL J. Biol. Chem. 275 (49), 38518-38523 (2000)
MEDLINE 20556293
PUBMED 10948191

REFERENCE
2 (bases 1 to 1353)
AUTHORS Small, K.M., Forbes, S.L., Brown, K.M. and Liggett, S.B.
TITLE Direct Submission
JOURNAL Submitted (26-OCT-2000) Internal Medicine, University of Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA
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GenCore version 5.1.3
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	41	100.0	1350	6	AX350512	AX350512 Sequence
2	41	100.0	1350	6	AX350513	AX350513 Sequence
3	41	100.0	1353	9	AF281308	AF281308 Homo sapi
4	41	100.0	1353	9	AF316894	AF316894 Homo sapi
5	41	100.0	1521	9	HUMADRA	M18415 Human plate
6	41	100.0	1941	9	AF262016	AF262016 Homo sapi
7	41	100.0	3604	9	HUMADRA2R	M23533 Human alpha
8	41	100.0	3612	9	AY032736	AY032736 Homo sapi
9	41	100.0	3653	9	AF284095	AF284095 Homo sapi
10	41	100.0	204908	9	AL158163	AL158163 Human DNA
11	32	78.0	1454	10	MUSALP2ADB	M99377 Mouse alpha
12	32	78.0	1552	10	RNU79031	U79031 Rattus norv
13	32	78.0	2291	10	CPUD25722	U25722 Cavia porce
14	32	78.0	204317	2	AC113491	AC113491 Mus muscu
15	30.4	74.1	1728	4	PIGAZAR	J05652 Porcine alp
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18	26.8	65.4	7353	6	AX344975	AX344975 Sequence
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20	26.2	63.9	576	6	AX119101	AX119101 Sequence
21	26.2	63.9	1330	9	BC007699	BC007699 Homo sapi
22	26.2	63.9	1353	9	BC011825	BC011825 Homo sapi
23	26.2	63.9	109891	9	HS112K5	D85987 Human DNA s
24	25.6	62.4	2150	1	STMCR1	D55783 Streptomyce
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26	25.2	61.5	7011	10	RATRBBI	M92905 Rat calcium
27	25.2	61.5	9695	10	AF055477	AF055477 Rattus no
28	25.2	61.5	77534	1	AF235504	AF235504 Streptomy
29	25.2	61.5	163198	2	ALC095367	ALC095367 Rattus no
30	25.2	61.5	230685	2	AL390719	AL390719 Homo sapi
31	25	61.0	62306	2	AC111609	AC111609 Rattus no
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34	24.6	60.0	1186	9	BC011933	BC011933 Homo sapi
35	24.6	60.0	1423	9	HS092980	U92980 Homo sapien
36	24.6	60.0	65612	9	AL136304	AL136304 Human DNA
37	24.6	60.0	92863	12	GGBILOCUS	AL023516 Gallus ga
38	24.4	59.5	1877	9	BC021901	BC021901 Homo sapi
39	24.4	59.5	2630	9	AF091035	AF091035 Homo sapi
40	24.4	59.5	60163	9	AC012018	AC012018 Homo sapi
41	24.2	59.0	17597	9	AL390760	AL390760 Human DNA
42	24.2	59.0	230255	10	AL645569	AL645569 Mouse DNA
43	24.2	59.0	231562	9	AC010148	AC010148 Homo sapi
44	24	58.5	1170	5	AB044371	AB044371 Gallus ga
45	24	58.5	106649	2	AC122626	AC122626 Rattus no

ALIGNMENTS

RESULT 1
AX350512
LOCUS AX350512 1350 bp DNA
DEFINITION Sequence 24 from Patent WO0179561.
ACCESSION AX350512
VERSION AX350512.1 GI:18616107
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
Liggett,S.B. and Small,K.M.
Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 24 25-OCT-2001;


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Db 547 AACCGCACCTGACACCGTACCACTATTATCTGACCTGGCGTGGCGACCTG 606
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OY 61 CTGGTGGCCACGCTCGTATCCCTTTCGCTGCGCCAAACAGGTCATGGCTACTGTAC 120
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Db 727 ATCTTAGCTTGTCCGACATCTCCGTGGAACGGTACTGGGCTGGCCATCTACTCAAG 786
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OY 421 TGCATGGGCTCTTCTGCTGCCCTCATCATGATCTCTGTACTAGTGGCATCTAC 480
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Db 952 TCGGTGTCTCTTCTACTGCGCATGGCGGTATGCTGTGTCATGTACTGCGGTGAC 1011
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OY 481 CAGATGC-----CAAGCGTGCACCCGCGTGCACCCAGCGCGGGGTCCGAGCGC 534
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OY 535 GTGCGCGCGCGCGCGGCGGCGACGAGCGCAAGGCCAACGGTCTGGGCGCGCGAGC 594
    |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1072 GCTTCCGAGGTGTGTGCGATCCATGCTGCGGCGCGCCACGCGCGCGCGAGGCGG 1131
    |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 595 GCGGCGCGCGGCGGAGAGCGCAACCGCTGCCACCGCATACAGGCGCGCGCTGGC 654
    |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1132 CAGGCGATGCGCAGCGCCCAAGGCGCACACCTTCCGAGCTGCTCTCCGTGCGCTGCTC 1191
    |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 655 GAGCCCGCGC 664
    |||| | | | |
Db 1192 AAGTCTCTCC 1201
    |||| | | | |
```

Search completed: February 13, 2003, 07:50:10
Job time : 113.488 secs

QY 369 GGGCGAGCGCGCTGCCAGATCAACGACACGAAAGTGGTACGTATCTCGTCGTGGCATCGG 428
Db 764 GATGTGGAGCTGTGTGGGAACACCTTCAGATCTCTACACCATCTACACCACTGTGG 7050
QY 429 CTCTTTCTTGGCTCCGTCGCATCATGATCCTGGTCTACGTGGGATCTACAGATCGC 4888
Db 704 GGCCCTTCTACATTTCCCTCTGGGTGTGCTCATCTTATATGGCCGGATCTACCGGGCTGC 6450
QY 489 CAAGGTCGCAACCGCGGTGCACACCGCGCGGGGTCTCGGACGCGCTCGCGCGC 544
Db 644 CCGGACCGCATCTCTGAATTCACACCTTCACTTATGGGAGAGCGCTTACACACGGGCC 589

```

RESULT 14
US-09-822-830A-178
? Sequence 178, Application US/09822830A
? Patent No. US20020142952A1
? GENERAL INFORMATION:
? APPLICANT: Genetics Institute, Inc.
? APPLICANT: Mong, Gordon G.
? APPLICANT: Clark, Hilary
? APPLICANT: Rechtel, Kim
? APPLICANT: Agostino, Michael J.
? APPLICANT: Howes, Steven H.
? APPLICANT: Resnick, Richard J.
? APPLICANT: Gulikote, Kamalakr
? APPLICANT: Graham, James R.
? TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
? FILE REFERENCE: GIN 6402
? CURRENT APPLICATION NUMBER: US/09/822,830A
? CURRENT FILING DATE: 2001-03-29
? PRIOR APPLICATION NUMBER: 60/195,604
? PRIOR FILING DATE: 2000-04-06
? NUMBER OF SEQ ID NOS: 631
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 178
? LENGTH: 2173
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-822-830A-178

```

Query Match	11.1%;	Score 130.4;	DB 10;	Length 2173;
Best Local Similarity	52.1%;	Pred. No. 6.3e-18;		
Matches 340;	Conservative 0;	Mismatches 306;	Indels 6;	Gaps 2

QY 27 CCCTTCCTGGAGTCTCTGGGCGCTGGGCGAATCTCTGGTGGGACAGCGCTCTCACTCCCTT 86

Db 1 CTTCTCTCTGCTCAACCTCGCCATCTCGAGCTTCTCTGGGCGCCTTCCTGCATCCCACT 60

QY 87 CTGCGTGGCGCAACGAGTGCATGGGCTACTGTGTACTTCGGGCAAGGCTTTGGTGGAGATCTA 146

Db 61 GATATGTACCCCTACGTGCTGACAGGCGCGGTGAGACCTTCGGCGGGGCGCTCTGCAAGCTGATG 120

QY 147 CCTGGCGCTCGACGTGCTCTTCTGCAAGTCTGCTCATCTGTGCACCTGTGTGGCCATCAAGCT 206

Db 121 GCTGTAGTGGAGCTACCTGCTGTGTGACCTCTCTGCGCTTCAACATCTGTGCTCATCAAGCTA 180

QY 207 GACGCGTACGTGCTCATACACAGGCGCATGAGTAC---AACCTGAAGGCGCACGCGCG 263

Db 181 CGACCGCTTCTGTGTGGTACCCGAGGCGGTCTCATACCGGGCGCCAGAGGCTGACACGCG 240

QY 264 CGCGATCAAGGCGCATCATCATACCGTGTGGTGTATCTCGGCGCCTCATCTCTTCCCGGC 323

Db 241 GCGGGCAGTGGCGAAGATGCTGCTGTGTGTGGTGTGCTGGCTTCTCTGTGTACGAGACCAGC 300

QY 324 GCTCATCTTCATCGAAGAAAGGAGGCGGCGGCGGCGGCGGACCGGCGGCGGCGGCGCTG 383

Db 301 CATCTGAGCGTGGAGTACCTGTCCGGGGGAGCTCATCCCGAGGGGCACTGCTATGC 360

QY 384 CGAGATCAACGACCGAAGAGTGTACGTATCTGCTGTGATGTGGGCTCTCTTCTCGGTCC 443

Db 361 CAGATCTTCTTCAACTGTGTATCTTCATACGCGCTTCAACCTCGAGATGTTCTTTACGCC 420

QY	444	CTGCCTCATCATGATCCTGGTCTCTACGGCCGATTTACCAAGATGCGCAGGGGTGGACCCG	503
Db	421	CTTCTCTAGCCTCATCCTCTTTAACTCTAGATCTTACTTAACATCTCAGAGGGCCACCCG	480
QY	504	CGTGCACACCCAGCCGCGCGGGGTCCGAGACCGCTGCGCCGCGCGCGCGGGGGGACCCGAGCG	553
Db	481	CCTCCGGCTGGATGGGGGTCTCAGAGCGACGCCGGCGCCGAGGCCCTCTCCGAGGGCCACGCC	540
QY	554	CAGGCCCAAGGCTGTG--GGCCCCGAGCGCAGCGCGGGCCCCGGGGGGGCGCAGAGGCCGA	620
Db	541	CTCACACACCCACACCGCTGGCTCTGTGGGCTGTCTGCGAGAGGGGACAGGGGAGGCCAT	600
QY	621	ACCGTGGCCCAACCAAGCTCAAGGGGGGCCCTTGGGAGAGCCCGCGCGGCCGAG	672
Db	601	GCCGCTGACACAGTTATGGGGTGGGTGAGGCGGCGCCCTAGACGCTCAGAGGCCGGG	652

```

1      RESULT 15
2      US-10-185-991-1
3      / Sequence 1, Application US/10185991
4      / Publication No. US20030022900A1
5      /
6      / GENERAL INFORMATION:
7      / APPLICANT: Charles Gluchowski, et al.
8      / TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
9      / TREAT BENIGN PROSTATIC HYPERPLASIA
10     /
11     / NUMBER OF SEQUENCES: 6
12     /
13     / CORRESPONDENCE ADDRESS:
14     / ADDRESSEE: COOPER & DUNHAM LLP
15     / STREET: 1185 Avenue of the Americas
16     / CITY: New York
17     / STATE: New York
18     / COUNTRY: U.S.A.
19     / ZIP: 10036
20     /
21     / COMPUTER READABLE FORM:
22     / MEDIUM TYPE: Floppy disk
23     / COMPUTER: IBM PC
24     / OPERATING SYSTEM: PC-DOS/MS-DOS
25     / SOFTWARE: Patentln Release #1.24
26     /
27     / CURRENT APPLICATION DATA:
28     / APPLICATION NUMBER: US/10/185,991
29     / FILING DATE: 28-Jun-2002
30     / CLASSIFICATION: <Unknown>
31     /
32     / PRIOR APPLICATION DATA:
33     / APPLICATION NUMBER: 09/444,783
34     / FILING DATE: <Unknown>
35     /
36     / ATTORNEY/AGENT INFORMATION:
37     / NAME: White, John P.
38     / REGISTRATION NUMBER: 28,678
39     / REFERENCE/DOCKET NUMBER: 41878-AA-PCT-US/JPM
40     /
41     / TELECOMMUNICATION INFORMATION:
42     / TELEPHONE: (212) 278-0400
43     / TELEFAX: (212) 391-0525
44     /
45     / INFORMATION FOR SEQ. ID NO: 1:
46     /
47     / SEQUENCE CHARACTERISTICS:
48     / LENGTH: 2140 base pairs
49     / TYPE: nucleic acid
50     / STRANDEDNESS: single
51     / TOPOLOGY: unknown
52     / MOLECULE TYPE: DNA (genomic)
53     /
54     / HYPOTHETICAL: N
55     / ANTI-SENSE: N
56     /
57     / FEATURE:
58     / NAME/KEY: CDS
59     / LOCATION: 178..1893
60     / OTHER INFORMATION:
61     /
62     / SEQUENCE DESCRIPTION: SEQ ID NO: 1:
63     /
64     / US-10-185-991-1

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Query Match	10.9%;	Score 128;	DB 9;	Length 2140;
Best Local Similarity	52.1%;	Pred. No. 1.9e-17;		
Matches 349;	Conservative	0;	Mismatches 300;	Indels 21;
				Gaps 2;

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; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/371,705
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1645
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (284)..(1414)
US-10-005-010-1
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Query Match      11.3%; Score 132.4; DB 12; Length 1645;
Best Local Similarity 54.7%; Pred. No. 2.4e-18;
Matches 293; Conservative 0; Mismatches 231; Indels 12; Gaps 1;
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QY 9 GCTCAAGGCGCCCAAAACCTCTTCTGCTGCTGCTGCGCCGCGACATCCTGTGGC 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 487 GCTCCACACCCCTGCGCAACTGATGCTCCCTGCGCACACGACCTCTTGTTC 546
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 69 CAGCTGCTATCCCTTCTCGCTGCGGACAGATCATGGCTACTGCTTGGCAA 128
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 547 CATCTTGTAATGCCATTCAGCATGCGCTATACCATCACCACTGGAACTTTGGCCA 606
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 129 GCGTTGGTGGAGATCATCTGCGCGCTCGACGTCTCTTCTGACGTCGTCATCGTGA 188
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 607 AATCTTGTTGACATCTGGCTGTCTCTGATCAGTGTGACAGCCCTCATCTGTGA 666
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 189 CTTGTGGCCATCAGCTTGACCGGCTACTGTCTCATACACAGCCATCGAGTACAACCT 248
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 667 TCTCTGTCTATGCTCTGTGACAGGACTGTGGCAATCACAGATGCCCTGGAATACAGTAA 726
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 249 GAAGCGACGCCCGCGCATCAAGCCATCATCATCGTGTGGCTATCTCGGCGT 308
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 727 ACCGAGAGCGGTGGCCACAGCGGCCACCATGATCGCCATTTGTGGCCATCTCCATCTG 786
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 309 CATCTCTTCCCGCCGCTATCTTCATCGAAGAAAGGCGGCGCGCCCGCAGCC 368
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 787 CATCTCCATCCCGCCGCTCTTCTGCGGAGGCAAG-----GCCAGAGAGA 834
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 369 GCGCGAGCGCGCTGCGAGATCAAGCAGAGAGAGTGTGATCTGCTGCTGCTGATCGG 428
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 835 GATGTGGAGATCTGTGTGAACACCTCTAGATCTCTACACCATCTACTCCACCTGTGG 894
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 429 CTCTCTTCTGCTCCCTGCTCATCATGATCTGTGTACGTGCGCATCTACAGATCGC 488
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 895 GGCCTTCTCATATCCCTCGGTGTGCTCATATCTATATGCGCGGATCTACGGGCTGC 954
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 489 CAAGCGTGGACCGCGGTGCCACCCAGCGCGCGGGGTCCGAGCCCGCTGCGCGC 544
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 955 CGGGAACCGCATCTGATTCACCCCTCACTTATGGAAGCGCTTACACACGCGCC 1010
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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RESULT 13

```

US-09-864-761-3769/c
; Sequence 3769, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmiga-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
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; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 3769
LENGTH: 1973
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL049576.15
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2
US-09-864-761-3769
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Query Match      11.3%; Score 132.4; DB 10; Length 1973;
Best Local Similarity 54.7%; Pred. No. 2.5e-18;
Matches 293; Conservative 0; Mismatches 231; Indels 12; Gaps 1;
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```

QY 9 GCTCAAGGCGCCCAAAACCTCTTCTGCTGCTGCTGCGCCGCGACATCCTGTGGC 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1112 GCTCCACACCCCTGCGCAACTGATGCTCCCTGCGCACACGACCTCTTGTTC 1053
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 69 CAGCTGCTATCCCTTCTCGCTGCGGACAGATCATGGCTACTGCTTGGCAA 128
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1052 CATCTTGTAATGCCATTCAGCATGCGCTATACCATCACCACTGGAACTTTGGCCA 993
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 129 GCGTTGGTGGAGATCATCTGCGCGCTCGACGTCTCTTCTGACGTCGTCATCTGTGCA 188
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 992 AATCTTGTTGACATCTGGCTGTCTCTGATCAGTGTGACACACCTCCATCTGTGA 933
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 189 CTTGTGGCCATCAGCTTGACCGCTACTGCTCATACACAGCCATCGAGTACAACCT 248
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 932 TCTCTGTGTAATGCTCTGTGACAGGTACTGGGCAATCAGATGCCCTGGAATACAGTAA 873
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 249 GAAGCGACCGCGCGCGCATCAAGGCAATCATCATCGCTGTGGCTATCTGCGCGT 308
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 872 ACCGAGAGCGGTGGCCAGCGGCCACCATGATGCGCATGTCTGCGCATCTCCATCTG 813
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 309 CATCTCTTCCCGCGCTATCTTCATCGAGAGAGAGGCGGGGGGGGGCGCGCAGCC 368
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 812 CATCTCCATCCCGCGCTCTTCTGCGGCGAGGCAAG-----GCCAGAGAGA 765
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```

CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/349,755
  FILING DATE: 08-Jul-1999
  CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/09/042,780
    FILING DATE: <Unknown>
    APPLICATION NUMBER: US 08/985,090
    FILING DATE: 04-DEC-1997
  ATTORNEY/AGENT INFORMATION:
    NAME: Elizabeth A. Hanley
    REGISTRATION NUMBER: 33,505
    REFERENCE/DOCKET NUMBER: MNI-032CP
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (617)227-7400
    TELEFAX: (617)742-4214
  INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 2689 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
    MOLECULE TYPE: cDNA
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 291..1625
      SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-349-755-1

Query Match      11.4%; Score 133; DB 9; Length 2689;
Best Local Similarity 52.0%; Pred. No. 1.9e-18;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;

10 CTCGAAGCGCGCCCAAACTCTGCTGCTGCGCTGCGCGGACATCGTGGTGGCC 69
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
483 CTCGCGACCGAGAACAACTTCTCGCTCAACCTCGGCATCTCGATCTCTGTCGGC 542
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
70 AGCCTGCTATCCCTTTCGCTGCGCAACGAGTCAATGGCTACTGTTCTGGCAAG 129
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
543 GCCTTTCGATCCCATGTATGTACCTACGCTGACAGCGCGCTGACCTTGGCGCG 602
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
130 GCTTGGTGAGATCTACCTGCGCTGACGCTCTTGTGACAGTGTGCTCATGTGCAC 189
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
603 GGCCTTGCAAGCTGGGTGTAGTGAATCACTGCTGTGACCTCTCTGCTTCAAC 662
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
190 CTGTGGCCATACAGCTGAGCCGCTACTGTGTCATCACACAGGCCATCGAGTAC---AAC 246
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
663 ATCGTGTCTATCAGCTAGACCGCTTCTGCTGCGTCAACCGAGCGGTCTATACCGGGCC 722
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
247 CTGAAGCGCAGCGCGCGCATCAAGGCCATCATCACCCTGTGGGTCTATCTGGCC 306
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
723 CAGCAGGCTGACACCGCGCGGAGTGCAGAGATGCTGTGTGTGGTGGCTTTC 782
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
307 GTCATCTCTTCCCGCGCTCATCTCATCGAAGAAAGGGCGCGCGCGCGCCAG 366
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
783 CTGCTGTACGACAGCATCTGAGCTGGAGTACCTGTCCGGGGGACAGTCCATCC 842
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
367 CCGCGCGAGCGCGCGCTGAGATCAAGCAAGCCAGAAAGTGTACATCTGTGTGATC 426
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
843 GAGGGGCACTGTATGCGAGTCTTCTACAACTGTACTTCCATCAACGCGCTTCCAC 902
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
427 GGCCTCTTTCGCTCCCTGCTCATCATGATCTGTGTCTACGTCATCTACAGATC 486
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
903 CTGAGTCTTTCACCGCTTCTCAGCGTACCTTCTTAACTCACTACATCTTACCTG 962
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
487 GCCAAGCGTGCACCGCGTGCACACAGCGCGCGGGGTGCGGACGCGCTGCGCGCG 546
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
963 ATCCAGAGGCGACCGCGCTCCGCTGAGTGGGCTTGAAGAGCAGCGCGCGCGCGCC 1022
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
547 CCGGGGGGACACGAGCGAGCCCAACGATCTG---GGCGCGAGCGCAAGCGGGCGCG 603
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1023 CCTCCGAGGCGCACCGCCTTACACACCGCCACCGCTGTGCTGTGGGCTGTGCGAAG 1082
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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```

604 GGGGCGCGAGAGCGGACCGCTGCGCCACCCAGCTCAAGCGCGCGCTGCGAGCGCGG 663
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1083 GGGCAGCGGAGGCGCATCGCTGACACAGTATGGGTGTAGCGCGCGCTAGCGCT 1142
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
664 CCGGCGCGG 672
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1143 GAGGCGCGG 1151
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 10
US-09-166-334-1
Sequence 1, Application US/09166334
Patent No. US20020168708A1
GENERAL INFORMATION:
  APPLICANT: Andrew D. J. Goodearl and Sandra Gluckman
  TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
  NUMBER OF SEQUENCES: 39
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: LAHIVE & COCKFIELD, LLP
    STREET: 28 State Street
    CITY: Boston
    STATE: Massachusetts
    COUNTRY: USA
  ZIP: 02109
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/166,334
    FILING DATE:
  CLASSIFICATION:
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US/09/042,780
      FILING DATE:
    APPLICATION NUMBER: US 08/985,090
      FILING DATE: 04-DEC-1997
  ATTORNEY/AGENT INFORMATION:
    NAME: Elizabeth A. Hanley
    REGISTRATION NUMBER: 33,505
    REFERENCE/DOCKET NUMBER: MNI-032CP
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (617)227-7400
    TELEFAX: (617)742-4214
  INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 2689 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: cDNA
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 291..1625
      SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-166-334-1

Query Match      11.4%; Score 133; DB 9; Length 2689;
Best Local Similarity 52.0%; Pred. No. 1.9e-18;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;

10 CTCGAAGCGCGCCCAAACTCTGCTGCTGCGCTGCGCGGACATCGTGGTGGCC 69
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
483 CTCGCGACCGAGAACAACTTCTCGCTCAACCTCGGCATCTCGATCTCTGTCGGC 542
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
70 AGCCTGCTATCCCTTTCGCTGCGCAACGAGTCAATGGGCTACTGTTCTGGCAAG 129
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
543 GCCTTTCGATCCCATGTATGTACCTACGCTGACAGCGCGCTGACCTTGGCGCG 602
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
130 GCTTGGTGAGATCTACCTGCGCTGACGCTCTTGTGACAGTGTGCTCATGTGCAC 189
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603 GGCCTTGCAAGCTGGGTGTAGTGAATCACTGCTGTGACCTCTCTGCTTCAAC 662
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Db 493 CTGCTGACGAGACCAACCATTCGAGCTGGAGTACCTGTCCGGGGGCACTCCATCC 552
QY 367 CCGCCGAGCCGCGCTGAGATCAACGACCAAGTGTACGTATCTGTGTCATC 426
Db 553 GAGGGCCACTGCTATGCGGAGATTCTTTACACAGTGTACTTCCATCAGCGCTCCACC 612
QY 427 GGCCTCTTCTGCTCCCTGCTCATCATGATCTGTGTACAGTGGGCACTACAGATC 486
Db 613 CTGAGTCTTTACGCCCTTCTCAGCGTCACTTTTAACTCAACATCTACCTGAAAC 672
QY 487 GCCAAGGTGTGACCCGCGGTGCGAACCCAGCGCCGGGGTCCGGAGCGGCTGCGCGC 546
Db 673 ATCCAGAGGCGCACCGCTCTCGGCTGTGATGAGGCTGTGAGAGGAGCGCGCCGACC 732
QY 547 CCGGGGCGACCGAGCGCGAGGCCCAACGCTGTG--GGCCCCGAGCGCGCGCGCG 603
Db 733 CCTCCGAGAGGCCAGGCCCTACACACCCAGCGCTGCTGGGCTGTGCGACAGAG 792
QY 604 GGGGCGCAGAGCGCGAAGCGCTGCGCCACCCAGCTCAACGCGCGCGCGCGAGCGCG 663
Db 793 GGGCAGGGGAGGCGCATGCGCTGTGACAGGTATGGGGTGGAGGCGCGCTGAGCGCT 852
QY 664 CCGGCGCGG 672
Db 853 GAGGCGCGG 861

RESULT 8
US-09-350-206-3

? Sequence 3, Application US/09350206
? Patent No. US2002009919A1

? GENERAL INFORMATION:
? APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman

? TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
? NUMBER OF SEQUENCES: 39

? CORRESPONDENCE ADDRESS:
? ADDRESSEE: LAHIVE & COCKFIELD, LLP

? STREET: 28 State Street
? CITY: Boston

? STATE: Massachusetts
? COUNTRY: USA

? ZIP: 02109

? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk

? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25

? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/350,206

? FILING DATE:
? CLASSIFICATION:

? PRIORITY APPLICATION DATA:
? APPLICATION NUMBER: 09/042,780

? FILING DATE:
? ATTORNEY/AGENT INFORMATION:

? NAME: Elizabeth A. Hanley
? REGISTRATION NUMBER: 33,505

? TELEPHONE: (617)227-7400
? TELEFAX: (617)742-4214

? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:

? LENGTH: 1335 base pairs
? TYPE: nucleic acid

? STRANDEDNESS: single
? TOPOLOGY: linear

? MOLECULE TYPE: cDNA
? FEATURE:

? NAME/KEY: CDS
? LOCATION: 1..1335

? US-09-350-206-3

Query Match 11.4%; Score 133; DB 10; Length 1335;
Best Local Similarity 52.0%; Pred. No. 1.8e-18;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;

QY 10 CTCMAAGCGCCCAAACTCTTCTGCTGTGTCTGTGGCTGGCGGACATCTGTGGCG 69
Db 193 CTCGCGACCCAGAACAACTTCTTCTGCTCAACCTCGGCATCTGCACTTCTGTGGC 252
QY 70 AGCGTGTATCCCTTTCGCTGCGTGGCCAGAGGATGATGCTGACTTCTGGCAAG 129
Db 253 GCCTTGTGATCTCCACTGTATGTACCTTACGTGTGACAGGCGCGGTGGACCTTGGCGG 312
QY 130 GCTTGTGTGAGATCTACCTGCGGCTGACGTGCTTCTTGTGACGTCTTCATCTGTGAC 189
Db 313 GCGCTGTGAGAGTGTGGGTGATGAGTACTGTCTGTGACCTCTTCTGCTTCAAC 372
QY 190 CTGTGGCCATACGCTGTGACGCTCTGTGTCTCATACAGAGCCATGTGATAC--AAC 246
Db 373 ATGCTGTCTATGACGTACAGACCGCTTCTGTGTGATACCCGAGCGGTCTCATACGGGCG 432
QY 247 CTGAGAGCGACGCGCGCGCATCAAGGCCATCATCATCATCATCATCATCATCATCAT 306
Db 433 CAGCAGGGTACACGCGGCGGCGAGTGGGAGATGCTGTGTGTGGGTGTGGGCTTTC 492
QY 307 GTCATCTCTTCCCGCGCTCATCTCTCATCTCATGAGAAAGGCGCGCGCGCGCGAG 366
Db 493 CTGCTGTACGAGACCGACCATCTGAGCTGTGAGTACCTGTCTGTGGGAGCTTCATATCCC 552
QY 367 CCGGCGGAGCGCGGCTGCGGATCAACGACCAAGATGTGATCTCATCTGTGTGATC 426
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QY 427 GGCCTCTTCTGCTCCCTGCTCATCATGATCTGTGTACGTGGCATCTTACAGATC 486
Db 613 CTGAGTCTTTACGCCCTTCTCAGCGTCACTTTTAACTCAAGCATCTTACCTGAAC 672
QY 487 GCCAAGCGTGTGACCGCGCGTGTGCCAACCCAGCGCGCGGCTGCGAGCGCGCGG 546
Db 673 ATCCAGAGGCGCACCGCTCTCGGCTGTGATGGGCTGTGAGAGCAGCGCGCCAGCGCC 732
QY 547 CCGGGGCGACCGAGCGCGACCCCAACGCTGTG--GGCCCCGAGCGCGCGCGCGCG 603
Db 733 CCTCCGAGAGGCCAGGCCCTACACACCCAGCGCTGTGCTGGGCTGTGCGACAGAG 792
QY 604 GGGGCGCAGAGCGCGAAGCGCTGCGCCACCCAGCTCAACGCGCGCGCGCGAGCGCG 663
Db 793 GGGCAGGGGAGGCGCATGCGCTGTGACAGGTATGGGGTGGAGGCGCGCTGAGCGCT 852
QY 664 CCGGCGCGG 672
Db 853 GAGGCGCGG 861

RESULT 9
US-09-349-755-1

? Sequence 1, Application US/09349755
? Patent No. US20020166131A1

? GENERAL INFORMATION:
? APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman

? TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
? NUMBER OF SEQUENCES: 39

? CORRESPONDENCE ADDRESS:
? ADDRESSEE: LAHIVE & COCKFIELD, LLP

? STREET: 28 State Street
? CITY: Boston

? STATE: Massachusetts
? COUNTRY: USA

? ZIP: 02109

? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk

? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25

NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1335
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-349-755-3

Query Match 11.4%; Score 133; DB 9; Length 1335;
Best Local Similarity 52.0%; Pred. No. 1.8e-18;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;

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QY 10 CTCGAAGCGCGCCAAACCTCTTCGTGCTCTCTGCTCGGCTCGGCGACATCCTGGTGCC 69
DB 193 CTCGCGACCCAGACACTCTTCCTGCTCAACCTGCGCATCTCCGACTTCTCTGCGGC 252
QY 70 ACGCTGTCATCCCTTCTTCGTGCGCCACGAGATCATGGCTACTGTAATTCGGCAAG 129
DB 253 GCCTTCTGATCCGATGATGATACCTTACGCTGACAGCGCGCTGACCTTCGGCGG 312
QY 130 GCTTGTGCGAGATCTACTGCGGCTGACGCTCTTCTTGACGTCGTCATCTGTCAC 189
DB 313 GGCCTCTGCAAGCTGTGGTAGTGACCTGCTGTCGACCTCTCTGCTTCAAC 372
QY 190 CTGTGGCCATGAGCTGAGCGCTACTGTGTCATCAGACAGCCATCGAGTAC---AAC 246
DB 373 ATGCTGCTATCAGCTACGACGCGCTCTGCTGCTCAGCCGAGCTCTCAATACCGGCGC 432
QY 247 CTGAAGCGGACCGCGCGCGCATCAAGGCCATCATCATCAGCTGCTGGTCTCTCGGCC 306
DB 433 CAGCAGGGGTGACAGCGGGGCGGACAGTGGGAGATGCTGTGGTGTGGTGTGGCTTC 492
QY 307 GTCATCTCTTCCCGCGCTCATCTTCATCGAAGAAAGGCGGCGGCGGCGCGCGAG 366
DB 493 CTGCTGTACGACCAAGCATCTGAGCTGGGAGTACTCTGTCGGGGGAGCTCCATCCCC 552
QY 367 CCGGCGAGCGCGCTGCGAGATCAAGCAGAGTGGTGGTATCTGCTGCTGATC 426
DB 553 GAGGGCAGCTGCTATGCGGAGTCTTCTTACAACTGTAATCTCTCATACGGCTTCACG 612
QY 427 GCGTCTTCTTCTGCTCCGCTGCTCATATCATCTGATCTGATGCGCATCTACAGATC 486
DB 613 CTGAGATCTTTCACCTCTCTCTCAGCTCACTTCTTAACCTACAGATCTACTGAC 672
QY 487 GCGAAGCGTGAAGCGGCGTGCACCCAGCGCGGGTCCGGAGCGCGCTGCCCGCG 546
DB 673 ATCTCAGAGGCGACCGCGCTCCGGTGGATGGGCTGAGAGGAGCGCGCGCGAGCCC 732
QY 547 CCGGGGGGACCGAGCGGCGCCCAACGATCTG---GGCCCGGAGCGGAGCGGCGCGCG 603
DB 733 CTTCCCGAGGCGCCAGCCCTTCAACACCCCGCGCTGCTGCTGCTGCTGCTGCTGCTG 792
QY 604 GGGGCGCGAGAGCGGAGCCGCTGCCACCACTCAAGCGCGCGCGCTGCGAGCGCGCG 663
DB 793 GGGCAGGGGAGGCGCATGCGCTGACAGGATATGGGTGAGGCGGCGCGCTGAGCGCT 852
QY 664 CCGGCGGCG 672
DB 853 GAGGCGGCG 861
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RESULT 7

US-09-166-334-3
Sequence 3, Application US/09166334
Patent No. US20020168708A1
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/166,334
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/042,780
FILING DATE:
APPLICATION NUMBER: US 08/985,090
FILING DATE: 04-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1335
US-09-166-334-3

Query Match 11.4%; Score 133; DB 9; Length 1335;
Best Local Similarity 52.0%; Pred. No. 1.8e-18;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;

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QY 10 CTCGAAGCGCGCCAAACCTCTTCGTGCTCTCTGCTCGGCTCGGCGACATCCTGGTGCC 69
DB 193 CTCGCGACCCAGACACTTCTTCCTGCTCAACCTGCGCATCTCCGACTTCTCTGCGGC 252
QY 70 ACGCTGTCATCCCTTCTTCGTGCGCCACGAGTCAAGGCTACTGTAATTCGGCAAG 129
DB 253 GCCTTCTGATCCGATGATGATACCTTACGCTGACAGCGCGCTGACCTTCGGCGG 312
QY 130 GCTTGTGCGAGATCTACTGCGGCTGACGCTCTTCTTGACAGTCTGTCATCTGTCAC 189
DB 313 GGCCTCTGCAAGCTGTGGTAGTGACCTGCTGTCGACCTCTCTGCTGCTGCTGCTG 372
QY 190 CTGTGGCCATGAGCTGAGCGCTACTGTGTCATCAGACAGCCATCGAGTAC---AAC 246
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QY 247 CTGAAGCGGACCGCGCGCGCATCAAGGCCATCATCATCAGCTGCTGGTCTCTCGGCC 306
DB 433 CAGCAGGGGTGACAGCGGGGCGGACAGTGGGAGATCTGCTGTGGTGTGGTGTGGCTTC 492
QY 307 GTCATCTCTTCCCGCGCTCATCTTCATCGAAGAAAGGCGGCGGCGGCGCGCGAG 366
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RESULT 5
US-09-954-531-995
; Sequence 995, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Can
; TITLE OR INVENTION: Gene Sets
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 995
; LENGTH: 2625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-995

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Query Match      12.1%; Score 141.4; DB 9; Length 2625;
Best Local Similarity 47.9%; Pred. No. 3.9e-20;
Matches 548; Conservative 0; Mismatches 576; Indels 21; Gaps 4;

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QY 7 GCGCTCAAGGGGCCCCAAACCTCTCTCTGCTGCTGCTGCGGCGGACATCCTGGTG 66
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DB 355 GCGCTGACAGACCCACCACTGATGATGATGATGATGATGATGATGATGATGATG 414
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QY 67 GCGACGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 126
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DB 415 GCGACACGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 474
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QY 127 AAGGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 186
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DB 475 AAGATTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 534
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QY 187 GACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 246
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DB 535 AACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 594
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QY 247 CTGAAGCGACGCGCGCGCGCATCAAGGCGCATCATCATCATCATCATCATCATCAT 306
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DB 595 ACGCGCTACAGCTCAAGGCGCGCGGTCAACCGCTCATCATCATCATCATCATCATCAT 654
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QY 307 GTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 366
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DB 655 TTTCACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 714
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QY 367 CCGGCGAGCGCGCGCTGCGAGATCAACAGCAAGAGTGTAGCTGCTGCTGCTGCTGCT 426
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DB 715 ATTGCAACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 762
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QY 427 GCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 486
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DB 763 GTGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 822
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QY 487 GCCAAGCGTGCAGCCGCGTGCACCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 546
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DB 823 CCGAAGCGAGTCAACACCAAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 882
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QY 547 CCGGCGGCGACGAGCGCGCAAGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 606
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DB 883 CTAAAGGCACTGTACTACCCCGACGACATGAATACTCTGACCGCTTATGATGAAGTCT 942
QY 607 GCGCGAGAGCGCGAACCCTGCTGCCACCAAGCTCAACGGCGCCCTGCGAGCCGCGCG 666
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 943 AATGGAGATTTCACATGAACAGCGGAGAGTGGAGGCTGCCCGCGAGCCAGGAGCTG 1002
QY 667 GCCGGCGCGCGGACACCGCGCTGACCTGAGCTGAGAGAGAGTGTCTTTCCGACACGCG 726
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DB 1003 GAGATGAGATGCTCTCCAGCACAGCCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1062
QY 727 GAGCGCTTCCAGGGCGCGCGCGAGACCGCGAGCGCGGCTCCCGGCGCAAGAGCGCGCG 786
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DB 1063 CCCAGCCACACAGCTGACTCTCCCGGACCGCTCCACACAGAGTCCACAGCACTGCT 1122
QY 787 GCGAGCCAGTGAAGCGGGCGACA---GCTGCCGCGCGCGCGCGCGCGCGCGCGCGCG 842
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DB 1123 GACAGCGCGCGCAACAGAGAAAGATGGGCTATGCCAAGAACACCCCAAGATTGCCAAG 1182
QY 843 GATCGGAGCGCGCGCTGCGAGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
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DB 1183 ATCTTGAATCCAGACCAATGCCAATGCAAAACCGGACCTCCTCAAGACATGAGC 1242
QY 901 CGCTGCGCGCGCGCGAGAACCGCGAAGCGCTTACGCTGCTGCGCGCTGCTGCTGCTGCT 960
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DB 1243 CGTAGAAGGCTGCCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1302
QY 961 GGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1017
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DB 1303 GCGGTGTTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1362
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QY 1018 GGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1077
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DB 1363 GACTGCAACATCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1422
QY 1078 TCGTTGAACCGGCTCATCTACCATCTTCAACCAAGATTTCCGCGCGCTTCAAGAG 1137
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DB 1423 GCGGTGAACCCCATCATCTACACCATCTTCAACCATTTGAGTTCGCAAGGCTTCTGAG 1482
QY 1138 ATCCT 1142
DB 1483 ATCCT 1487

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RESULT 6
US-09-349-755-3
; Sequence 3, Application US/09349755
; Patent No. US20020166131A1
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/349,755
; FILING DATE: 08-Jul-1999
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,780
; FILING DATE: <unknown>
; APPLICATION NUMBER: US 08/985,090
; FILING DATE: 04-DEC-1997
; ATTORNEY/AGENT INFORMATION:

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QY	481	CAGATGCGCAAGCGTCGACACCGCGTGGCCACCA-----GCCCGC	521
Db	589	CTGATGCGCCAAAGCGACCAACCGCAGAGGTCTCCAGGGCCAAAGGGGGGCGTGGGAGAGGT	648
QY	522	GGGTCGGGAAGCGCGTCGGCGCGCGCGCGGGGGGACACCGAGCCGACCCCAAGCGTGT--	579
Db	649	GAGTTCACAGACGCCCGACCCGACCCATGATGTTGGGGCTTTGGCTTACGCCAAACTGCAACC	708
QY	580	-----GGCCCCGAGCGACGCGGGGCGCGGGGGGCGCAAG	615
Db	709	CTGAGCTCTGTGGCTTCTGCCAGAGAGTCAACGCGACACTCGAAGTTCAGTGGGGGAAG	768
QY	616	GCCGAACCGCTGCGCCACACCGACTCAACGGGGGCCCTTGGGAGACCCGCGCGCGCGCGCG	675
Db	769	GAGAGGGGGAGACCCCTTGAAATCTGGGAGACCCGGGCTTGTCCACCCAGTTGGGCTGC	828
QY	676	GCGACACCCGACCGCTGACCTGGAGAGAGGTGCTTTCGACACCGCGCGCGCTT	735
Db	829	CTTCCCAACTCAGGCCCGAGGGCCAGAGAGGGGTTTGGGGGCAATCTTCACAGAGATGAA	888
QY	736	CCAGGGCCCCGACAGACCCGAGCGCGGTCCCCGGGGGCAAGGCAAGGCCGACGAGCCAG	795
Db	889	GCTTAAAGAGAGAGAAAGAGAGAGAGAGTGTGAACCCGAGGCACTGCAGTGTCTCCG	948
QY	796	GTAAGCCGGGCGCACACTGCGCGCGCGCGCGCGCGCGCGCGAGATCGGAGACGCCG	855
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QY	856	GCTCAGAGGGCGCGGGGAGAGAGCGGTGGGGCTGCCA-----AGCGTTCGGCTGG	906
Db	1009	CGTGGCAGAGTGTCTCTGGGCGAGGGGCGTGGGTGCTTAAGTGGGCAAGTGGGGTCCA	1068
QY	907	CGCGGGGGGCGAAGCCCGAGAAAGCGCTTACGTTGCTGTGGCCGTGCTCATTCGAGTg	966
Db	1069	CGGGCGACGCTGACCCCGGAGAAAGCGTTTACTTGTGTGGCTTGGTTCATTTGGCGTT	1128
QY	967	TTTCGTGTGCTGTGTTTCCCTTCTTCTTCACTTACACGCTCACGGCGGTGGG-----	1020
Db	1129	TTTGGGCTCTCTGTTGCCCTTCTTCTTCAAGCTACAGCCTGGGCGCCATCTGGCCGAAG	1188
QY	1021	---TGCCTCGGCGACGAGCGACTTTCAAATTCCTTCTTGTGGTGGCTACTGCAACAGC	1077
Db	1189	CACGTGCAAGGTGCCCCATGGCTTCTTCAGATTTCTTCTTGATTCGGCTAAGTSCAACAAC	1248
QY	1078	TGCTTGAACCGCGTATCTACCATCTTCAACCAACGATTTCCGCGCGCTTCAAGAAG	1137
Db	1249	TCACGACACCTGTATCTACCATCTTCAACCAAGAGACTTCCGCGTGCCTTCCGGAGG	1308
QY	1138	ATCCTCTGCG	1148
Db	1309	ATCCTGTGCG	1319
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US-10-077-870-3			
; Sequence 3, Application US/10077870			
; Publication No. US20030003470A1			
; GENERAL INFORMATION:			
; APPLICANT: Salonen, Jukka T			
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof			
; FILE REFERENCE: 0933-0183P			
; CURRENT APPLICATION NUMBER: US/10/077,870			
; CURRENT FILING DATE: 2002-05-21			
; PRIOR APPLICATION NUMBER: FI 20010323			
; PRIOR FILING DATE: 2001-02-20			
; NUMBER OF SEQ ID NOS: 10			
; SOFTWARE: PatentIn Ver. 3.1			
; SEQ ID NO 3			
; LENGTH: 1353			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			

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: LOCATION: (1)...(1350)
: OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein
US-10-077-870-3

Query Match          34.3%; Score 400.8; DB 9; Length 1353;
Best Local Similarity 63.3%; Pred. No. 2.2e-72;
Matches 772; Conservative 0; Mismatches 367; Indels 81; Gaps 77

OY 1 AGCCGCGGCGCTCAAGAGCGGCGCCCAAAACCGCTCTCTCGTGTGTCTCTGTGAGCCTCGGCGCGACATC 60
Db 118 ACCCGCTGCTGTGGGGCCCCCTCAGAACCGTGTCTGTGTGTCTGTGCTGGCGCGCGACATC 177
OY 61 CTGTGTGGCCACGCTGTCATCCCTTTCTCTCTGTGGCCACAGAGTCAATGGGCTACTGTGTAC 120
Db 178 CTGTGTGGCCACGCTCATCATCTCCCTTTCTCTGTGGCCACAGAGTCAATGGGCTACTGTGTAC 237
OY 121 TTTCGGCAGAGCTTGTGTGGGAGATCTCAACCGGGGCGGTGAGCTGTCCTCTTCTGCACGTCGTAC 180
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1 NAME/KEY: terminator
2 LOCATION: 1864..1866
3 OTHER INFORMATION: /note="Bacteriorhodopsin stop
4 OTHER INFORMATION: codon."
5 FEATURE:
6 NAME/KEY: mutation
7 LOCATION: replace(213, "")
8 OTHER INFORMATION: /note="G to T mutation removes
9 OTHER INFORMATION: AlwNI restriction site."
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11 NAME/KEY: misc-feature
12 LOCATION: 427..435
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16 LOCATION: replace(930, "")
17 OTHER INFORMATION: /note="G to A mutation removes
18 OTHER INFORMATION: AlwNI restriction site."
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20 NAME/KEY: mutation
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35 LOCATION: replace(1863, "")
36 OTHER INFORMATION: /note="C to T mutation removes
37 OTHER INFORMATION: AlwNI restriction site."
38 FEATURE:
39 NAME/KEY: terminator
40 LOCATION: 1813..1815
41 OTHER INFORMATION: /note="Muscardinic "OMI" stop
42 OTHER INFORMATION: codon."
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44 US-08-767-993-6

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Qy	727	GAGCGGCTCCAGGGGCCCCAGACCCGAGCGCGGTCGCCGGGG--CAAAAGCAAGCGCC	785
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Qy	786	AGCGAGCCAGTGAAGCCGGGGCAGACGCTGCCGGGGCGGGGGGGGAGCAGGGGAT	845
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Search completed: February 13, 2003, 07:46:58
Job time : 106.502 secs

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; NAME/KEY: misc_feature
; LOCATION: 376..414
; OTHER INFORMATION: /note="Bacteriorhodopsin
; OTHER INFORMATION: pre-sequence."
; FEATURE:

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Page 9

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QY	69	CACGCTGCTATCCCTTTTCTGCTGGCCAAAGAGTCATGGCTACTGTGTTAGCTGGGCAA	128	
Db	547	CATCTTGTGTAATGGCCCATCAGCATGCGCTATTAACATCACCACCACTGGAACTTTGGCCA	606	
QY	129	GGCTTGGTCCGAGATCTACTGCGCTGCACGTGCTCTTCTGTGACGTCGTCCATGTGCA	188	
Db	607	AATCTTGTGTGACATCTGGCTGTCTTACATCATCAGCTGCTCACGCCCTCATCTCTGCA	666	
QY	189	CGTGTGGCCATCAGCCTTGAGCCGCTACTAGTGCATCAGACAGGCCATCGAGACAACT	248	
Db	667	TCTCTGTGTCATGTGCTCTGTGACAGTATGGGCATACAGATGGCCCTTGGAATACGTAA	726	
QY	249	GAAGGCGACAGCGCGCGCGCATCAAGGCCATCATCATCACCCTGTGGGTATCTCGGCCGT	308	
Db	727	ACGCAAGAGCGCTGGCCACGCGGCCACCACTGATCGCATTTGCTGGGGCATCTTCATCTCG	786	

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Dn      /8/ CACTTCATCCCCCGCTCTTCTTGCGGCGAGGCCAAG-----GCCACGAGAGA
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Db      835 GAGTGTGAGCATGTCTGTGTGTAAACCTCTCAGATCTCTTACACCATCTACTTCACTGTGG
Qy      429 CTCCTTCTTGCGTCCCTGCGCTCAATCAATGATCTGCTGTACGTGGCATCTTACAGATGCG
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Db      895 GGGCTTCTACATTCCTCGCTGGGTGTGCTATCATCATATATAGCGGAGATCACGGGGCTGC
Qy      489 CAAGCTCTCACCGCCGTCGACCCAGCCAGCGCGGGGGCCGAGAGCGCTGCGCGGC 544
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RESULT 13
; Sequence 1, Application US/08194338
; Patent No. 5474898
;
; GENERAL INFORMATION:
;
; APPLICANT: Venter, John C.
; APPLICANT: Fraser, Claire M.
; APPLICANT: McCombie, William R.
; TITLE OF INVENTION: OCTOPAMINE RECEPTOR
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbie, Martens, Olson and Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,338
; FILING DATE: 08-FEB-1994
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,174
; FILING DATE: 28-MAR-1991
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH101.001DV1

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RESULT 10
US-09-642-855-5
; Sequence 5, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/642,855
; PRIOR FILING DATE: 2000-08-21
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-855-5

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Best Local Similarity 52.0%; Pred. No. 2.2e-16;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;

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RESULT 11
US-09-642-514-5
; Sequence 5, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: ORN1290
; CURRENT APPLICATION NUMBER: US/09/642,514
; PRIOR FILING DATE: 2000-08-21
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-514-5

Query Match 11.4%; Score 133; DB 4; Length 2699;
Best Local Similarity 52.0%; Pred. No. 2.2e-16;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;

QY 10 CTCAGGCGGCCCAAACTCTCTGCTGTCTGCTGCGCTGCGCGACATCTGGTGGC 69
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Db 491 CTCGGACCCAGAACACTTCTCTGCTCAACCTCGCATTCGCACTTCTGCTGGC 550
QY 70 ACGCTGCTATCCTTTCTGCTGGCCAGAGGTATATGGGCTACTGCTCTCGGCAAG 129
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Db 671 ATCTGTGCATCAGCTACGACCGCTCTCTGCTGCTACCGAGGGGTCTCATACGGGGCC 730
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    || || || || || || || || || || || || || || || || || || || ||
Db 731 CAGAGGGGTGACAGCGCGCGGAGTGGGAGAGTGTCTGTGGTGTGGCTTTC 790
QY 307 GTCATCTCTTCCGCGCGCTCATCTCATCGAAGAAAGGGCGCGCGCGCGCGAG 366
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QY	10	CTCAAGGCGGCCAAAAACCTTTCCTGGGTCTCTGGCCCTCGGCCCAACATCTCGTGGCGCC	69
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RESULT 9
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: Sequence 5, Application US/09167354A
: Patent No. 6136559
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: GENERAL INFORMATION:
: APPLICANT: Lovenberg, Timothy
: APPLICANT: Erlander, Mark
: APPLICANT: Pyati, Jayashree
: APPLICANT: Huvar, Arne
: TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
: FILE REFERENCE: JMW
: CURRENT APPLICATION NUMBER: US/09/167,354A
: CURRENT FILING DATE: 1998-10-07
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 5
: LENGTH: 2699
: TYPE: DNA
:
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: CDNA
: US-09-167-354-5

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QY	70	ACGCTGTCATCCCTTCTTCTGCTGGCCCAACGAGTCAATGAGGCTACTGTCTTCTGGCAAG	129	111	111	111	111	111
Db	551	GCCCTTCTGCATCCCACTGTATATACCTACAGTGTGACAGCGCCGTGGACCTTCTGGCGG	610	111	111	111	111	111
QY	130	GCCTTGGGGAATCTACTGGCGCTCCAGCTGCTCTTCTGACAGTGTCCATCTGAC	189	111	111	111	111	111
Db	611	GGCCTTGCAACTGTGGCTGGTACTGGACACTCTGCTGTACACTCTCTGCTTCAAC	670	111	111	111	111	111
QY	190	CTTGTGGCCATGAGCCTGGACCGGTACAGTGGTCCATACACAGGCACTCAGATAC	246	111	111	111	111	111
Db	671	ATCGTCTATATAGCTACGACCGCTTCTCTTCTGGTACCGAGCGGTCTATACCGGGCC	730	111	111	111	111	111
QY	247	CTGAAAGCGACCGCGCGCGCATCAAGGCCATCATCAACCGTGTGGGTCACTTCGGCC	306	111	111	111	111	111
Db	731	CACAGAGGAGACACGGGGGGGAGATGGGGAAGATGCTGCTGTGGGTGCTGTGGCTTC	790	111	111	111	111	111
QY	307	GTCTATCTCTTCCCGCCGCTCATCTCCATCGAAGAAGGGGGGGCGGCGGCCCGAC	366	111	111	111	111	111
Db	791	CTGCTGTATAGGACACGACCATCTCTGAGCTGGAGATACCTGTCTGGGGGCACTCTCATCCCG	850	111	111	111	111	111
QY	367	CGGGGCGACCGCGCTGGAGATCAAGACACCAAGATGGTACGTCTCTGCTGTCATC	426	111	111	111	111	111
Db	851	GAGGGCACTGCTATAGCCGAGTCTTCTTACAAAGTACTCTCTCATCAACGAGCTTCACAC	910	111	111	111	111	111
QY	427	GCGTCTCTTCTGCTCCCTGCGCTATATGATCTGTGCTACGAGGCACTTACACAGATC	486	111	111	111	111	111
Db	911	CTGAGATCTTACGCCCTTCTCTAGGCTCACTCTTCTTAACTCAACACTTACCTGTAAC	970	111	111	111	111	111
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Db 433 CACGACGGTGTACACGCGGCGGCGCATGCGGAGATGCTGTGTGGTGTGCTGCTTC 492
QY 307 GTGATCTCTTCCCGCGGCTCATCTCCATCGAGAGAGGGGCGGCGCGCGCGAG 366
Db 493 CTCTCTAGGACGACGACATCTGAGCTGGAGTACTCTCCGGGGGCGACCTCCATCCCC 552
QY 367 CCGGCGAGCGCGCTGCGGATCAACGACGACGAGAGTGTAGCTCATCTCTGTGTGATC 426
Db 553 GAGGGCAGCTATGCTGCGGATCTCTCAAGTGTACTCTCATACAGGCTTCACAC 612
QY 427 GGTCTCTTCTTCCCTCCCTGCTCATCATGATCTGTGTAGTGGGCTATACGATC 486
Db 613 CTGAGATCTTTAGCGCTTCCTCAGCGTCACTCTTAACCTCAGCATCTTCAAG 672
QY 487 GCGAAGGTGTGACCGCGCGGCGGACCGGCGGCTGCGGCGCGCTGCGCGCGCG 546
Db 673 ATCCAGAGGCGCACCGGCTCCGGCTGAGTGGGGCTCGAGAGGCGACCGGCGCGAGCC 732
QY 547 CCGGGGGGCGACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 603
Db 733 CCGCGGAGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 792
QY 604 GGGGGGCGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 663
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Db 853 GAGGCGGCGG 861

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RESULT 7

US-08-985-090-1
 ; Sequence 1, Application US/08985090
 ; Patent No. 5885893

GENERAL INFORMATION:

APPLICANT: Andrew D.J. Goodearl
 TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USRS THEREFOR
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentln Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/985,090
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Jean M. Silverl
 REGISTRATION NUMBER: 39,030
 REFERENCE/DOCKET NUMBER: MNI-032
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)742-4214
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2689 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 FEATURE:

NAME/KEY: CDS
 LOCATION: 291..1625
 US-08-985-090-1

Query Match 11.4%; Score 133; DB 2; Length 2689;
 Best Local Similarity 52.0%; Pred. No. 2,2e-16;
 Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;

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QY 10 CTGAAGGCGCCCAAAACCTTCTCCTGCTGTCTGTGGCTGCGGCGGACATCGTGGCC 69
Db 483 CTCCGACACCAAGAAACCTTCTCCTGCTGTCTGTGGCTGCGGCGGACATCGTGGCC 542
QY 70 ACGCTGCTATCCCTTCTCCTGCTGTCTGTGGCTGCGGCGGACATCGTGGCTGCGGAG 129
Db 543 GCTTCTGCTATCCCTGCTGTCTGTGGCTGCGGCGGACATCGTGGCTGCGGAG 602
QY 130 GCTTGTGCGAGATCTTACCTGCGGCTGCGGCTGCTGTCTGTGGCTGCGGAG 189
Db 603 GCGCTCTGCAAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 662
QY 190 CTGTGCGGCTATGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTG 246
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QY 247 CTGAAGGCGCGCGCGCGCGCATCAAGGCGCATCATCATCATCATCATCATCATCAT 306
Db 723 CAGCAGGGGTGAGACCGGGGCGGCGGAGGAGATGCTGTGTGTGTGTGTGTGTGTGT 782
QY 307 GTGATCTCTTCCCGCGGCTCATCTCCATCGAGAGAGGGGCGGCGGCGGCGGAG 366
Db 783 CTGCTGTAGGACGACGCGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCT 842
QY 367 CCGGCGGCGCGCGCGCTGCGGATCAAGGCGAGAGGAGTGTGCTGTGCTGTGCTG 426
Db 843 GAGGGCAGCTGCTATGCGGAGTCTTCTTACAGCTGTGCTGTGCTGTGCTGTGCTG 902
QY 427 GGTCTCTTCTTCTGCTGCTGCTGCTCATCATCATCATCATCATCATCATCATCAT 486
Db 903 CTGAGTCTTCTTACGCGCTTCTTCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 962
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Db 963 ATCCAGAGGCGCACCGGCTCGGCTGTGAGTGGGCTTCGAGAGGCGACCGGCGGAG 1022
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Db 1083 GGGCAGGGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1142
QY 664 CCGGCGGCGG 672
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RESULT 8

US-09-165-543-1
 ; Sequence 1, Application US/09165543
 ; Patent No. 6093545

GENERAL INFORMATION:

APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
 TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:

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Oy 487 GCCAAGGTCGACCCCGCGGACACCCAGCCCGGGGTCCGGACCGCTGCGCGCGG 546
Db 673 ATCCAGAGGGCACCGCCCTCCGGCTGGATGGGGCTCGAGAGGACACCGCCCGAGCC 732
Oy 547 CCGGGGGGACCGAGCGACGAGGCTG---GGCCCCGAGGCGACCGCGGGCGG 603
Db 733 CTTCCCGAGGGCCACCCCTCACCACCCACCGCTGCTGGGGGTGTCGGCAGAG 792
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Oy 664 CCGGCGCGG 672
Db 853 GAGGCGCGG 861
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RESULT 5
; Sequence 6, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyall, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; CURRENT APPLICATION NUMBER: US/09/642, 855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167, 354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
; US-09-642-855-6
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Query Match 11.4%; Score 133; DB 4; Length 1335;
Best Local Similarity 52.0%; Pred. No. 2e-16;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;
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Oy 70 ACGCTGTCATCCCTTCTCTGCTGCGCAAGAGGTCAATGGGCTACGTACTTGGCAAG 129
Db 253 GCGTTTGCATCCACATGTATGTATACCTAGTGTGACAGCCGCTGAGACTTGGCGG 312
Oy 130 GCTTGGCGAGATCTACCTGCGCTGAGCTGCTCTTTCGACAGTCTGCATCTGAC 189
Db 313 GCGCTTGCAGAGCTGTGGTGTAGTGTACTCTGTCGACCTCTGCTGCTCAAC 372
Oy 190 CTGTGGCCATCAAGCCCTGAGCTACTGTATCATCAACAGGCAATCGATGAC---AAC 246
Db 373 ATGCTGCTATCAAGCTACGACCGCTTCTCTGCTGACCGGAGCGGTCTATCCGGGCC 432
Oy 247 CTGAAGGCGACCGCGCGCATCAAGGCCATCATCAACCGTGTGGGTCAATCTGCGCC 306
Db 433 CAGAGGAGTACACGCGCGCGAGTGGGAAAGATGCTGTGTGGGTGGTGGCTTTC 492
Oy 307 GTGATCTCTTCCGCGCTCATCTCATGAGAGAGGCGCGCGCGCGCGCGCGAG 366
Db 493 CTGCTGTACGAGACGACGATCTGAGCTGGAGTACCTGTGCGGGGAGGCTTCATCC 552
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Oy 367 CCGGCGGACCGCGCTCGAGATCAACGACGAGTGTACTGATCTGCTGTCGATC 426
Db 553 GAGGCGCACCTGATGAGAGTCTTTCACAACTGTACTTCTTCATACGAGGCTTCCACC 612
Oy 427 GGTCTCTTCTTCTGCTCCCTGCTCATCATCATCTGTGTCTGATGCGCATCTACAGATC 486
Db 613 CTGAGATTCTTTACGCCCTTCTCAGAGTCACCTTTTAACCTGACATCTACCTGAC 672
Oy 487 GCCAAGCTCGACCCCGGTGCGACCCAGCCCGGGGTCCGGACGCGCTGCGCGCGG 546
Db 673 ATCCAGAGGGCACCGCCCTCCGGCTGGATGGGGCTCGAGAGGACCGCGCGAGCC 732
Oy 547 CCGGGGGGACCGAGCGAGCGCCCAAGGCTG---GGCCCCGAGGCGACCGCGGGCGG 603
Db 733 CTTCCCGAGGGCCACCCCTCACCACCCACCGCTGCTGGGGTGTGAGCGCGCTAGCGCT 792
Oy 604 GGGGGGCGAGAGCGCGCAACCGCTCCACCCAGCTCAACGGCGCCCTGCGAGCGCG 663
Db 793 GGGCAGGGGGAGGCGCATGCGCGCTGCACAGGTATGGGGTGGTGAAGCGCGCTAGCGCT 852
Oy 664 CCGGCGCGG 672
Db 853 GAGGCGCGG 861
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RESULT 6
; Sequence 6, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyall, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; CURRENT APPLICATION NUMBER: US/09/642, 514
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167, 354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
; US-09-642-514-6
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Query Match 11.4%; Score 133; DB 4; Length 1335;
Best Local Similarity 52.0%; Pred. No. 2e-16;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;
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Oy 10 CTCGAAGCGGCCCCAAACCTTCTCTGCTGCTGCGCTCGCGGACATCTGTTGGCC 69
Db 193 CTCGGACCCGAGAACACTTCTTCTCTCAACCTCGCATCTCCGACTTCTGTCGGC 252
Oy 70 ACGCTGTCATCCCTTCTCTGCTGCGCAAGAGGTCAATGGGCTACGTACTTGGCAAG 129
Db 253 GCGTTTGCATCCACATGTATGTATACCTAGTGTGACAGCCGCTGAGACTTGGCGG 312
Oy 130 GCTTGGCGAGATCTACCTGCGCTGAGCTGCTCTTTCGACAGTCTGCATCTGAC 189
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Oy 247 CTGAAGGCGACCGCGCGCATCAAGGCCATCATCAACCGTGTGGGTATCTGCGCC 306
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Thu Feb 20 09:21:29 2003

us-09-636-259b-1.rni

Page 3

STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1335
US-09-165-543-3

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QY	70 ACGCTCGTCACTCCCTTCTTCGCTGGCGCAAGAGTCAATGGCTACTGGTACTTTCGGCAG	129		
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QY	307 GTTCATCTCTTCCCGCGCTCATCTTCATCTGAGAAAGAGGGCGGCGCGGCCCGCGAG	366		
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3  ; Sequence 6, Application US/09167354A
4  ; Patent No. 6136559
5  ;
6  ; GENERAL INFORMATION:
7  ;
8  ; APPLICANT: Lovenberg, Timothy
9  ; APPLICANT: Erlender, Mark
10 ; APPLICANT: Pyatt, Jayashree
11 ; APPLICANT: Huver, Arne
12 ;
13 ; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
14 ;
15 ; FILE REFERENCE: SUBTYPE
16 ;
17 ; FILE REFERENCE: JMW
18 ;
19 ; CURRENT APPLICATION NUMBER: US/09/167,354A
20 ;
21 ; CURRENT FILING DATE: 1998-10-07
22 ;
23 ; NUMBER OF SEQ ID NOS: 8
24 ;
25 ; SOFTWARE: PatentIn Ver. 2.0
26 ;
27 ; SEQ. ID NO 6
28 ;
29 ; LENGTH: 1335
30 ;
31 ; TYPE: DNA
32 ;
33 ; ORGANISM: Artificial Sequence
34 ;
35 ; FEATURE:
36 ;
37 ; OTHER INFORMATION: Description of Artificial Sequence:CDNA
38 ;
39 US-09-167-354-6

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Best Local Similarity	52.0%;	Pred. No. 2e-16;		
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Db 193	CTCCGCACCCAGAAACACTTCTTCCTCACTGCACTGCCATCTCCGACTCTTCCTGTGGG	252		
QY 70	ACGCTGCTATCCCTTTCTCTGCTGGCCCAAGAGTATATGGGCTACAGTACTCTCGGCAAG	129		
Db 253	GCCCTTCGCACTCCACACTGATATGATACCTACGATGTGTGACAGGCGGCTTGACCTTCGGCGG	312		
QY 130	GCTTGTGCGAGATCTACCTACGCGCGCTCGAGCGTCTCTTCTGCAAGCTGCATCTGTGCAC	189		
Db 313	GGCCTCTGCAAAAGCTGTGGTGTGTAGTGTGACACTGCTGTGTGCACCTCTTGCCCTTCAC	372		
QY 190	CTGTGCGCCATCACTCTGAGACCGCTACTGTGTGCATTCACACAGGCGCATCGAGTAC---AAC	246		
Db 373	ATCTGTGCTACACTTACGACCCGCTCTCTGTGCTGCACCCGAGCGGTCTCATATACGGGGCC	432		
QY 247	CTGAAGCGCACCGCGCGCGCGCATAAAGGCCATTCATCATCAACCGTGTGGGTATCTCGGCC	306		
Db 433	CAGCAGGGTGTACACAGCGGCGGGCGAGTGGGGAAGATGCTGTGTGGTGTCTTGCCCTTC	492		
QY 307	GTCATCTCTCTCCGCGCGCTCATCTCCATCTGAGAAAGAGGGCGGGCGGGCGGCCGACG	366		
Db 493	CTGCTGTCTGAGACACAGCCATCTTAGCTGGGAGTACCTGTCCGGGGGACGCTCATCCCC	552		
QY 367	CCGGCCGAGCGCGCGTGTGAGATCAACGACCCAGAGTGTACGTCATCTCTGCTGTGCATC	426		
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Db 867 GCTGTGGCTACCTGGAGTGTGCTGTGCTACCTAGTCCATCCGACCTGTGTGCAT 926
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RESULT 2
US-08-985-090-3
; Sequence 3, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentio Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silverl
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
;
US-08-985-090-3
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Query Match      11.4%; Score 133; DB 2; Length 1335;
Best Local Similarity 52.0%; Pred. No.2e-16;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;
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Db 313 GGCCTCTCAAGCTGTGGCTGTGTAGTGTAGTACTGTGTGTGTGTGTGTGTGTGTGTGT 372
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QY 190 CTGTGCGCATCAGCTGTGACCGCTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 246
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 373 ATCTGTGTATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 432
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 247 CTGAAGCGCAGCGCGCGCGCGCATCAAGGCGCATATCATACCGGTGGGTCATCTGGCG 306
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 433 CAGCAGGGGTGACAGCGCGCGGCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 492
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 307 GTCATCTCTTCCGCGCTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCT 366
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 493 CTGCTGTACGAGCAGCAGCATCTGAGCTGTGAGTACCTGTGCGGGGCGAGTCCATCC 552
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 367 CCGGCGGAGCGCGCGCTGCGGATCAAGACAGCAGAGGTGATCTGTCGTGTGTGTGTGT 426
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 553 GAGGCGCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 612
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 427 GGTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 486
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 613 CTGAGTTCCTTACGCGCTTCTCTGAGGTACCTTCTTAACTTCAAGTCTTAACTTCAAG 672
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 673 ATTCAGAGGGGCGACCGCTCTGCGCTGTGATGGGGTCTGAGAGGCGACCGCGCGG 732
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 547 CCGGGGGGCGACCGGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 603
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 733 CTCTCCGAGGCGGAGCGGCTTACCAACCGGCGGCTGTGTGGGTGTGTGTGTGTGTGT 792
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Db 793 GGGCAGCGGGGAGCGCATGCGCTGTGACAGGTATGGGGTGTGTGTGTGTGTGTGTGT 852
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QY 664 CCGGCGCGG 672
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Db 853 GAGGCGGG 861
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RESULT 3
US-09-165-543-3
; Sequence 3, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
```

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 13, 2003, 06:16:02 : Search time 62.5019 Seconds
(without alignments)
5740.812 Million cell updates/sec

Title: US-09-636-259B-1

Perfect score: 1170
Sequence: 1 agccgcgcgcctcaagcgcgc.....ggagacgaagcgcgcgtg 1170

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_Patents_NA:*
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6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	155.4	13.3	3335	1 US-07-676-174A-1	Sequence 1, Appl1
2	133	11.4	1335	2 US-08-985-090-3	Sequence 3, Appl1
3	133	11.4	1335	3 US-09-165-543-3	Sequence 3, Appl1
4	133	11.4	1335	4 US-09-167-354-6	Sequence 6, Appl1
5	133	11.4	1335	5 US-09-642-835-6	Sequence 6, Appl1
6	133	11.4	1335	6 US-08-985-090-1	Sequence 1, Appl1
7	133	11.4	2689	2 US-08-985-090-1	Sequence 1, Appl1
8	133	11.4	2689	3 US-09-165-543-1	Sequence 5, Appl1
9	133	11.4	2699	4 US-09-167-354-5	Sequence 5, Appl1
10	133	11.4	2699	5 US-09-642-855-5	Sequence 5, Appl1
11	133	11.4	2699	6 US-09-642-854-5	Sequence 5, Appl1
12	133.4	11.3	1645	2 US-08-461-812-1	Sequence 1, Appl1
13	133.4	11.3	3335	1 US-08-194-338-1	Sequence 1, Appl1
14	130.4	11.1	1956	1 US-08-313-553-6	Sequence 6, Appl1
15	130.4	11.1	1956	3 US-08-767-993-6	Sequence 6, Appl1
16	129	11.0	2428	3 US-08-475-742-15	Sequence 15, Appl1
17	128	10.9	1621	1 US-08-722-001-13	Sequence 13, Appl1
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23	128	10.9	2140	3 US-08-244-354-1	Sequence 1, Appl1
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26	128	10.9	2140	4 US-09-688-415-1	Sequence 1, Appl1
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28	127.8	10.9	1610	1 US-08-056-051-5	Sequence 5, Appl1
29	127.8	10.9	1610	1 US-07-928-611-21	Sequence 21, Appl1
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31	127.8	10.9	1610	4 US-09-060-694-21	Sequence 21, Appl1
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34	126.4	10.8	1776	1 US-08-722-001-29	Sequence 29, Appl1
35	120.8	10.3	1581	1 US-08-313-553-8	Sequence 8, Appl1
36	120.8	10.3	1581	3 US-08-767-993-8	Sequence 8, Appl1
37	120	10.3	1601	1 US-08-722-001-27	Sequence 7, Appl1
38	120	10.3	1997	1 US-08-722-001-11	Sequence 7, Appl1
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40	119.2	10.2	1673	1 US-07-791-936A-1	Sequence 11, Appl1
41	119.2	10.2	1673	1 US-08-383-781B-1	Sequence 1, Appl1
42	119.2	10.2	1771	2 US-07-968-267B-1	Sequence 1, Appl1
43	119.2	10.2	1771	4 US-09-168-510-1	Sequence 1, Appl1
44	119.2	10.2	2463	1 US-08-370-542-1	Sequence 1, Appl1
45	119.2	10.2	2463	1 US-08-542-358-1	Sequence 1, Appl1

ALIGNMENTS

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RESULT 1
US-07-676-174A-1
; Sequence 1, Application US/07676174A
; Patent No. 534776
; GENERAL INFORMATION:
; APPLICANT: Ventor, J. Craig
; TITLE OF INVENTION: Octopamine receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Eleventh Floor, 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/676,174A
; FILING DATE: 19910328
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/5683/79117/KIK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)861-3000
; TELEFAX: (202)822-8944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3335 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 319..2121
; US-07-676-174A-1
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Query Match 13.3% Score 155.4: DB 1: Length 3335:
Best Local Similarity 56.6% Pred. No. 1.7e-20;
Matches 313; Conservative 0; Mismatches 231; Indels 9; Gaps 1;

QY 21 CCAAAACCTCTCTCGTGTCTGCGCTCGCGACATCTGTCGACACGCTCGTCAT 80
DB 747 CCAAACTCTTCAATGATTTTCGTCGCGGCGGCGATCTACGGTGCCTCTGTCGCT 806


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QY 433 TTCTTGCTCCCTGCCTCATCATGATCCCTGCTACGTGGCGCATCTACCAAGATGCCAAG 492
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Db 241 TTCTTGCGCGCCTGCCTCATCATGTGTGTACGGCGCGCATCTACCACTCTGTCAG 300
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    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 553 GGCACCGAGCGCAGGCCCAACGGTCTGGGCCCGAGCGCAGCGCGGGCCCGGGGGCGCA 612
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 GAGTCCATCAGATGAGCGAGGTGAACGGCAAGGAGAGCGCGCGCGGCGAGGGGAACGGA 420
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QY 613 GAGCCCGAA 621
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Db 421 AACGAGAA 429
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Job time : 2343.51 secs

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Best Local Similarity	80.78;	Pred. No. 5.5e-26;		

1 AGCCGCGGCTCAAGGCGCCCAAAACCTCTTCTGTGTCTGTGGCTCGGCGGACATC 60

b
597 AGCCGCGGCTCAGAGCGCGCAGAACCTCTTCTGTGTTCTTGGCCACCGCGCAATC 655

[illegible]

121 TTGGCGAAGGCTTGGTGGCAGATCTACCTGGCGCTCGAGCGTCTCTTCTGCAGTGTGTC 180

[illegible][illegible]

777 ATGCTCTCAATTTGGTGTTCAGTACCGCATTGCATCACACAGGCCAATCGAG 240

ATGCGCCATCCTGCGCAATTAAGCTTTGACCCCTACTGGTCTGTACGACGACGGCGGTCCAG 836

241 TTACAACCTGAGCGCACGCGCGCGCCGATCAAGGC 275

837 TACACCTGAAGAGGACCCCTCAGCGCGTMAGGGC 871

ESQUISA 15

REAR
DOOR

REAR DOOR

LOCUS	DEFINITION	777 bp	DNA	linear	GSS 14-SEP
LREAZAR	Lamprey alpha2 adrenergic receptor gene fragment, genomic surv				

sequence.
ACCESSION
AL606561

AL606561.1 GI:15620571
GSS: Alpha2 adrenergic receptor gene

ORGANISM Lethenteron reissneri.
SOURCE Lethenteron reissneri.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia

REFERENCE
1 (bases 1 to 777)
Petrionymzontidiomies; Petromyzontidae; Lethenteron.

AUTHORS	TITLE
Hunter, C. and Elgar, G.	Alpha2 adrenergic receptor gene

Unpublished
JOURNAL
REFERENCE
2 (bases 1 to 777)

AUTHORS
Hunter, C.
TITLE
Direct Submissions

Submitted (14-SEP-2001) MRC Human Genome Mapping Project Resource Centre

Centre Hinxton, Cambridge, CB10 1SB. UK Email:
biohelp@hmp.mrc.ac.uk

source	Location/Qualifiers
1.	.777

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/organism="Leithenteron reissneri"  
/db xref="taxon:7753"
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SE COUNT	169 a	237 c	241 g	130 t
IGIN				

Query Match 15.98; Score 185.8; DB 17; Length 777;
Best Local Similarity 64.68; Pred. No. 6e-25;

Matches 277; Conservative 0; Mismatches 152; Indels 0; Gaps

193 TGGCCATCAGCCTGGACCCGCTACTGTCTCATCACACAGGCCATCGAGTACAACCTGAAG 252

1 TGGCCATCAGCCCTGACCGCTACTGTGCGTGTGCGAGGCGGTGAGTACACATCAAG 60

253 CGCAGCGCGCGGCATCAAGGCCATCATCACCGTGTTGGTCAATCTCGGCCGTCAATC 312

61 CGCAGCCGGCGAGTGAGCGCATCGTCGTGTGGTTCATCGCCATCGCCATC 120

[illegible][illegible]

121 TCTCTCCCTCCATCTCCATGAACTGAAGAACCGGACAGCAGCAGGAGGCTGGT 180
373 ATGG

3/3 GAGCCGGCGTCCGAGATCAACGACAGAGTGGTACGTCTCTCGTCATCGGCTCC 432

181 CGGCCCAACTGCGAGCTCAACACGACGACCTGTACATCCTGGGCTCGTGCATCGGATCG 240


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Plate: LAM11671 row: m column: 11
High quality sequence stop: 716.
Location/Qualifiers
1..893
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HUC-56237"

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FEATURES	SOURCE
Location/Qualifiers	1..893
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:5266354"	
/clone_1lb="NH_MGC_97"	

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/note="Organ: testis; Vector: pBluescript (modified
pBluescript KS+); Site.1: BamHI; Site.2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTNN-3',
size-selected for average insert size 2.2 kb and

```

normalized to R0F 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC library."

Query Match	19.7%	Score 230.6;	DB 13;	Length 893;
Best Local Similarity	81.0%;	Pred. No. 2.8e-33;		
Matches 406; Conservative	0;	Mismatches 74;	Indels 21;	Gaps 11.
QY	1	AGCGGCGCTCAAGGCGCCCAAAACCTCTTCTTGCTGCTGCTCTGAGCTTGG--CCGACA	58	

Db 393 AGCCGGCGCTAAGGCGCCCCAAGACTCTCTCGTGTCGTGACACTCGGACAAAT 452

Oy 59 TCCGTGTGGCCACGCTCGT-CATCCCTTTCGCTGGCCCAAGGTCAATGGGCTACTGG 117

Db 453 TCCGTGTGGCCACGCTCGTACATCCCTTTCGCTGGCCCAAGGTCAATGGGCTACTGG 512

QY 118 TACTTCGGGCA -GGCTTTGTGTCG -AGATCTACCTGGCGCTGCAGCGCTCTTCTGCACGT 175
|||||
Db 513 TACTTCGGGCAAGGCGCTGTGTCGAAGATCTACCTGGCGCTGCAGCGCTCTTCTGCACGT 572
|||||
QY 176 -CGTCATCTGTCACCTCTGCGCATAGGCTGAGCGCTACTGTTCCATTCACACAGGCC 234
|||||

DB	573	ACGTCCATCGTGCACACTCTGTGGCCATCATAGCCCTGAGCCGCTACTAGTGCTCATCACAGGGCC	632
QY	235	ATCGAGTTCACACCTTGAAAGCGCAGCCGCGCGCATCAAGGCCATCATCACCGGTGG	294
Db	633	ATCGAGTTCACACCTTGAAAGCGCAGCCGCGCGCATCAAGGCCATCATCACCGGTGG	692

[illegible]

CGAGGATGGTCTGTACAGCCGCCTTCCTGCTGCCGCTCATCATGATCC 460
||||| || | |||| ||||| ||||| ||
GGTAGCATTATTGAGATCGTGCAATGGATPACTTTGTTGGTCCGCTGTCATCAAGATCC 872

TGCTCTAAGCTGGCATTAACC 481

RESULT 12

873	TTG-CAACGCCGCATATACC	892
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LOCUS	1135 bp	mRNA	linear	EST 16-FEB-2001
DEFINITION	AL544577.L11.NFL006.P12 Homo sapiens cDNA clone CS01021YC24 3 prime, mRNA sequence.			
ACCESSION	AL544577			
VERSION	AL544577.1	GI:12877057		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			

Query Match	26.5%;	Score 310.2;	DB 14;	Length 988;
Best Local Similarity	74.3%;	Pred. No. 4.2e-48;		
Matches 423; Conservative	0;	Mismatches 133;	Indels 13;	Gaps 2.

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DD007YE02"
/clone_1id="LTI_NF001_NBC4"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and

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OY	886	GCTGCGAAGCGTGGCCGTGGCGGGCGGCACAGACCAGAGACGCTTCACGTTGCTG	945
Dd	685	AACACCAAAGGGTCCCGTGATGAGGGGACAGACAGAACGGGAAGAAGTTTCACTTTCGTT	744
OY	946	CTGGCCGTGTGCATCGAGTAGTTCGTGTGTGTGTGCCGTGCCCTTCCTTCACCTTCACG	1005
Dd	745	CTGGCGGGTGGTGGATGGGGCTTCGTGCATCATCTGCTGGTCCACTTCATTCTTCACCTACG	804
OY	1006	CTCAGCGCCGTTCGGG-----TGTCTCGTCGACGACGACGCTTCCTTCAAATTC	1050
Dd	805	CTGACCGCGGTGTGCAAGAGCTGCTGTGCTCTCCACACCTTCCTTCAAATTC	855

RESULT 8	LOCUS	BM352981/c	358 bp	mRNA	linear EST 07-JAN-2002		
DEFINITION		BM352981	1969H02.y1 HR85 islet Homo sapiens cDNA 5' similar to SW:A2AA_HUMAN				
ACCESSION		P08913 ALPHA-2A ADRENERGIC RECEPTOR ; mRNA sequence.					
VERSION		BM352981					
KEYWORDS		EST . GI:18085339					
SOURCE		human.					
ORGANISM		Homo sapiens					
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 358)					
AUTHORS		Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Keastner,K., Lemishke,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Merris,M., Page,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Meising,B., Ritter,E., Konko,I., Bennett,J., Cardenas ,M., Gibbons,M., McCann,R., Cole,R., Tsagarelshvili,R., Williams,T., Jackson,Y. and Bowers,Y.					
TITLE		Endocrine Pancreas Consortium					
JOURNAL		Unpublished (2000)					
COMMENT		Other ESTs: 1969H02.xl Contact: Douglas Melton, Klaus H. Keastner, & Hiroshi Inoue Endocrine Pancreas Consortium Harvard University, Howard Hughes Medical Institute Depte of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138 Tel.: 617-495-1812 Fax: 617-495-8557 Email: dmelton@biohp.harvard.edu Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@lm.wustl.edu) Possible reversed clone: similarity on wrong strand Seg primer: -40RP from GIBCO High quality sequence stop: 342. Location/Qualifiers 1..358 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_id="HR85 islet" /tissue_type="Purified pancreatic islet" /lab_host="DH10B" /note="Organ: Pancreas. Vector: pBluescript SK(-). Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size. XhoI site was destroyed after directional cloning. Amplified once. Contact Information: Hiroshi Inoue, MD, Metabolism Div. (Alan Pernutt lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@lumate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."					

BASE COUNT	76 a	114 c	115 g	53 t
ORIGIN				

Query Match	27.3%	Score 319.4	DB 13	Length 358
Best Local Similarity	99.7%	Pred. No. 7e-50,		
Matches 320:	Conservative	0.0		

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Location/Qualifiers
1. 1077
/organism="Homo sapiens"
/adb_xref="taxon:9606"
/clone="CSOD1021YC24"
/clone_1db="LRI_NF1006.PL2"
/tissue_type="placenta"
/note="vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-c1g(c/dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
Eco RV sites of the pcMVSPORT 6
cloned into the Not I and Eco RV sites of the pcMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive

```

Rockville, Maryland 20850, USA Fax : (1)
Email : fliang@lifetech.com URL :

a	397	c	385	g	168	t	3	others
---	-----	---	-----	---	-----	---	---	--------

27.6%; SCORE 322.6; DB 9; LENGCH 10000;
78 18: Pred NO. 3.1e-50;

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conservative 0; Mismatches 104; Indels 13; gaps 27

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AAACCTCTTCCGTGTCTCTGGCCTCGGCCGACATCCTGCTGGCCACGCT / 4

5AACCCTCTTCCCTGGTGTGCGTGGCCCTCGGCCGACATCCTGGTGGCCACGCT 549

TTTCTCGCTGGCCACGAGGTATGGGCTACTGGTACTTCGGCAAGGCTTG 134

TTCTCTCGTTGGCCACGAGCTCATGGCCCTACTGGTACTTCGGGCAGGTGTG 609

TTACCTGGCGCTCGACGTGCTTCTGACAGTGTGCATCGTGCACCTGTG 194

TTATCTGGCGCTCGATGTGCTGTTTGCACCTCGTCGATCGTCATCTGTG 669

CTGGACCGCTACTGGTCCATCACACAGGCCATCGAGTACAACCTGAAGC 254

CTGACGGCGGTGAGTACAACCTGAACG 729

...TTCATTCACCCCT-GTGGGTCAATCTGGCCGTCATCT 313

789

373

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[illegible]

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CCCTGCCTCATCATGATCCCTGGTCTACGTCGCGCATCTACCAAGATCCCGGAGG 755

CCCTGCCTCATCATGGGCGCTGGTCTACGGCGGCACCTACCGAGTGGCCAGC 35/

GCCTGCCACCCAGCCGCCGGGTCCGGACGCCGTGCCCGCCGCCGCC 548

GCACGCTCAGCGAGAGCGCGCCCCCGTGGGCCCGACGGTGGCTC 1012

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alpha2 adrenergic receptor gene fragment probably subtype

omic survey sequence.

0.1 GI:15591915

ota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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mRNA sequence.
 ACCESSION B1838282
 VERSION B1838282.1 GI:15949832
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 740)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution Information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLML1559 row: 1 column: 04
 High quality sequence stop: 740.
 Location/Qualifiers
 1..740
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="5222475"
 /clone_lib="NIH_MGC_120"
 /lab_host="DH10B"
 /note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site:1; NotI: Site:2; EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."
 BASE COUNT 115 a 240 c 235 g 150 t
 ORIGIN
 Query Match 33.8%; Score 395; DB 13; Length 740;
 Best Local Similarity 100.0%; Pred. No. 6.5e-64;
 Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 LOCUS BB643669/c
 DEFINITION BB643669 RIKEN full-length enriched, adult male corpora quadrigemina Mus musculus cDNA clone B30352011 5', mRNA sequence.
 ACCESSION BB643669
 VERSION BB643669.1 GI:16478370
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 691)
 AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Kono,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
 RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
 COMMENT Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 Wagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo,S., Shingawa,A., Saito,T., Kiyosawa,H., Yamakawa,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.
 e mouse tissues.
 Location/Qualifiers
 1..691
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone_image="B30352011"
 /clone_lib="RIKEN full-length enriched, adult male corpora quadrigemina"
 /sex="male"
 /tissue_type="corpora quadrigemina"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in

Fax: 617-495-8557
 Email: dmeltone@biohp.harvard.edu
 Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center For information on
 obtaining a clone please contact: Juliana Brown
 (brown@fas.harvard.edu)
 Possible reversed clone: similarity on wrong strand
 Seq primer: -40RP from Gibco
 High quality sequence stop: 445.
 Location/Qualifiers
 1..561
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6136374"
 /clone.lib="Melton Normalized Human Islet 4 N4-HIS 1"
 /sex="Both"
 /tissue_type="Islets of Langerhans"
 /dev_stage="Adult"
 /lab_host="DH10B"
 /note="Organ: Pancreas; Vector: pSPORT1; Site:1: Not 1;
 Site:2: Sal 1; Starting library constructed using
 SuperScript Plasmid Library kit (Life Technologies). cDNA
 made by oligo-dT priming. Size-selected by column
 fractionation; average insert size 1.08 kb. Library was
 amplified once on solid support and plasmid DNA from
 library was prepared. The library DNA was normalized by
 method #4 from Bonaldo, Lennon, and Soares 1996 Genome
 Research 6:791-806; 0.5 microgram single-stranded library
 plasmid DNA was mixed with 5 micrograms PCR product
 representing library inserts and hybridized to an EcoT of
 20. Single-stranded (unhybridized) plasmids were isolated
 by hydroxyapatite chromatography and used to make this
 library."

BASE COUNT 63 a 215 c 210 g 73 t
 ORIGIN

Query Match 47.9% Score 561; DB 14; Length 561;
 Best Local Similarity 100.0%; Pred. No. 7.5e-95;

Matches 561; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 430 TCTTCTTCTGCTCCCTGCTCATCATGATCTGCTACGTCGTCACGATCTACGATGCC 489
 DB 561 TCTTCTTCTGCTCCCTGCTCATCATGATCTGCTACGTCGTCACGATCTACGATGCC 502
 QY 490 AAGCTGCGACCGCGTCCGACCCGCGCGGGGTCCGACGCGCTGCGCGCGCGCG 549
 DB 501 AAGCTGCGACCGCGTCCGACCCGCGCGGGGTCCGACGCGCTGCGCGCGCGCG 442
 QY 550 GGGGCGACCGACGCGACGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 609
 DB 441 GGGGCGACCGACGCGACGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 382
 QY 610 GCAAGAGCGCAACCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 669
 DB 381 GCAAGAGCGCAACCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 322
 QY 670 GGGCGCGCGACCGACGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 729
 DB 321 GGGCGCGCGCGACCGACGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 262
 QY 730 CGGCTCCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 789
 DB 261 CGGCTCCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 202
 QY 790 AGCCAGGTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 849
 DB 201 AGCCAGGTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 142
 QY 850 ACGCCGCGCTCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 909
 DB 141 ACGCCGCGCTCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 82
 QY 910 GGGCGCGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 969

Db 81 GGGCGCGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22
 QY 970 GTGGTGTGCGGTTCCTCCCTTC 990
 DB 21 GTGGTGTGCGGTTCCTCCCTTC 1

RESULT 2
 BM967243/c
 LOCUS
 DEFINITION 492 bp mRNA linear EST 29-Apr-2002
 1j32c09.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
 CDNA clone IMAGE:613636 5' similar to SW:42AA_HUMAN P08913

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 492)
 Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
 Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
 Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
 , M., Gibbons,M., McCann,R., Cole,R., Tsagaris,I., Williams,T.,
 Jackson,Y. and Bowers,Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Other ESTs: 1j32c09.x1

TITLE
 JOURNAL
 COMMENT
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557

FEATURES
 Source
 1..492
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:613636"
 /clone.lib="Melton Normalized Human Islet 4 N4-HIS 1"
 /sex="Both"
 /tissue_type="Islets of Langerhans"
 /dev_stage="Adult"
 /lab_host="DH10B"
 /note="Organ: Pancreas; Vector: pSPORT1; Site:1: Not 1;
 Site:2: Sal 1; Starting library constructed using
 SuperScript Plasmid Library kit (Life Technologies). cDNA
 made by oligo-dT priming. Size-selected by column
 fractionation; average insert size 1.08 kb. Library was
 amplified once on solid support and plasmid DNA from
 library was prepared. The library DNA was normalized by
 method #4 from Bonaldo, Lennon, and Soares 1996 Genome
 Research 6:791-806; 0.5 microgram single-stranded library
 plasmid DNA was mixed with 5 micrograms PCR product
 representing library inserts and hybridized to an EcoT of
 20. Single-stranded (unhybridized) plasmids were isolated
 by hydroxyapatite chromatography and used to make this
 library."

BASE COUNT 44 a 202 c 182 g 64 t
 ORIGIN

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 12:34:42 : Search time 2326.51 Seconds
(without alignments)
8144.696 Million cell updates/sec

Title: US-09-636-259B-1
Perfect score: 1 agccgcgcgcctcaagcgcc.....ggacacggaagcgatcgtg 1170
Sequence: 170

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: em_estba:
2: em_esthm:
3: em_estin:
4: em_estnu:
5: em_estov:
6: em_estpl:
7: em_estro:
8: em_hic:
9: gb_est1:
10: gb_est2:
11: gb_hic:
12: gb_est3:
13: gb_est4:
14: gb_est5:
15: em_estfun:
16: em_estom:
17: gb_gss:
18: em_gss_hum:
19: em_gss_iny:
20: em_gss_pln:
21: em_gss_vtl:
22: em_gss_fun:
23: em_gss_mam:
24: em_gss_mus:
25: em_gss_other:
26: em_gss_pro:
27: em_gss_rtd:

Pred. No. is the number of results predicted by chance a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	561	47.9	561	14	BM967248
2	490.4	41.9	492	14	BM967243
3	453	38.7	453	14	BQ129312
4	395	33.8	740	13	BI838282
5	373	31.9	691	10	BB643669
6	322.6	27.6	1077	9	AL544609

C	8	320.2	27.4	855	17	CGAA2AAR	AL606540 Chicken a
	9	319.4	27.3	358	13	BM352981	BM352981 1669h02.Y
	10	310.2	26.5	988	14	BQ887729	BQ887729 AGNCOURT
	11	283.2	24.2	867	9	AL530418	AL530418 AL530418
	12	230.6	19.7	893	13	BI459381	BI459381 603200147
	13	199.8	17.1	1135	9	AL544577	AL544577 AL544577
	14	194.2	16.6	350	10	BE648878	BE648878 UI-M-BH2.
	15	191.4	16.4	896	17	CNS03BQW	AL236849 Tetradon
	16	185.6	15.9	777	17	LRFA2AAR	AL606541 Lamprey a
	17	181.2	15.5	966	17	CGAA2AAR	AL606541 Chicken a
	18	179.4	15.3	1010	17	CNS02MW2	AL606595 Tetradon
	19	175.8	15.0	921	17	CGAA2AAR	AL284651 Tetradon
	20	173.4	14.8	691	17	HIPRA2AAR	AL606565 Herring a
	21	172.6	14.7	882	17	HIPRA2AAR	AL606580 Sea Horse
	22	172.2	14.7	697	17	RESA2AAR	AL606568 Sea Horse
	23	171.4	14.6	872	17	ECGA2AAR	AL606551 Frog alph
	24	169.6	14.5	825	17	ARUA2AAR	AL606560 Horse alp
	25	167.8	14.3	890	17	CNS02MW9	AL606576 Sturgeon
	26	166.8	14.3	693	17	ARUA2AAR	AL606574 Tetradon
	27	164.8	14.1	723	17	AGAA2A2AAR	AL606581 Tothcarp
	28	163.4	14.0	829	17	AL549866	AL549866 AL549866
	29	161.8	13.8	705	17	HGRA2AAR	AL606570 Shark alp
	30	160.6	13.7	805	17	CNS03CEB	AL237702 Tetradon
	31	160.2	13.7	753	17	SCAA2AAR	AL606564 Ostrich a
	32	160	13.6	788	17	DREA2AAR	AL606584 Zebrafish
	33	159.4	13.6	699	17	LOSA2AAR	AL606553 Gar alpha
	34	158.6	13.6	981	17	HIPRA2AAR	AL606569 Sea Horse
	35	154.4	13.2	872	9	AL573897	AL573897 AL573897
	36	151.4	12.9	860	17	CNS03HKO	AL244403 Tetradon
	37	151	12.9	780	17	CCLA2AAR	AL606557 Herring a
	38	148.8	12.7	800	17	T39448	T39448 ya06a09.12
	39	146.4	12.5	301	14	BM647571	BM647571 170060873
	40	143.4	12.3	535	13	BM647571	AL613341 fd43d01.x
	41	142.8	12.1	451	9	BI836679	BI836679 603089610
	42	141.4	12.1	702	13	BI836679	AL606579 Tothcarp
	43	141.4	12.1	798	17	AGAA2AAR	AK018378 Mus muscu
	44	140.8	12.0	2146	11	AK018378	AK018378 Mus muscu
	45	140.4	12.0	975	17	CNS039RV	AL234292 Tetradon

ALIGNMENTS

RESULT 1
LOCUS BM967248/C 561 bp mRNA linear EST 29-APR-2002
DEFINITION l332d04.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
CDNA clone IMAGE:6136374 5' similar to SW:42AA_HUMAN P08913

ACCESSION BM967248
VERSION BM967248.1 GI:19561047
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 561)
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS Melton,D., Brown,J., Kently,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scarsee,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Merra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Rheising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarisshvill,R., Williams,T., Jackson,Y., and Bowers,Y.,
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: l332d04.x1

TITLE JOURNAL
COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812

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•
•

Db 1249 TCACTGAACCTGTATATCTACACATCTTCACACAGACTTCGCCGCTCTCCGAGG 1308
 OY 1138 ATCTCTGTG 1148
 Db 1309 ATCTGTGCGG 1319
 RESULT 15
 AA199906
 ID AA199906 standard; DNA; 1344 BP.
 AC AA199906;
 DT 18-FEB-2002 (first entry)
 DE Human alpha-2BAR third intracellular loop variant encoding DNA.
 XX
 KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
 KW polymorphic site; allelic variant; cardiovascular disease;
 KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
 KW phosphorylation; inositol phosphate; alpha-2BAR; chromosome 2; ds.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1344
 FT /*tag= a
 FT /*product= "alpha-2BAR"
 FT /note= "sequence is deleted for a 9 nucleotide
 FT polymorphic site found at nucleotides 901-909
 FT of the wildtype alpha-2BAR protein (AA199905)"
 XX
 PN WO200179561-A2.
 XX 25-OCT-2001.
 XX 17-APR-2001; 2001WO-US12575.
 XX 17-APR-2000; 2000US-0551744.
 XX 10-AUG-2000; 2000US-0636259.
 XX 19-OCT-2000; 2000US-0692077.
 PA (LIGG/) LIGGETT S B.
 PA (SMAL/) SMALL K M.
 XX
 PI Liggett SB, Small KM;
 DR WPI: 2001-611728/70.
 DR P-PSDB: AAM52118.
 XX
 PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 PT determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting
 XX a polymorphic site -
 PS
 PS Claim 5; Page 144-145; 163pp; English.
 XX
 CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC or (i), a site comprising cytosine or guanine at position 753 of (IIIV)
 CC positions 961-972 of (III). The method may be used for genotyping at
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
 CC polymorphic site which correlate to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. ephedrine,

CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHR933 and
 CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
 CC rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC levels). The present sequence is that of the third intracellular loop of
 CC the human alpha-2BAR variant, the sequence is deleted for a 9 nucleotide
 CC polymorphic site found at nucleotides 901-909 of the wildtype gene
 CC (AA199905).
 CC
 SQ Sequence 1344 BP; 220 A; 458 C; 400 G; 266 T; 0 other;

Query Match 34.4%; Score 402.2; DB 23; Length 1344;
 Best Local Similarity 63.4%; Pred. No. 1.4e-57;
 Matches 769; Conservative 0; Mismatches 368; Indels 76; Gaps 7;

OY 1 AGCGCGGCTCTCAAGCGCCCAAACTCTTCTGCTGTCTGCGCTGCGGACATC 60
 Db 118 AGCGGCTCTGCTGCGCCCTCAGAACCTGTCCTGCTGCTGCGCGCGCGCATC 177
 OY 61 CTGCTGCGCACGCTGCTATCCCTTCTGCTGCGCAACGAGTCATGGCTACTGTAC 120
 Db 178 CTGCTGCGCACGCTCATCATCCCTTCTGCTGCGCAACGAGTCGCTGCTGTAC 237
 OY 121 TTGCGCAAGCTTGTGCGGAGATCTACTGCGCTGCAGCTGCTCTTCTGACGTGTC 180
 Db 238 TTGCGCGCGAGCTGTGTGAGAGTGTACCTGCGCTGCACGCTCTTCTGACCTGTGC 297
 OY 181 ATCTGTCACCTGTGCGCATGAGCTGAGCGCTGACGCTGCTGCTGCTGCTGCTGCTG 240
 Db 298 ATCTGTCACCTGTGCGCATGAGCTGAGCGCTGACGCTGCTGCTGCTGCTGCTGCTG 357
 OY 241 TACAACTGAAAGCGCAGCGCGCGCATCAAGCGCATCATCATCACTGCTGCTGCTG 300
 Db 358 TACAACTGAAAGCGCAGCGCGCGCATCAAGCGCATCATCATCACTGCTGCTGCTG 417
 OY 301 TCGGCGCTATCTCTTCCGCGCTCATCTCCATCGAAGAAAGGCGCGCGCGCGG 360
 Db 418 GCGCGCTATCTCTTCCGCGCTCATCTCCATCGAAGAAAGGCGCGCGCGCGG 468
 OY 361 CCGCAGCGCGCGCGCGCGCTGCGAGATCAAGCAGCAGAGTGTATCATCTGCTG 420
 Db 469 CAGCGCGCGCGCGCGCGCGCGCGCGAGTCAACAGAGAGCGCTGTAATCTGCGCTG 528
 OY 421 TGCATGCGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 Db 529 AGCATCGAGATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 588
 OY 481 CAGATCGCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 Db 589 CTGATCGCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 646
 OY 541 GCG 600
 Db 647 GTGAGTCAAGCAGCG 706
 OY 601 CCGGCG-----GCGCAGAGCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCG 655
 Db 707 CCGTGGCGCTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 766
 OY 656 AGCG 715
 Db 767 AGAGAGGCG 826
 OY 716 CCGACAGCGCGCGCGCG-----CTCAGCGCG 743
 Db 827 CCGTTCGCAACTGAGCGCAGCGCGCAGAGAGGCTGTTGTGGGCACTCTCAAGAGTG 886
 OY 744 CCGCAGACCGCAGCGCGCTCCCGCGCGCAGAGCGCGCGCGCGCGCGCGCGCGCG 803
 Db 887 AAGCTGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 946


```
RESULT 13
AA064890
ID AA064890 standard; DNA; 1382 BP.
XX
XX AA064890.
AC
XX
XX 01-FEB-1995 (first entry)
DE
XX Human derived adrenaline alpha 2CII receptor DNA.
XX
XX adrenaline receptor; alpha CII; screening; detection; pharmacology;
KM drugs; ds.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
FH 1.2
FT 5'UTR /tag= a
FT /note= "5'-non translated region"
FT CDS /tag= b
FT /product= adrenaline alpha CII receptor
FT misc_feature /tag= b
FT /note= "encodes Met; this codon may or may not be
FT present, but can only be present if
FT misc_feature /note= "this sequence may or may not be present"
FT 3'UTR /tag= c
FT /note= "3'-non-translated region"
FT
FT
XX JP06121686-A.
XX
XX
XX 06-MAY-1994.
XX
XX 12-OCT-1992; 92JP-0272744.
XX
XX 12-OCT-1992; 92JP-0272744.
XX
XX 12-OCT-1992; 92JP-0272744.
XX
XX (ASAH ) ASAH KASEI KOYO KK.
XX
XX WPI; 1994-185923/23.
XX
XX P-PSDB; AAR54834.
XX
XX
XX Adrenaline receptor gene encoding alpha 2CII receptor - for
XX screening drugs reactive to the alpha 2CII receptor
XX
XX Claim 1; Page 9-11; 13pp; Japanese.
XX
XX This sequence encodes the amino acid sequence of a polypeptide
XX (AAR54834) that constitutes human derived adrenaline alpha 2CII
XX receptor. this can be used for the study of the pharmacological
XX importance of the gene expression in humans.
XX
XX Sequence 1382 BP; 165 A; 480 C; 497 G; 240 T; 0 other;
XX
Query Match 40.1%; Score 468.8; DB 15; Length 1382;
Best Local Similarity 66.2%; Pred. No. 1.6e-68;
Matches 778; Conservative 0; Mismatches 347; Indels 51; Gaps 5;
```

```

Db 357 TTTGGGCGAGGTGTGTGCGCGCGGTGTACCTGGGCGCTGATGCTGTTTGGACCTGTCG 416
Qy 181 ATGTCGACCTGTGTGCGCCATCAGCCCGCTACTGTGTCATACACAGGACCTGAG 240
Db 417 ATGTCGATCTGTGTGCTTGTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 476
Qy 241 TACACCTGAAAGCGACAGCGCGCGCATCAAGGACCATCATCATGAGGCGGCGGTCATC 300
Db 477 TACACCTGAAAGCGACAGCGCGCGCATCAAGGACCATCATCATGAGGCGGCGGTCATC 536
Qy 301 TGGCGCGTCATCTCTTCCCGCGCTCATCTTCATGAGAAAGAGGCGGCGGCGGCG 360
Db 537 TGGCGCGTCATCTCTTCCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 593
Qy 361 CCGCAGCCCGCGAGCGCGCGGTGCGAGATCAACGACGAGAGTGGTACGATCTGCTG 420
Db 594 -----GCTTACCGCGAGTGTGCGCGCTCAACGACGAGACCTGTATCTTCTCTCC 644
Qy 421 TGCATCGCTCTTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
Db 645 TGCATCGCTCTTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 704
Qy 481 CAGATCGCCAGCGTCGACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 705 CGAGTGGCCAGACCTGCGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 764
Qy 541 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
Db 765 GGTGCGTCCCGGACATACGA -----AAACGCGCTGGGCGCGCGCGCGCGCGCG 815
Qy 601 CCGGGGCGCGCAGAGCGCGGAAACCGCTGCGCACAGCTCAACGCGCGCGCGCGCGCG 660
Db 816 GAGAACGGG-----CACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 862
Qy 661 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
Db 863 GAGCAGCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 922
Qy 721 CACGCGGAGCGCGCTCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
Db 923 GCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 982
Qy 781 GCCGAGCGAGCCAGGTCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
Db 983 GCGCGTACCGCTGCGAGGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1042
Qy 841 GGGATCGGAGCGCGCGCTGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
Db 1043 CTCGCTGAGATTCTTCTGTCGCGCGCGCGCGCGCG-----GCGCGCAGCGCGTGC 1094
Qy 901 CGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
Db 1095 CGCGCAGAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1154
Qy 961 GGAATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1017
Db 1155 GGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1214
Qy 1018 -----GGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1071
Db 1215 CCGGAGGCGCTGCGAGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1274
Qy 1072 AACAGCTGCTGTAACCGCGCGCATCTACACATCTTCAACACAGATTTCCGCGCGCTTC 1131
Db 1275 AACAGCTGCTGTAACCGCGCGCATCTACACAGATTTCCGCGCGCATCTTC 1134
Qy 1132 AAGAAGATCTCTGTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1167
Db 1335 AACGACATCTCTTCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1370
```

RESULT 14

SQ Sequence 1383 BP; 164 A; 482 C; 500 G; 237 T; 0 other;

[illegible]

QY	361	CCGACGCCGGCCGACGCCGGCGCTGCGAGATCAACGACCAAGAGTGTACCTATCTGTCG	420
Db	593	-----CCATACCCGAGTGTGGGCCCTCAACGACGAGACCTGGTATCTCTCTCC	64.2
QY	421	TGCATGGCTCCCTTCTTCTGCTCCCTGACATCATATGATCTGTGCTTAAAGTTCGATATAC	480
Db	643	TGCATGGCTCCCTTCTTCTGCTCCCTGACATCATATGATCTGTGCTTAAAGTTCGATATAC	70.2
QY	481	CAGATGCCAAGCGTTCGACCCCGCTGCGACCCGACCCGCGGGTCCGAGACCGCTGCGC	54.0
Db	703	CGAGTGGCCAAAGGCTGCGACGCGCACAGCTCAGCGAAGAGCGGCCCGCTGGGCCGAC	76.2
QY	541	GGCGCGCGGGGGGGCGACCGAGGCGAGGCCCAACGCTCTGTGGCCCCGAGCGACGCGGGC	60.0
Db	763	GGTGTCTCCCGCTACCTACCAAAACGGGCTGTGGCGGGCGGAGCGAGCGAGAACGGCG	82.2
QY	601	CCGGGGGGGGCGCAGAGGCGCACCGCTGCCCAACCGCTCAACGGCGCGCCCTGGCGAC-C	65.9
Db	823	ACTGCGCGC-----CCCGCGCGCGACCTGGAGCGCGGACGACGACGAC	86.5
QY	660	CGCGCGCGCGGGGGCGCGCGGACACCGACGCGCTGGACCTGGAGAGAGCTGCTTCCGA	71.9
Db	866	CGAGGGGGCGAGAGCGCGCGCGCGCGGGCGGTGCGCGCGGGGGCGCGCGCGCGAGCGG	92.5
QY	720	CCACGCGGAGCGCGCTCCAGAGGCCCGCGAGACCCGAGCGCGCGTCCCGGGGGCAAGGCAA	77.9
Db	926	GGCGGAGGGGGGGCGCGGGCGGTGCGAGACGGGACGAGGGCGCGGGCGCGGCGCTGAGT	98.5
QY	780	GGCGCGAGCGAGACCGAGTGAAGCCGGCGGACACCTCGCGGGCGCGGGCGGGGGCGAC	83.9
Db	986	CGGGGGCGCTGACCGCTTCAGAGTCCCGCGGGCGCGGTGGCGCGCTTCGCGCGCAGCT	104.4
QY	840	GGGAGATCGGGAAGCGCGCTGACAGGGCGGGGAGAGGACCGGTGGGGCTGCGAAGCGTC	89.9
Db	1046	CGCGCTCGGTGAGTCTTCTCTGTGCGCGCGCGCGCGCGCGCGCGAG-----CAGCGTGTG	110.0
QY	900	GGCGCTGGCGGGGGCGGCAAAACCGGAGAAAGCGCTTACGCTGTGCGCGCTGTGCTAT	95.9
Db	1101	CGGCGCAAGGTGGCGCCGAGGGCGCGGAGAAAGCGCTTACCTTGTGCTGGCTGTGCTAT	116.6
QY	960	CGAGTGTTCGGGGTGTCTGTTTCCCTTCTTCTTCTTACCTAACGCTACGCGCGCTC--	101.1
Db	1161	GGGCGTGTCTGCTCTGTCTGTGTCCTTCTTCTTCTTATCATAGGCTCTTACGGCATCTG	122.0
QY	1018	-----GGTGTCTCCGTGCGCACGACGCTCTTCAATTTCTTCTGTGGTGGCGTACG	107.0
Db	1221	CGCGAGGCGCTGCGCAGGAGCGCGCGCGCGCTTCAAGTTCTTCTGTGATGGCTACG	128.0
QY	1071	CACAGCGTCTGTGAACCGCGGCTATCTACACATCTTCAACACAGATTTCCGCGCGCTT	113.0
Db	1281	CACAGCGTCTGTGAACCGCGGCTATCTACAGGCTTCAACACAGATTTCCGCGCATCTT	134.0
QY	1131	CAGAGATCTCTGTGCGGGGGGACGAGAGCGGATC 1167	
Db	1341	CAGGACATCTCTTCCGAGGAGGAGAGAGGCGCTC 1377	
RESULT 12			
AA199933			
ID	AA199933 standard; DNA: 1371 BP.		
XX	AA199933;		
XX	18-FEB-2002 (first entry)		
XX	Human alpha-2CAR variant encoding DNA.		
DE	Human: genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;		
KM	polymorphic site; allelic variant; cardiovascular disease;		
FM	central nervous system disease; adenylyl cyclase; MAP kinase activity;		
KM	phosphorylation; inositol phosphate; alpha-2CAR; chromosome 4; ds.		

XX (EPiG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI WPI: 2002-154759/20.
 XX Novel nucleic acid useful for diagnosis and therapy of behavioral
 PT disorder, neurological disorder and cancer, comprises a sequence of a
 PT segment of chemically pretreated DNA of adrenergic alpha-1c-receptor
 PT gene -
 PS Claim 1; Page 32-36; 190pp; English.
 XX The invention relates to nucleic acids comprising a segment of chemically
 CC pretreated DNA of adrenergic alpha-1c-receptor gene. The invention also
 CC relates to oligonucleotides or peptide nucleic acid (PNA) oligomers
 CC useful for detecting cytosine methylations. The pretreated DNA is useful
 CC for the diagnosis or therapy of behavioural disorders, neurological
 CC disorders and cancer, in particular major depressive disorder, Tourette's
 CC syndrome, schizophrenia, psychiatric and neurological disorders, smoking,
 CC drug abuse, alcoholism, personality traits, compulsive gambling, human
 CC immunodeficiency virus dementia, migraine, behaviour in patients with
 CC and schizoaffective patients, and suicidal behaviour. In patients with
 CC schizophrenia, the nucleic acid is useful for detecting the methylation
 CC state of all CpG dinucleotides and/or single nucleotide polymorphisms
 CC (SNPs). The present sequence is human chemically treated genomic DNA.
 XX
 XX Sequence 7353 BP; 1544 A; 384 C; 1956 G; 3469 T; 0 other:
 SQ
 Query Match 62.0%; Score 725.2; DB 24; Length 7353;
 Best Local Similarity 76.2%; Pred. No. 1.3e-110;
 Matches 892; Conservative 0; Mismatches 278; Indels 0; Gaps 0;

QY 601 CCGGGGGCGCAGAGCCCAACCGCTGCGCCACCACTCAAGGGGCCCTGGCGGCC 660
 |||||
 Db 5781 TCGGGGGCGGTAGAGGTCAATCGTTTATTTAGTTTAAAGGGCTTTTGGCAGTTTC 5840
 QY 661 GCGCGGGGGCGCGCGCAGACAGCGCTGACCTGAGAGAGACTGCTTCCGAC 720
 |||||
 Db 5841 GCGTCGGTCGGGTCGCGCCATATCGACGGCTTGAGATTGAGAGAGAGTCTTTTCCAT 5900
 QY 721 CACGCCAGCGGCTCTCAGGGCCCGCAGACCCGAGCGGGTCCCGGGGCAAGGCAAG 780
 |||||
 Db 5901 TACGTGAGCGCTTTTACGTTTCTAGATTCGACCGCGGTTTGGGGTAAAGGTAAAG 5960
 QY 781 GCCCGAGCCAGCAGTGAAGCGGACAGCGCTCGCGGGCGCGGGCGGCGAGC 840
 |||||
 Db 5961 GTTCGACCGAGTTAGGTGAAGTCGGGCGATATGTTTGTCCGCGCGGGTCCGGGCGAGC 6020
 QY 841 GGGATCGGAGCGCGCGCTGAGGGCGGGGAGAGCGCTCGGGCTGCCAAGCGCTG 900
 |||||
 Db 6021 GGGATCGGAGCGTTCGTTTGAAGGTCGGGAGAGCGCTCGGGGTTGTTAAGCGCTG 6080
 QY 901 CGTCGCGCGGGCGGCAAGACCGGAGAACGCTTCACGTTGCTGGCGCGGTGCATC 960
 |||||
 Db 6081 CTTGGCGCGGGCGGTGAATCGGAGAACGTTTACGTTGCTGTTGCTGCTGATTC 6140
 QY 961 GGAGTGTTCGTGGTGTCTGGTTCCCTCTCTTCACTACAGCTACAGCGCGCTCGGG 1020
 |||||
 Db 6141 GGAGTGTTCGTGGTGTCTGGTTCCCTCTCTTCACTACAGCTACAGCGCGCTCGGG 6200
 QY 1021 TGTCTCCGTGCGACGACGCTCTTCAATTCCTCTCTGTTGGCTCTCAACAGCTGC 1080
 |||||
 Db 6201 TGTTCGTTGTTACGTTACGTTTAAATTTTGGTTCGTTATTTGTAATGATTCG 6260
 QY 1081 TTGAACCGGTCATCTACACCATCTTCACACGATTTCCGCGCGCTTCAGAGATTC 1140
 |||||
 Db 6261 TTGAATTCGTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 6320
 QY 1141 CTCTGTCGGGGGAGCAGGAGACGGATGCTG 1170
 |||||
 Db 6321 TTTTGTGCGGGGAGATGAGAACGGATGCTG 6350
 RESULT 11
 AA199931
 ID AA199931 standard; DNA; 1383 BP.
 AC AA199931;
 DT 18-FEB-2002 (first entry)
 DE Human alpha-2CAR encoding DNA.
 KW Human: genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
 KW polymorphic site; allelic variant; cardiovascular disease;
 KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
 KW phosphorylation; inositol phosphate; alpha-2CAR; chromosome 4; ds.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 1.1386
 FT CDS
 FT /tag= a
 FT /product= "alpha-2CAR"
 FT /note= "sequence includes a 12 nucleotide polymorphic
 FT site at nucleotides 961-972 absent in the
 FT alpha-2CAR variant (AA199933)"
 XX
 PN WO200179561-A2.
 XX 25-OCT-2001.
 PD
 XX 17-APR-2001; 2001WO-US12575.
 PF
 XX

[illegible]

OY 1021 TGCATCCGTGCCACGCGCAGCTTCAATTCTTCCTGGTTGGGTA CTGAACAAGCTCG 1080
 ||| | | | | | | | | |
D6 6201 TGTTTTTGTTTAGCACACTTTTAAAAAATTTTTTTTTTTTTTTTCCCCCCCCCCATAAAATCATATCCCCTCCACC

Accession	Species	Gene	Protein	Accession	Species	Gene	Protein
QY 1081	TTGAAACCGGTCATCTACACCATCTTCAACACGATTTTCGGCGCGCCCTTCAGAGATC	1140		QY 1141	CTCTGTCGGGGGCGACGAGACGGATCGTG	1170	
Db 6261	TTTTGATTCGGGTTATTATTATATTATTTATTTACGATTTTCCTCGCGTTTTAAGAGATT	6320		Db 6321	TTTGTGCGGGGGGATAGAGACGGATCGTG	6350	
RESULT 10							
AAD28362							
ID AAD28362	standard; DNA; 7353 BP.						
AC AAD28362;							
DT 22-APR-2002	(first entry)						
DE Human	chemically treated genomic DNA #3.						
KW Human;	cytostatic; antidepressant; neuroleptic; nootropic; antiaddictive;						
KW adrenergic	alpha-1C-receptor; cytosine methylation; therapy; alcoholism						
KW behavioural	disorder; neurological; psychiatric; cancer; schizophrenia;						
KW Tourrette's	syndrome; smoking; human immunodeficiency virus dementia;						
KW drug	abuse; miltaraine; ds.						
OS Homo sapiens.							
PN MO2000202809-A2.							
PD 10-JAN-2002.							
XX 02-JUL-2001;	2001WO-EP07540.						
XX 30-JUN-2000;	2000DE-1032529.						
PR 01-SEP-2000;	2000DE-1043826.						

XX 07-MAR-2002.
 PD 01-SEP-2001; 2001WO-EPI0074.
 PF 01-SEP-2000; 2000DE-1043826.
 PR 05-SEP-2000; 2000DE-1044543.
 XX (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K, Guetlig D;
 PI WPI: 2002-371829/40.
 DR
 XX Determining the degree of cytosine methylation in genomic DNA, useful
 PT for diagnosis and prognosis, comprises selective hybridization of
 PT amplicons from chemically treated DNA -
 XX
 XX Claim 12: 56bp + Sequence listing: 56bp; German.
 XX
 CC This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridised to two classes, each with at least one
 CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
 CC and the degree of hybridisation to both classes is determined from the
 CC label on the amplicon. From the ratio of labels hybridised to the two
 CC classes of oligomers, the degree of methylation is calculated. The method
 CC is used: (i) for diagnosis and/or prognosis of side effects of
 CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
 CC of the central nervous, cardiovascular, gastrointestinal and respiratory
 CC systems etc., particularly by detecting mutations or single nucleotide
 CC polymorphisms (SNP s); and (ii) for differentiation of cell or tissue
 CC types and for investigating cell differentiation. The method allows the
 CC methylation status of many C residues to be determined simultaneously.
 CC AB013410-AB054121 represent genomic DNA sequences used to illustrate the
 CC method for determining the degree of cytosine methylation described in
 CC the disclosure of the invention.
 CC
 XX
 XX Sequence 1733 BP; 685 A; 585 C; 211 G; 252 T; 0 other:
 SQ
 Query Match 62.0%; Score 725.2; DB 24; Length 1733;
 Best Local Similarity 76.2%; Pred. No. 1.4e-110;
 Matches 892; Conservative 0; Mismatches 278; Indels 0; Gaps 0;

Db 933 TCGTACGCTGCTGAGTCCGCTTGGCAGATTACGATTAGAACTGGTATTTCTCG 874
 Qy 421 TGCATCGGCTCTCTTCTGCTCCCTGCTCATCATGATCTCTAGTGGCATCTAC 480
 Db 873 TGTATCGGTTTATTTTTCGTTTGTATTATATCATATTTTGTATGCTGCTTTTAT 814
 Qy 481 CAAATGCCCAAGGCTGCGACCCGCTGACACCGCCGCGGCTCCGACCGCTCGCC 540
 Db 813 TAGATCGTTAAGGCTGCTATTCGCTGTTATTTAGTCGTCGGGGTTCCGACGTCGTC 754
 Qy 541 GCGCCCGCGGGGGGACCGACCGACCGACCGACCGCTGCTGGCCCGGACGCGCGGCG 600
 Db 753 GCGTCGTCGGGGGTTATCGAGCTAGATTACGTTTACGTTTACGAGGTGCGGGGT 694
 Qy 601 CCGGGGGGCGCAGAGCCGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 Db 693 TCGGGGGGCGCTAAGGCTGCAATGCTGTTTATTTAGTTTACGCGCTTTTGGCGAGTTC 634
 Qy 661 GCGCGCGCGCGCGCGCGACCGACCGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 Db 633 GCGTCGCTCGGGTCCGCGCATTCGACCGCTGATTTGAGAGAGATTCTGTTTCGAT 574
 Qy 721 CACGCGAGCGGCTCCAGGCGCCCGACACCGAGCGCGCTCCCGGGCAGAGCGTAC 780
 Db 573 TACGTCAGCGGCTTTTATGAGGTTTCTGATTCGATTCGAGCGGCTTTGCGGTTAAGTAA 514
 Qy 781 GCGCGACGAGCCAGGTTGAAGCGGCGGACCGCTGCGCGCGCGCGCGCGCGCGCGAGC 840
 Db 513 GTTCGAGGAGTTAGGTTGATGCTCGGCGATAGTTTGTTCGGGGCGGCTGCGGGCGAGC 454
 Qy 841 GGGATCGGAGCGCGCGCTGACGCGCGGGGAGGAGCGCGCTCGGCGCTGCCAAGCGCTCG 900
 Db 453 GGGATCGGAGCGCGGTTGAGGCTCGGGGAGGAGCGCGCTCGGCGGTTTAAAGCGCTCG 394
 Qy 901 CGCTGCGCGCGCGCGCAGAACCGGAGAACGCTTCACGTTGCTGCGCGCTGCTGCTATC 960
 Db 393 CGTTGCGCGCGCGCGTAAATCGAGAACGCTTTACGTTGCTGCTGCTGCTGCTATC 334
 Qy 961 GAGAGGTTCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
 Db 333 GAGAGGTTCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 274
 Qy 1021 TGCTCGTGCACGACCGCTCTTCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
 Db 273 TGTTCGCTGCTACGACGCTTTTAAATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 214
 Qy 1081 TTGAACCGCGGCTATCATCATCTTCAACACGATTTCCCGCGGCTTCAAGAACATC 1140
 Db 213 TTGAATTCGCTATTTATTTATTTTAAATTACGATTTTCGCGGCTTTTAAAGAACAT 154
 Qy 1141 CTCTGTCGGGGGAGACGAAAGCGATCTG 1170
 Db 153 TTTTGTGCGGGGAGTAAAGAACGAGATCTG 124

RESULT 9
 ABL32072
 ID ABL32072 standard; DNA; 7353 BP.
 XX
 XX ABL32072;
 XX
 XX 26-MAR-2002 (first entry)
 XX
 XX Human immune system associated gene SEQ ID NO: 45.
 DE Human immune system disease; cytosine methylation; antistimatic;
 KW Human: immune system disease; antianemic; cytosinatic; noctropic;
 KW antiantisclerotic; antianemic; cytosinatic; ophthalmological;
 KW neuroprotective; anti-HIV; anticonvulsant; antidiabetic; antipsoriatic;
 KW antineumatic; antianthrill; antidiabetic; antipsoriatic;
 KW antineumatic; cancer; eye disease; arteriosclerosis; anaemia;
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
 KW gene; ds.

KW	Tourette's syndrome; smoking; human immunodeficiency virus dementia;
KW	drug abuse; migraine; ds.
XX	
XX	Homo sapiens.
PN	MO200202809-A2.
PD	10-JAN-2002.
XX	
XX	02-JUL-2001; 2001WO-EP07540.
PF	30-JUN-2000; 2000DE-1032529.
PR	01-SEP-2000; 2000DE-1043826.
PA	(EPIG-) EPIGENOMICS AG.
PI	Olek A, Piepenbrock C, Berlin K;
DR	WPI; 2002-154759/20.
XX	
PT	Novel nucleic acid useful for diagnosis and therapy of behavioral
PT	disorder, neurological disorder and cancer, comprises a sequence of a
PT	segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
PT	gene -
PS	
XX	Claim 1; Page 36-40; 190pp; English.
CC	The invention relates to nucleic acids comprising a segment of chemically
CC	pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also
CC	relates to oligonucleotides or peptide nucleic acid (PNA) oligomers
CC	useful for detecting cytosine methylations. The pretreated DNA is useful
CC	for the diagnosis or therapy of behavioural disorders, neurological
CC	disorders and cancer, in particular major depressive disorder, Tourette's
CC	syndrome, schizophrenia, psychiatric and neurological disorders, smoking,
CC	drug abuse, alcoholism, personality traits, compulsive gambling, human
CC	immunodeficiency virus dementia, migraine, behaviours in patients with
CC	schizophrenia. The nucleic acid is useful for detecting the methylation
CC	state of all CpG dinucleotides and/or single nucleotide polymorphisms
CC	(SNPs). The present sequence is human chemically treated genomic DNA.
XX	
SQ	Sequence 7353 BP; 1713 A; 384 C; 2140 G; 3116 T; 0 other;
	Query Match 68.7%; Score 804.2; DB 24; Length 7353;
	Best Local Similarity 80.5%; Pred. No.1,4e-123; Indels 0;
	Matches 941; Conservative 0; Mismatches 228; Gaps 0;
QY	1 AGCGGGCGGTCAAGGCGGCCAAAACCTTTCCTGGTGCTGTGGCGCTGC CGCATC 60
DB	2173 AACCGCGGTCAAAAGCCCCCAAACCTTCTCTAATCTCTAACCTCGACGCATC 2114
QY	61 CTGTGGCCACGCTGCTCATCCCTTTCTGCTGGCCACAAGAGTCATGGGCTACTG 120
DB	2113 CTATTAAACGAGCTGCTCATCCCTTTCTGCTTAACACGAATCAATAACTAATAC 2054
QY	121 TTGGCAAGCTTGSTGGAGATTACCTGGCGCTGACGTGCTCTCTCACGTGCTC 180
DB	2053 TTGCACAAATTAATAGAAATTTACTTAAGCTGACGACTCTTCAAGTGTGC 1994
QY	181 ATCGACACTGTGCGGCATAGCCTGGACCGCTACTGTGTCATACACAGGCCATGAG 240
DB	1993 ATCGACACTTAATAGCGATCAACCTAAACGCTACTAATTCACACAAACCATGAA 1934
QY	241 TACAACCTGAAGCGACGCGCGCGCGCATCAAGCGCATCATACACGTTGGGTATC 300
DB	1933 TACAACCTTAAGAAGCGACCGCGCGCATCAAAACCATCATCATACCGTTAATAATC 1874
QY	301 TCGGCGGTATCTCTTCCCGCGCTCATCTCCATCGAAGAGGCGCGCGCGCGCGC 360
DB	1873 TCGACCGGTATCTCTTCCCGCGCTCATCTCCATCGAAGAAAAAGAGAGAGAGAC 1814
QY	361 CCGCAGCGCGCGGACCGCGCTGCGAGATCAAGACCAAGAGTGTACGTATCTCGTCG 420

Db	1813	CCGGAAACCGACGAAACCGCGCTACGAAATCAACAACCAAAAAATATATACGATCTCTGTCG	1754
Qy	421	TGCATGGGCTCTCTTCTTCGCTCTCTCTCATTCATGATCTGCTTACGTGCGCATCTAC	480
Db	1753	TACATGCACCTCTCTTTGGCTCTCTTACCTCATCATTAATCCATATCTACATGACATCTTAC	1694
Qy	481	CAGATCGCCAAAGCGTGTGCACCCGCGTGGCACACCGCGCGGGGTCCGAGCGCGCTCGCC	540
Db	1693	CAAAATCCCAAGAGTGTGCACCCGCGTACACCCAAACCGCGGAATCCGAACGCGCTGCGCC	1634
Qy	541	GGCGCGCGGGGGGAGCCAGAGGCGCAAGGCGCAACGGTCTGTGGCCCGCGAGCCAGCGGGCG	600
Db	1633	GGCGCGCGGAAAAACACACCGGAAGCAACCCAAACGATCTTAAACCCCGGAACCAACGAGAAC	1574
Qy	601	CCGGGGGCGCGAGAGCGCCGAACCGCTGCGCCACCCAGCTCAACGGCGCCCTCGGCGAGGCC	660
Db	1573	CCGAAAAACCGAAAAACCGAACCGGCTACCCACCACTCACTACAGAGCGCCCTTAAGAAACCG	1514
Qy	661	GGCGCGCGCGGGGCGCGCGCGACACCGACCGCGCTGAGCTCTGAGAGAGCTGTCTTCCGAC	720
Db	1513	GGCGCGGACCGAACCGCGCGCGACACCGACCGCGCTAACTTAAACAAAAAACTCTCTTCCGAC	1454
Qy	721	CACGCGGAGCGGCTCTCCAGGGCCCCCGCCAAACCGAGCGGGGCGCCCGGGGCGAAAGCAAG	780
Db	1453	CACGCGGAAACACCTCTCCAAAAACCCCGGAACCCGAGACCGGATCCCGGAAACAAAAACAAA	1394
Qy	781	GGCCGAGCGACCCAGGTGGAAGCGGGGAGCGCTGCCGCGGCGCGGCGCGGGGCGGCGACG	840
Db	1393	ACCCGACGAAACCAATTAATAAACGAAACGACAACTTACCGCGACGCGAAACGAAAAACGACG	1334
Qy	841	GGGATCGGGAGCGCGGCTGCAAGGGCGCGGGGAGAGAGCGGTGCGGGGCTGCGCAAGCGCTCG	900
Db	1333	AAAAATCGAAACGCGCGACTACATAACCGAAAAACGAAAAACGCGTGAACCTAACCAAAACGTCG	1274
Qy	901	CGGTGGCGGGGCGCGGCGAGAACCGCGAAGACGCTTCACGTTGCTGCTGCGCGTGGCTATC	960
Db	1273	CGGTAAACCGGAACGACAAACCCGGGAAAAACGGTTCACGTTGCTGCTTAACTAACCTATCTAC	1214
Qy	961	GGAGTTCGTGTTGTTGCTGCTGCTTCTTCTTCACTTACACGCTACACGGCGCGTGGG	1020
Db	1213	GAAATATTGTGTAATTACTAATTTCCCTTCTTCTTCACTACGCTACACGACGCTGCAG	1154
Qy	1021	TGTCGCTGCCACGAGCGCTCTCAAAATTCCTTCTTGTTGCTGCTGCTTACGCAACAGCTCG	1080
Db	1153	TACTCCGTACACGACGCTCTTCAAAATTTCTTCTTAAATTGCTAATGACTACTACAAACAATCG	1094
Qy	1081	TTGAAACCGCGTATCTACACATCTTCAACACGATTTCCGCGCGGCGCTTCAAGAAATC	1140
Db	1093	TTAAACCCGATCATCTACACCTTCTTCAACACGATTTCCGCGCGCTTCAAAAAATC	1034
Qy	1141	CTCTGTCCGGGGGAGAGGAGGAGGATCGT	1169
Db	1033	CTCTATCGAAAAAACAAAAACGATTCGT	1005
RESULT 7			
ABQ47498			
ID	ABQ47498 standard; DNA; 1733 BP.		
AC	ABQ47498;		
XX	12-JUL-2002 (first entry)		
DT	Oligonucleotide for detecting cytosine methylation seq ID NO 34089.		
DE			
XX	Human; cytosine methylation; 5'-CpG-3': uracil; cytosine; diagnosis;		
XX	drug; side effect; cancer; central nervous system; cardiovascular;		
KW	gastrointestinal; respiratory system; single nucleotide polymorphism;		
KX	SNP; cell differentiation; ds.		
OS	Homo sapiens.		
XX	WO200218632-A2.		
PN			

XX 12-JUL-2002 (first entry)
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 34092.
XX
XX Human; cytosine methylation; 5'-CpG-3'; urec11; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
PN WO200218632-A2.
XX
XX 07-MAR-2002.
XX
XX 01-SEP-2001; 2001WO-EP10074.
XX
XX 01-SEP-2000; 2000DE-10A3826.
PR 05-SEP-2000; 2000DE-10A4543.
XX
XX (EP1G-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
PI WPI; 2002-371829/40.
XX
XX Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC AB013410-AB094121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
XX Sequence 1733 BP; 626 A; 625 C; 211 G; 271 T; 0 other;
SQ
Query Match 68.7%; Score 804.2; DB 24; Length 1733;
Best Local Similarity 80.5%; Pred. No. 1.5e-123;
Matches 941; Conservative 0; Mismatches 228; Indels 0; Gaps 0;
OY 1 ACCGCGGCGCTCAAGCGCCCAAAACCTCTTCGTGTCTCTGCGCTCGCGGACATC 60
DB 441 AACCGCGCGCTCAAAACCGCCCAAAACCTCTTCATATATCTCAACCTCGACGACATC 500
OY 61 CTGGTGGCCACGCTGTCATCCCTTTCTGCTGCGCAACGAGGTATGGGCTACGTAC 120
DB 501 CTAATTAACCAACGCTGTCATCCCTTTCTGCTACCAACGAATATATAAAGCTAAATAC 560
OY 121 TTGCGGAGAGCTGTGTCGAGATCTACCTGGGCTGAGAGCTCTCTTCGACGTCGTC 180
DB 561 TTGCGAGAAAGCTTAATACGAATCTACCTACGCTGACGACGTCCTTCTACACGTCGTC 620
OY 181 ATGCTGACACTGTGCGCATCAAGCTGACCGCTACTGTGTCATCATCACACAGGCAATCGAG 240

DB 621 ATGCTACACCTATACGCGCATCAACCTTAACCGCTACTAATCTCATCACAAACCATCGAA 680
OY 241 TACAACTGAAAGGACAGCGCGCCGCGCATCAAGGCCATCATCATCAGCGTGGTCATC 300
DB 681 TACAACTTAAGGACAGCGCGCGCGCGCATCAAAACCATCATCATCAGCGTAAATCATC 740
OY 301 TCGGCGCTCATCTCTTCCTTCGCGCGCTCATCTCATGAGAGAGAGGCGCGCGCGCGG 360
DB 741 TCGACCGTCATCTCTTCCTTCGCGCGCTCATCTCATGAGAGAGAGAGAGAGAGAG 800
OY 361 CCGCAGCG 420
DB 801 CCGCAGCG 860
OY 421 TGCATCGGCTCTCTTCCTTCGCTGCTGCTCATCATGATCTCTGCTCATGCGCGCATCTAC 480
DB 861 TACATCGACTCTCTTCCTTCGCTGCTGCTCATCATGATCTCTGCTCATGCGCGCATCTAC 920
OY 481 CAGATCGCAAGCGTTCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
DB 921 CAATCGCGCAAGCGTTCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 980
OY 541 GCG 600
DB 981 GCG 1040
OY 601 CCGGCG 660
DB 1041 CCGAAGAAACCG 1100
OY 661 GCG 720
DB 1101 GCG 1160
OY 721 CAGCGCGAGCGCGCTTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
DB 1161 CAGCGCGAGCGCGCTTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1220
OY 781 GCGCGCGAGCGCGCTTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
DB 1221 ACCGAGCGAGCGCGCTTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1280
OY 841 GCGAGCGAGCGCGCGCTTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
DB 1281 AAATGCGAGCGCGCGCTTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1340
OY 901 CGGTGCG 960
DB 1341 CGGTGCG 1400
OY 961 GGAATGCGCGCGCGCGCTTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
DB 1401 GGAATGCGCGCGCGCGCTTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1460
OY 1021 TCGTCCG 1080
DB 1461 TACTCG 1520
OY 1081 TTGAGCG 1140
DB 1521 TTGAGCG 1180
OY 1141 CTCTGCG 1200
DB 1581 CTCTGCG 1600
RESULT 5
ABL32073/c standard; DNA: 7353 BP.
ID ABL32073
XX ABL32073;
AC

XX 12-JUL-2002 (first entry)
XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 34091.
DE Human: cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX Homo sapiens.
OS
XX
XX MO200218632-A2.
XX
XX 07-MAR-2002.
XX
XX 01-SEP-2001; 2001WO-EP10074.
XX
XX 01-SEP-2000; 2000DE-1043826.
XX 05-SEP-2000; 2000DE-1044543.
XX
XX (EPIC-) EPIDENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
XX WPI; 2002-371829/40.
XX
XX Determining the degree of cytosine methylation in genomic DNA, useful
XX for diagnosis and prognosis, comprises selective hybridization of
XX amplicons from chemically treated DNA -
XX
XX Claim 12: 56pp + Sequence Listing: 56pp; German.
XX
XX This invention describes a novel method for determining the degree of
XX methylation of a particular cytosine in a motif 5'-CpG-3', present in a
XX genomic sample of DNA. The sample is treated chemically to convert
XX cytosine (C) but not methylated C, to uracil, then part of the genomic
XX DNA that contains the target C is amplified to form a labeled amplicon.
XX The amplicon is hybridised to two classes, each with at least one
XX member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers.
XX and the degree of hybridisation to both classes is determined from the
XX label on the amplicon. From the ratio of labels hybridised to the two
XX classes of oligomers, the degree of methylation is calculated. The method
XX is used: (i) for diagnosis and/or prognosis of side effects of
XX therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
XX of the central nervous, cardiovascular, gastrointestinal and respiratory
XX systems etc., particularly for detecting mutations or single nucleotide
XX polymorphisms (SNP/s); and (ii) for differentiation of cell or tissue
XX types and for investigating cell differentiation. The method allows the
XX methylation status of many C residues to be determined simultaneously.
XX ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
XX method for determining the degree of cytosine methylation described in
XX the disclosure of the invention.
XX
XX Sequence 1733 BP: 271 A; 211 C; 625 G; 626 T; 0 other;
XX
XX Query Match 68.7%; Score 804.2; DB 24; Length 1733;
XX Best Local Similarity 80.5%; Pred. No. 1.5e-123;
XX Matches 941; Conservative 0; Mismatches 228; Indels 0; Gaps 0;

DB 1113 ATCGTACACCTATACGGCATCAACCTTAACCGGTACTAATCCATCCACAAACCATCGAA 1054
QY 241 TACAACCTGAAGGCGACGCGCGCGCATCAAGCCATCATCATCAGCGTGGGTATC 300
DB 1053 TACAACCTGAAGGCGACGCGCGCGCATCAAGCCATCATCATCAGCGTGGGTATC 994
QY 301 TCGGCGGTCAATCTCTTCCCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGG 360
DB 993 TCGACCGTCAATCTCTTCCCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGG 934
QY 361 CCGGACGCGCGCGCGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGG 420
DB 933 CCGGACGCGCGCGCGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGG 874
QY 421 TGCATGCGCTCTTCTTCCCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGG 480
DB 873 TACATGCGCTCTTCTTCCCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGG 814
QY 481 CAGATGCGCGCGCGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGGCGG 540
DB 813 CAGATGCGCGCGCGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGGCGG 754
QY 541 GCGCGCGCGCGCGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGGCGG 600
DB 753 GCGCGCGCGCGCGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGGCGG 694
QY 601 CCGGCGCGCGCGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGGCGGCGG 660
DB 693 CCGGCGCGCGCGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGGCGGCGG 634
QY 661 GCGCGCGCGCGCGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGGCGGCGG 720
DB 633 GCGCGCGCGCGCGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGGCGGCGG 574
QY 721 CAGCGCGCGCGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGGCGGCGGCGG 780
DB 573 CAGCGCGCGCGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGGCGGCGGCGG 514
QY 781 GCGCGCGCGCGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGGCGGCGGCGG 840
DB 513 ACCCGAGCGCGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGGCGGCGGCGG 454
QY 841 GCGATGCGCGCGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGGCGGCGGCGG 900
DB 453 AAAATGGAAGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGGCGGCGGCGG 394
QY 901 GCGTGGCGCGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 960
DB 393 GCGTGGCGCGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 334
QY 961 GAGTGGCGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1020
DB 333 GAAATGGAAGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 274
QY 1021 TGCATGCGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1080
DB 273 TACATGCGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 214
QY 1081 TGAACCGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1140
DB 213 TGAACCGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 154
QY 1141 CTCTGCGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1169
DB 153 CTCTGCGCGCGGTCAATCTCCATGAGAAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 125

RESULT 4
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ID ABQ47501 standard; DNA; 1733 BP.
XX
XX AC ABQ47501;

```
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FT      replace(/53,/c)
FT      /*tag= b
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PM      WO200179561-A2.
XX
XX      25-OCT-2001.
XX
XX      17-APR-2001; 2001WO-US12575.
XX
XX      17-APR-2000; 2000US-0551744.
XX      10-AUG-2000; 2000US-0636259.
XX      19-OCT-2000; 2000US-0692077.
XX
XX      (LIGG/) LIGGETT S B.
XX      (SMALL/) SMALL K M.
XX
XX      Liggett SB, Small KM;
XX
XX      WPI: 2001-611728/70.
XX      P-PSDB: AAM52123.
XX
XX      Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
XX      determining whether an individual is at increased risk of developing a
XX      disease associated with the corresponding receptor comprises detecting
XX      a polymorphic site -
XX
XX      Disclosure; Page 152; 163pp; English.
XX
XX      The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
XX      receptor gene (I)-(III) by detecting a polymorphic site, comprising:
XX      (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
XX      alpha2A or alpha2C or fragment or complement of; and
XX      (b) detecting a polymorphic site comprising nucleotide positions 901-909
XX      of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
XX      or a site comprising (A) (ggggcgggcg) or (B) (ggggcgctgag) at
XX      positions 961-972 of (III). The method may be used for genotyping an
XX      alpha2B, alpha2A or alpha2C receptor gene and further used to determine
XX      whether an individual is at increased risk of developing a disease
XX      associated with alpha2B, alpha2A or alpha2C, comprising detecting a
XX      polymorphic site which correlate to disease selected from cardiovascular
XX      disease, central nervous system disease and combinations of these. In
XX      addition, the technique may be used to predict an individual's response
XX      to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
XX      norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
XX      combinations of these) or antagonist (e.g. yohimbine, prazosin, AKC 239,
XX      rauwolfscine, idazoxan, tolazolan, phentolamine and combinations of
XX      these) by detecting the polymorphic site and correlating the site to a
XX      predetermined response (where the response is correlated to adenylyl
XX      cyclase, MAP kinase activity, phosphorylation or inositol phosphate
XX      levels). The present sequence is that of the human alpha-2AR variant
XX      gene.
XX
XX      Sequence 1350 BP; 199 A; 489 C; 442 G; 220 T; 0 other;
XX
XX      Query Match      99.9%; Score 1168.4; DB 23; Length 1350;
XX      Best Local Similarity 99.9%; Pred. No. 2,7e-183;
XX      Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db      361 ATCTGACCTGTGGCCATCAAGCTTGAGCCGCTACTGGTCCATCAACAGGCAATCGAG 420
Qy      241 TACAACTGAAGGAGCAGAGCGCGCGCATCAAGGCCATCATCAACGCTGGGTATC 300
Db      421 TACAACTGAAGGAGCAGAGCGCGCGCATCAAGGCCATCATCAACGCTGGGTATC 480
Qy      301 TCGGCGGTATCTCTCTTCCCGCGCTCATCTCCATGAGAGAGGCGCGCGCGCG 360
Db      481 TCGGCGGTATCTCTCTTCCCGCGCTCATCTCCATGAGAGAGGCGCGCGCGCG 540
Qy      361 CCGGAGCGCGCGAGCGCGCGCTCGAGATCAAGACAGAGAGTGTATCATCTCTCG 420
Db      541 CCGGAGCGCGCGAGCGCGCGCTCGAGATCAAGACAGAGAGTGTATCATCTCTCG 600
Qy      421 TGCATCGGCTCTCTCTTCCGCTCCCTGCTCATATGATCTGCTCTACGTCGCACTAC 480
Db      601 TGCATCGGCTCTCTCTTCCGCTCCCTGCTCATATGATCTGCTCTACGTCGCACTAC 660
Qy      481 CAGATCGCCAAAGCTTGCACCCCGGTGTCACCCAGCGCGCGGGGTCCGGAGCGCTCGCC 540
Db      661 CAGATCGCCAAAGCTTGCACCCCGGTGTCACCCAGCGCGCGGGGTCCGGAGCGCTCGCC 720
Qy      541 GCGCGCGCGGGGCGACCGAGCGAGCGCGCCCAACGCTCTGAGGCCCGGCGCGCG 600
Db      721 GCGCGCGCGGGGCGACCGAGCGAGCGCGCCCAACGCTCTGAGGCCCGGCGCGCG 780
Qy      601 CCGGAGCGCGCGAGAGCGCGCATCCGCAAGCTCAAGCGCGCGCGCTGCGAGCGCC 660
Db      781 CCGGAGCGCGCGAGAGCGCGCATCCGCAAGCTCAAGCGCGCGCGCTGCGAGCGCC 840
Qy      661 GCGCGCGCGGGGCGCGCGCGAGCACCGCGCTGAGCTGAGAGAGCTGCTCTTCGAC 720
Db      841 GCGCGCGCGGGGCGCGCGCGAGCACCGCGCTGAGCTGAGAGAGCTGCTCTTCGAC 900
Qy      721 CACGCGAGCGGCTCTCAAGGGCGCGCGAGACCGGAGCGCGGTCCCGGGGCAAGGCAAG 780
Db      901 CACGCGAGCGGCTCTCAAGGGCGCGCGAGACCGGAGCGCGGTCCCGGGGCAAGGCAAG 960
Qy      781 GCGCGAGGAGCGAGGTAAAGCGGGGCGAGACGCTGCGCGCGCGCGCGCGCGCG 840
Db      961 GCGCGAGGAGCGAGGTAAAGCGGGGCGAGACGCTGCGCGCGCGCGCGCGCGCG 1020
Qy      841 GGGATCGGAGCGCGCGCTGCAAGGGCGCGGGGAGAGGCGCGTGGCGCGCAAGGCGTCG 900
Db      1021 GGGATCGGAGCGCGCGCTGCAAGGGCGCGGGGAGAGGCGCGTGGCGCGCAAGGCGTCG 1080
Qy      901 CGCTGGCGCGGGCGCGAGAACCGGAGAGCGCTTACGTTCTGCTGGCGGTGCTATC 960
Db      1081 CGCTGGCGCGGGCGCGAGAACCGGAGAGCGCTTACGTTCTGCTGGCGGTGCTATC 1140
Qy      961 GGAAGTGTGAGTGTGCTGCTGCTTCCCTTCTTCTACCTACAGGCTCAGGGCGTGGG 1020
Db      1141 GGAAGTGTGAGTGTGCTGCTGCTTCCCTTCTTCTACCTACAGGCTCAGGGCGTGGG 1200
Qy      1021 TGGTCCGTCGACGCGAGCGCTTCAAAATCTTCTTCTGCTGAGCTACGAAAGCTCG 1080
Db      1201 TGGTCCGTCGACGCGAGCGCTTCAAAATCTTCTTCTGCTGAGCTACGAAAGCTCG 1260
Qy      1081 TTGAACCGGCTCATCTACACCATCTTCAACACAGATTTCCGCGCGCTTCAAGAGATC 1140
Db      1261 TTGAACCGGCTCATCTACACCATCTTCAACACAGATTTCCGCGCGCTTCAAGAGATC 1320
Qy      1141 CTCTGTGCGGGGAGAGAGGAGGATCGTG 1170
Db      1321 CTCTGTGCGGGGAGAGAGGAGGATCGTG 1350
```

RESULT 3
AB047500/c
ID AB047500 standard; DNA: 1733 BP.
XX
AC AB047500;

XX (LIGG/) LIGGETT S B.
 PA (SMAL/) SMALL K M.
 XX
 PI Lliggett SB, Small KM;
 XX
 DR WPI: 2001-611728/70.
 DR P-FSDB: AAM52122.
 XX
 PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 PT determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting
 PT a polymorphic site -

PS Example 7; Page 151; 163pp; English.

CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
 CC or a site comprising (A) (999g999g99) or (B) (999g99g99g) at
 CC positions 961-972 of (III). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2C, comprising detecting a
 CC polymorphic site which correlate to disease and selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. yohimbine, UK14304, BHT933 and
 CC norphenephine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
 CC combinations of these) or antagonist (e.g. epinephrine, prazosin, AHC 239,
 CC rauvolfine, idazoxan, tolazoline, phenolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC levels). The present sequence is that of the human alpha-2AAR gene
 CC (Genbank Accession AF281308).

XX Sequence 1350 BP; 199 A; 490 C; 441 G; 220 T; 0 other;

Query Match 100.0%; Score 1170; DB 23; Length 1350;
 Best Local Similarity 100.0%; Pred. No. 1.5e-183;

Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCGCGGCTCAAGGCGCCCAAAACCTTCTGAGGTCTGGGCTTGGGCGGCAGATC 60
 DB 181 AGCCGCGGCTCAAGGCGCCCAAAACCTTCTGAGGTCTGGGCTTGGGCGGCAGATC 240
 QY 61 CTGGTGGCCAGGCTGCTATCCCTTTCGCTGGCCAAAGGTCATGGGCTACTGTATC 120
 DB 241 CTGGTGGCCAGGCTGCTATCCCTTTCGCTGGCCAAAGGTCATGGGCTACTGTATC 300
 QY 121 TTGGGCAAGGCTTGGTGGAGATCTACCTGGGCTGGAGCTGCTTTCGACGTCGTC 180
 DB 301 TTGGGCAAGGCTTGGTGGAGATCTACCTGGGCTGGAGCTGCTTTCGACGTCGTC 360
 QY 181 ATGCTGACCTGTGGCCATCAAGCTGGACCGCTACTGGTGCATCACAGGCGCATCGAG 240
 DB 361 ATGCTGACCTGTGGCCATCAAGCTGGACCGCTACTGGTGCATCACAGGCGCATCGAG 420
 QY 241 TACAACCTGAAGGCGGCGCGCCGATCAAGGCGATCATCATCAGCTGGGTCATC 300
 DB 421 TACAACCTGAAGGCGGCGCGCCGATCAAGGCGATCATCATCAGCTGGGTCATC 480
 QY 301 TCGGCGCTCATCTCTTCCGCGCTCATCTCCATGAGAAAGGCGCGCGCGCGCG 360
 DB 481 TCGGCGCTCATCTCTTCCGCGCTCATCTCCATGAGAAAGGCGCGCGCGCGCG 540
 QY 361 CCGGAGCGCGCGCGCGCGCTGCGAGATCAAGAGACAGAACTGTAGTCACTCTGTCG 420
 DB 541 CCGGAGCGCGCGCGCGCGCTGCGAGATCAAGAGACAGAACTGTAGTCACTCTGTCG 600

QY 421 TGCATCGGCTCTTCTTCCGCTCCCTGCTCATGATGATCTGTGTTACGTGCGCATTC 480
 DB 601 TGCATCGGCTCTTCTTCCGCTCCCTGCTCATGATGATCTGTGTTACGTGCGCATTC 660
 QY 481 CAGATCGCAAGGCTGCGACCCGCGCTGCGACCCAGCCGCGCGGGTTCGAGCCGTCG 540
 DB 661 CAGATCGCAAGGCTGCGACCCGCGCTGCGACCCAGCCGCGCGGGTTCGAGCCGTCG 720
 QY 541 GCGCGCGCGGGGCGACCGAGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 600
 DB 721 GCGCGCGCGGGGCGACCGAGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 780
 QY 601 CCGGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 660
 DB 781 CCGGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 840
 QY 661 GCGCGCGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 720
 DB 841 GCGCGCGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 900
 QY 721 CAGCGCGAGGCGGCTTCCAGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 960
 DB 901 CAGCGCGAGGCGGCTTCCAGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 960
 QY 781 GCGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 840
 DB 961 GCGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1020
 QY 841 GCGGATCGGAGCGCGGCTGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 900
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 QY 1021 TGCCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1080
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 QY 1081 TTGAACCGCGGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1140
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 DB 1321 CTCTGTGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1350

RESULT 2
 AA19918
 ID AA19918 standard; DNA: 1350 BP.

AC AA19918;

DT 18-FEB-2002 (first entry)

DE Human alpha-2AAR variant encoding DNA.

XX Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;

KW polymorphic site; allelic variant; cardiovascular disease;

KW central nervous system disease; adenylyl cyclase; MAP kinase activity;

XX phosphorylation; inositol phosphate; alpha-2AAR; chromosome 10; ds.

OS Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 1..1353

Db 291 CTGGTGGCCACGCTGTCATTCCTTTCTTTGGCCACGAGGTATAGGTTACTGTAC 350
QY 121 TTGCGCAAGGCTTGTCGATCTACTGCGCTCGAGCTGCTTTCTGACAGTCGCC 180
Db 351 TTTGGTAAGGTGTGTGTGATCTATTGGCTCTCGAGTGTCTTTTGTGACAGTCGCC 410
QY 181 ATGTGACCTGTGTGCGCATCAGCTGAGCCGCTACTGTGTCATCACAGGCGCATCGAG 240
Db 411 ATAGTGACCTGTGTGCGCATCAGCTTGAACCGTACTGTCATCACAGGCGCATCGAG 470
QY 241 TACAACTGAAGGCGAGCGCGCGCGCATCAAGCGCATCATCATCAGCTGTGGGTATC 300
Db 471 TACAACTGAAGGCGAGCGCGCGCGCATCAAGCGCATCATCATCAGCTGTGGGTATC 530
QY 301 TCGGCGGTATCTCTTCCCGCGCTCATCTCATGAGAGAGGCGCGCGCGCGCG 360
Db 531 TCGGCGGTATCTCTTCCCGCGCATCTCATGAGAGAGGCGCGCGCGCGCGCG 590
QY 361 CCGGAGCGCGCGCGCGCGCGCGCGCATCAAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 591 CAGCAGCGCGCGCGCGCGCGCGCGCATCAAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 421 TGCATGCGCTCTCTTCTGCTCCCTGCGCTCATCATGATCTGTACTGCGCATCTAC 480
Db 651 TGCATGCGCTCTCTTCTGCGCTGCTGCTCATCATGATCTGTACTGCGCATCTAC 710
QY 481 CAGATGCGCAAGCTGTGCGACCGCGCTGCGACCGCGCGCGCGCGCGCGCGCGCG 540
Db 711 CAGATGCGCAAGCTGTGCGACCGCGCTGCGACCGCGCGCGCGCGCGCGCGCGCG 770
QY 541 GCG 600
Db 771 GCG 830
QY 601 CCGGAGGCGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
Db 831 CCCAGCGCGCGTGAAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 890
QY 661 GCG 720
Db 891 GCG 950
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Search completed: February 15, 2003, 16:43:17
Job time : 3906.63 secs

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DB 421 TACAACTGAAAGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
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QY 1081 TTGAACCGCGCTCATCTTCAACCATCTTCAACCATCTTCAACCATCTTCAAC 1140
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QY 1141 CTCTGTGCGGCG 1170
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mammalia: Eutheria: Rodentia: Sclurognathini: Muridae: Murinae: Mus.
Mus musculus
Mus musculus (strain 129/Sv) DNA.

REFERENCE
AUTHORS
TITLE
Link, R., Daunt, D., Barsh, G., Chrusciel, A., and Kobilka, B.
Cloning of two mouse genes encoding alpha 2-adrenergic receptor
subtypes and identification of a single amino acid in the mouse
alpha 2-C10 homolog responsible for an interspecies variation in
antagonist binding
Mol. Pharmacol. 42 (1), 16-27 (1992)
JOURNAL
MEDLINE
PUBMED
92342131
FEATURES
source

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BASE COUNT 229 a 481 c 467 g 277 t
ORIGIN

Query Match 80.4% Score 941.2; DB 10; Length 1454;
Best Local Similarity 87.8%; Pred. No. 1.3e-114;
Matches 1027; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

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DB 231 AGTGGCGCGCTCAAAACCTTCTGCTGCTCTGAGCCTCGCCGACATC 290
QY 61 CTGTGGCCACGCTGCTCATCCCTTCTGCTGCTGAGCCTCGCCGACATC 120
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JOURNAL Submitted (20-NOV-1996) Cell Biology, UMDNJ-SOM, 2 Medical Ctr.
Dr., Stratford, NJ 08044, USA
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Best Local Similarity 88.5%; Pred. No. 1.6e-116;
Matches 1036; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

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DEFINITION
ACCESSION M62372.1 GI:206615
VERSION alpha-2-adrenergic receptor; transmembrane protein.
KEYWORDS Rattus norvegicus (strain Sprague-Dawley) adult liver DNA.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1380)
AUTHORS Lanier, S.M., Downing, S., Duzic, E. and Homcy, C.J.
TITLES Isolation of rat genomic clones encoding subtypes of the alpha
2-adrenergic receptor. Identification of a unique receptor subtype
JOURNAL J. Biol. Chem. 266 (16), 10470-10478 (1991)
MEDLINE 91244823
PUBMED 1645350
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PUBMED 8573196
 REFERENCE 2 (bases 1 to 2291)
 AUTHORS Richman, J.G.
 TITLE Direct Submission
 JOURNAL Submitted (26-APR-1995) Jeremy G. Richman, University of Arizona,
 Pharmacology and Toxicology, College of Pharmacy, Room 235, Tucson,
 AZ 85721, USA

FEATURES
 Location/Qualifiers

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Query Match 83.7% Score 979.4; DB 10; Length 2291;
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ACCESSION U79031
VERSION U79031.1 GI:3282234
KEYWORDS
SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1552)
AUTHORS Chabberg, S.C., Duda, T., Rhine, J.A. and Sharma, R.K.
TITLE Molecular cloning, sequencing and expression of an alpha
2-adrenergic receptor complementary DNA from rat brain
Mol. Cell. Biochem. 97 (2), 161-172 (1990)
JOURNAL Mol. Cell. Biochem. 144 (2), 181-190 (1995)
MEDLINE 95349560
PUBMED 7623790
JOURNAL Mol. Cell. Biochem. 144 (2), 181-190 (1995)
MEDLINE 95349560
PUBMED 7623790
REFERENCE 3 (bases 1 to 1552)
AUTHORS Venkataraman, V., Duda, T.M. and Sharma, R.K.
TITLE Direct Submission

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KEYWORDS alpha-2A-adrenergic receptor.
 SOURCE Porcine liver DNA.
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 REFERENCE 1 (bases 1 to 1728)
 AUTHORS Guyer,C.A., Horstman,D.A., Wilson,A.L., Clark,J.D., Kragoe,E.J., Jr. and Limbird,L.E.
 JOURNAL Unpublished (1990)
 REFERENCE 2 (bases 70 to 1582)
 AUTHORS Guyer,C.A., Horstman,D.A., Wilson,A.L., Clark,J.D., Cragoe,E.J., Jr. and Limbird,L.E.
 TITLE Cloning, sequencing, and expression of the gene encoding the porcine alpha 2-adrenergic receptor. Allosteric modulation by Na⁺, H⁺, and amiloride analogs
 JOURNAL J. Biol. Chem. 265 (28), 17307-17317 (1990)
 MEDLINE 91009167
 PUBMED 2170371
 COMMENT Draft entry and computer-readable sequence for [J. Biol. Chem. (1990) In press] kindly submitted by C.A.Guyer, 02-AUG-1990.
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 VERSION U25722.1 GI:818874
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 ORGANISM Cavia porcellus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
 REFERENCE 1 (bases 1 to 2291)
 AUTHORS Svensson,S.P., Bailey,T.J., Porter,A.C., Richman,J.G. and Regan,J.W.
 TITLE Heterologous expression of the cloned guinea pig alpha 2A, alpha 2B, and alpha 2C adrenoceptor subtypes. Radioligand binding and functional coupling to a cAMP-responsive reporter gene
 JOURNAL Biochem. Pharmacol. 51 (3), 291-300 (1996)
 MEDLINE 96152573

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Best Local Similarity			
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Db	959	CAGCGCGACCGGCTCTCAGGGCCCCGACAGACCAGCGCGGCTCCCGGGGCAAGAGGCAAG	1018
Oy	781	GCCCGAGCAGACCAAGTGAAGCGCGGCGACAGCCCTGCCGCGGGCGCGCGCGGGGCGACG	840
Db	1019	GCCCGAGCAGACCAAGTGAAGCGCGGCGACAGCCCTGCCGCGGGCGCGCGCGGGGCGACG	1077
Oy	841	GGGATGGGAGCGCCGCGGTGACAGGGCCGGGGGAGAGAGCGCTCGGGGCTCCCAAGAGCGTCG	900
Db	1078	GGGATGGGAGCGCCGCGGTGACAGGGCCGGGGGAGAGAGCGCTCGGGGCTCCCAAGAGCGTCG	1137
Oy	901	CGGTGGCGGGGCGCGCGGTGACAGGGCCGGGGGAGAGAGCGCTTCAGGCTGTGCGCGGTGCAT	959
Db	1138	CGGTGGCGGGGCGGGGAGAAACCTCGAAGAGCGCTTCAGGCTGTGCGCGGTGCAT	1197
Oy	960	CGGAGTGTTCGTGTGTGCTGTGCTCCCTCTCTTCACCTCAACGCTACAGGCGCGTGG	1019
Db	1198	CGGAGTGTTCGTGTGTGCTGTGCTCCCTCTCTTCACCTCAACGCTACAGGCGCGTGG	1257
Oy	1020	GTGCTCCGCTGCGCAGCAGCGCTCTTCAAAATCTTCTGTGTTGGCTACTGCAACAGCTC	1079
Db	1258	GTGCTCCGCTGCGCAGCAGCGCTCTTCAAAATCTTCTGTGTTGGCTACTGCAACAGCTC	1317
Oy	1080	GTTGAACCCGGTCACTATACACCAATCTTCAACACACGATTTCCCGCGGCTTCAAGAAAT	1139
Db	1318	GTTGAACCCGGTCACTATACACCAATCTTCAACACACGATTTCCCGCGGCTTCAAGAAAT	1377
Oy	1140	CCTCTGTGCGGGGAGCAGAGAGCGGATCTGTG	1170
Db	1378	CCTCTGTGCGGGGAGCAGAGAGCGGATCTGTG	1408
RESULT 11			
PIGA2AR			
LOCUS	PIGA2AR	1728 bp	DNA linear
DEFINITION	Porcine alpha2A-adrenergic receptor (PORA2AR)	gene,	MAN 27-APR-1997
ACCESSION	J05652		
VERSION	J05652.1	GI:1561303	

	Matches	1169;	Conservative	0;	Mismatches	0;	Indels	2;	Gaps	2;
QY	1	AGCGCGCGCGCTCAAGAGCGGCCAAAACCTCTTCTCGTGTGTCTCTGGCCCTCGGCCGACATC	60							
Db	2258	AGCCGCGCGCTCAAGAGGGGCCAAAACCTCTCTCGTGTGTCTCTGGCCGCGGACATC	2317							
QY	61	CTGGTGGCCACGCTTCGTTCATCCCTTTCTCTGCTGTGGCCACGAGAGTCAATGGAGTACTAGTAC	120							
Db	2318	CTGGTGGCCACGCTTCGTTCATCCCTTTCTCTGCTGTGGCCACGAGGTCAATGGGTACTAGTAC	2377							
QY	121	TTGGGCAAGGCTTGTGTGCGAGATCTACTCTTGGCGCTGACGTGCTCTTGTGACAGTGTGC	180							
Db	2378	TTGGGCAAGGCTTGTGTGCGAGATCTACTCTTGGCGCTGACGTGCTCTTGTGACAGTGTGC	2437							
QY	181	ATCTGTGACCTGTGTGCGCCATCATGACCTGTGACCCGCTACTGTGTCTCATCTACACAGGCGCATCGAG	240							
Db	2438	ATCTGTGACCTGTGTGCGCCATCATGACCTGTGACCCGCTACTGTGTCTCATCTACACAGGCGCATCGAG	2497							
QY	241	TACCACTGAAAGCGGCACAGCGCGCGCGCATCAAGGCCATCATCATCACCTGTGGGTATC	300							
Db	2498	TACCACTGAAAGCGGCACAGCGCGCGCGCATCAAGGCCATCATCATCACCTGTGGGTATC	2557							
QY	301	TCGGCGGTGATCTCTCTTTCCTCCGCGCTCATCTCATCTGAGAAAGAGGCGGCGCGCGCGC	360							
Db	2558	TCGGCGGTGATCTCTCTTTCCTCCGCGCTCATCTCATCTGAGAAAGAGGCGGCGCGCGCGC	2617							
QY	361	CCGCGAGCGGCGCCAGACCGCGCTGCGAGATCAACACACAGAAAGTGTACGTATCTCTGCG	420							
Db	2618	CCGCGAGCGGCGCCAGACCGCGCTGCGAGATCAACACACAGAAAGTGTACGTATCTCTGCG	2677							
QY	421	TGCATCGGCTCTCTTCTTGTGCTCCGCTCATCATCATCATCTGTGTCTACGTGTGCGATCTAC	480							
Db	2678	TGCATCGGCTCTCTTCTTGTGCTCCGCTCATCATCATCATCTGTGTCTACGTGTGCGATCTAC	2737							
QY	481	CAGATCGCCAAAGCGTGTGACACCCGCGTGTGCCACCCAGCCGCGCGGGGTCCGGAGAGCCGTGGCC	540							
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Db	2918	GGCGCGCGCGGGCGCGCGGACACCGAGCGGCTGTGACCTGTGGAGAGAGGCTCGTCTCCGAC	2977							
QY	721	CAGCGCGACCGGCTCCAGAGGCGCCCGCACACCGAGCGCGGTCTCCCGGGGCAAAAGGCAAG	780							
Db	2978	CAGCGCGAGCGGCTCCAGAGGCGCCCGCACACCGAGCGCGGTCTCCCGGGGCAAAAGGCAAG	3037							
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QY	841	GGGATGGGAGCGCGCGGCTGCAGGGCGCGGGGGAGAGGAGCGGCTGGGGGCTCCAAAGCGTGC	900							
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QY	901	CGGTGGGGGCGAGG - GGCAGAACCGCGAGAGAGCGCTTACGTTTGTGTGTGCGGTGTGAT	959							
Db	3157	CGGTGGGGGCGAGG - GGCAGAACCGCGAGAGAGCGCTTACGTTTGTGTGTGCGGTGTGAT	3216							
QY	960	CGGAGTTCGTGTGTGTGTGTGTGTCCCTTCTTCTTCACTTACACTACAGCTCAGCGCGGTGG	1019							
Db	3217	CGGAGTTCGTGTGTGTGTGTGTGTCCCTTCTTCTTCACTTACACTACAGCTCAGCGCGGTGG	3276							
QY	1020	GTTGCTCGGTGCGACGACGCTGTTCAAATTTCTTCTGTGTGGGTACTGTCAACAGCTC	1079							
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Query Match	Best Local Similarity	Score	ID	DB	Length
Query Match	Best Local Similarity	Score	ID <td>DB <td>Length</td> </td>	DB <td>Length</td>	Length
Matches 1169; Conservative	99.9%; Pred. No. 1.9e-144;	168.4; DB 6;	199 a	489 c	220 t
	0; Mismatches 1; Indels 0; Gaps 0;				
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181	AGCCGCGGCTCAAGAGCGGCCCAAAACCTTCTTCGTGTCTGTGGCTTCGGCCGACATC	240			
61	CTGGTGGCCAGGCTTCGTATCCCTTTCGGTGGCCAAACAGGTTCATGGCTACTGTAC	120			
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121	TTCGGCAAGGCTTGGTGGAGATCTACCTGGCGCTGACGCTCTTCTCTGACGTGTC	180			
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421	TACAACTGGAACGCGACGCGCGCGCATCAAGGCCATCATACCGTGTGGTATC	480			
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481	TGCGCCGTATCTCTTCCCGCGCTCATCTGCATGGAAGAAAGGGGGCGCGCGGC	540			
361	CCGACACCGCGGAGCGCGCGCTGCGAGATCAACGACGAAAGGTATCTATCTGTC	420			
541	CCGACACCGCGGAGCGCGCGCTGCGAGATCAACGACGAAAGGTATCTATCTGTC	600			
421	TGCAATGGCTCTTCTTCCCTCCCTGCTCATCATGATCGGTATGATGTCGATCTAC	480			
601	TGCAATGGCTCTTCTTCCCTCCCTGCTCATCATGATCGGTATGATGTCGATCTAC	560			
481	CAGATGCGCAAGAGGTGCGACCGCGCGTGCACACCGCGCGGGTCCGAGCGCGTGGC	540			
661	CAGATGCGCAAGAGGTGCGACCGCGCGTGCACACCGCGCGGGTCCGAGCGCGTGGC	720			
541	CGCGCGCGGGGGGACCGAGCGGACCGGACCGGATCGTGTGGCCCGAGCGCGGGG	600			
721	CGCGCGCGGGGGGACCGAGCGGACCGGATCGTGTGGCCCGAGCGCGGGG	780			
601	CGCGGGGGCGCAAGAGCGCGTGGCCACCGTCAACGAGGCGCCCTTGGCGAGCC	660			
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841	CGCGCGCGCGGGCGCGCGACCGAGCGCGTGGAGAGTCTGTCTTCCGAC	900			
721	CAGCGCGAGGGGCTTCCAGGGGCCCGAGACCGGAGTCCCGGGGCGAAAGCGAAG	780			
901	CAGCGCGAGGGGCTTCCAGGGGCCCGAGACCGGAGTCCCGGGGCGAAAGCGAAG	960			
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961	GCCGCGAGCGAGCGAGTGAAGCCGGGCGACAGCTCCCGCGCGCGCGGGGGAAG	1020			
841	GGGATCGGGAGCGCGGCTGCAAGGCGCGGGGAGAGAGCGGTGGCAAGGGCTG	900			
1021	GGGATCGGGAGCGCGGCTGCAAGGCGCGGGGAGAGAGCGGTGGCAAGGGCTG	1080			
901	CGCGGGCGGGGGGCGAAGCCGGGAAACCGGGAACCGCTTCACTTCTGCTGCGGATGATC	960			
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LOCUS
DEFINITION Homo sapiens alpha-2A adrenergic receptor mRNA, complete cds.
ACCESSION AF284095
VERSION AF284095.1 GI:13447750
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS Mao, Z.-M., Tang, K., Li, B.-M. and Jing, N.-H.
TITLE Cloning and expression of human alpha-2A adrenergic receptor in
SY5Y cells
JOURNAL Unpublished
2 (bases 1 to 3653)
REFERENCE
AUTHORS Mao, Z.-M., Tang, K., Li, B.-M. and Jing, N.-H.
TITLE Direct Submission
JOURNAL Submitted (01-JUL-2000) Shanghai Institute of Physiology, Chinese
Academy of Sciences, 320 Yue Yang Road, Shanghai 200031, P. R. China
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Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

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Query Match 100.0%; Score 1170; DB 9; Length 1353;
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RESULT 3
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LOCUS Homo sapiens adrenergic receptor alpha-2A gene, complete cds.
DEFINITION AF262016
ACCESSION AF262016
VERSION AF262016.2 GI:9864781
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1941)
Castellano,M., Giacche',M., Rossi,F., Rivadosi,F., Perani,C.,
Beschi,M. and Agabiti Rosel,E.
A search for genetic variability in the human alpha-2 adrenergic
receptor on chromosome 10
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1941)
Castellano,M., Giacche',M., Rossi,F., Rivadosi,F., Perani,C.,
Beschi,M. and Agabiti Rosel,E.
Direct Submission
JOURNAL Submitted (29-Apr-2000) Medical and Surgical Sciences, University
of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy
3 (bases 1 to 1941)
Castellano,M., Giacche',M., Rossi,F., Rivadosi,F., Perani,C.,
Beschi,M. and Agabiti Rosel,E.
Direct Submission
JOURNAL Submitted (22-Aug-2000) Medical and Surgical Sciences, University
of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy
REMARK Sequence update by submitter
COMMENT On Aug 22, 2000 this sequence version replaced gi:9837145.
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FEATURES Liggett, Stephen B. (US) ; Small, Kersten M. (US)
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DEFINITION Homo sapiens alpha 2A adrenergic receptor (ADRA2A) gene, complete cds.
ACCESSION AF281308
VERSION AF281308.1 GI:9652209
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1353)
AUTHORS Small, K.M., Forbes, S.L., Brown, K.M. and Liggett, S.B.
TITLE An asn to lys polymorphism in the third intracellular loop of the human alpha 2A-adrenergic receptor imparts enhanced agonist-promoted G1 coupling
JOURNAL J. Biol. Chem. 275 (49), 38518-38523 (2000)
MEDLINE 20556293
PUBMED 10948191
REFERENCE 2 (bases 1 to 1353)
AUTHORS Small, K.M., Forbes, S.L., Bridges, K.M. and Liggett, S.B.
TITLE Direct Submission
JOURNAL Submitted (22-JUN-2000) Internal Medicine, University of Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA
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ORIGIN

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Thu Feb 20 09:21:27 2003

us-09-636-259b-1.rge

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Run on: February 15, 2003, 12:29:07 ; Search time 3468.63 Seconds
(without alignments)
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Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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5	1170	100.0	3653	9 AF284095	AF284095 Homo sapi
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11	984.4	84.1	1728	4 PIGA2AR	PIGA2AR
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14	944.4	80.7	1380	10 RRG20	RRG20
15	941.2	80.4	1454	10 MUSALP2ADB	MUSALP2ADB
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17	931	79.6	2923	4 BT079030	BT079030 Bos tauru
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19	804.2	68.7	7353	6 AX348496	AX348496 Sequence
20	725.2	62.0	7353	6 AX344974	AX344974 Sequence
21	725.2	62.0	7353	6 AX348495	AX348495 Sequence
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ALIGNMENTS

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DEFINITION Sequence 24 from Patent WO0179561.
ACCESSION AX350512
VERSION AX350512.1 GI:18616107
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS 1
TITLE Liggett,S.B. and Small,K.M.
JOURNAL Alpha-2 adrenergic receptor polymorphisms
Patent: WO 0179561-A 24 25-OCT-2001;

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RESULT 15
US-10-166-101-6
; Sequence 6, Application US/10166101
; Publication No. US20030008823A1
; GENERAL INFORMATION:
; APPLICANT: Weinmann, Richard L.
; APPLICANT: Branchek, Theresa
; TITLE OF INVENTION: DNA Encoding A 5-HT1F Receptor And Uses Thereof
; FILE REFERENCE: 39318-C
; CURRENT APPLICATION NUMBER: US/10/166,101
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 09/246,075
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 08/483,222
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/117,006
; PRIOR FILING DATE: 1994-08-22
; PRIOR APPLICATION NUMBER: PCT/US93/00149
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: 07/817,920
; PRIOR FILING DATE: 1992-01-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 6
; LENGTH: 390
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; ORGANISM: Homo sapiens
US-10-166-101-6
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Query Match 23.3%; Score 555; DB 9; Length 390;
Best Local Similarity 30.2%; Pred. No. 4.2e-28;
Matches 138; Conservative 59; Mismatches 154; Indels 106; Gaps 12;

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OY 116 FCTSSIVHLCATSLDRYSITQAIENLKRTPRRIRKAIITVWYISAVISFPLISIEKK 175
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OY 234 RG-----PDVAAPPGGTERRPNGLGPERSAGPGGAABEPLPTQLNG-APGEPAAPAGPRD 287
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Db 292 ----VRSDALLEKKRLMAAREKAKTKTGLTILGAFIVCWLPEFTLISLWPICDACWFH 347
OY 405 RTLFKEFFWGYCNSLNPVITYIFNHDERRAFKKIL 441
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 348 LAIFDPEFTWGLYLN-LINDIITYTMSNEDFKQAFHKL 383
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Search completed: February 14, 2003, 13:48:59
Job time : 15.5 secs


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RESULT 11
US-10-005-010-4
: Sequence 4, Application US/10005010
: Patent No. US20020115149A1
: GENERAL INFORMATION:
: APPLICANT: Weinsbach et al, Richard L.
: TITLE OF INVENTION: Method of Obtaining A Composition Comprising A 5-HT1D
: FILE REFERENCE: 36536-B A
: CURRENT APPLICATION NUMBER: US/10/005,010
: CURRENT FILING DATE: 2001-10-29
: PRIOR APPLICATION NUMBER: 09/371,705
: PRIOR FILING DATE: 1999-08-05
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 4
: LENGTH: 390
: TYPE: PRN
: ORGANISM: Homo sapiens
: US-10-005-010-4

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22 NANFTGPNQTSNSTLPQDLITRAISVGLVGAFILEAIVGNILVILSVACNRHLRIPTN 81

Db 362 FIVALLVPECESSCHMPTLLGAIINWLGYSNSLNPVIYAYENKDFONAFKKIKLFCOR 421

RESULT 8
US-09-993-844-6
; Sequence 6, Application US/09993844
; Patent No. US20020106739A1
; GENERAL INFORMATION:
; APPLICANT: Oakley, Robert H.
; APPLICANT: Barak, Lawrence S.
; APPLICANT: Laporte, Stephanie A.
; APPLICANT: Caron, Marc G.
; TITLE OF INVENTION: Modified G-protein Coupled Receptors
; FILE REFERENCE: 033072-026
; CURRENT APPLICATION NUMBER: US/09/993,844
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/245,772
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/260,363
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: amino acid sequence of 5HT1AR-V2R chimera
; OTHER INFORMATION: expressed from the pEARB-1/5HT1AR vector
US-09-993-844-6

Query Match 24.7%; Score 589; DB 10; Length 451;
Best Local Similarity 34.0%; Pred. No. 3,6e-30;
Matches 165; Conservative 61; Mismatches 163; Indels 96; Gaps 20;

QY 1 MGSLQPDAGNSWNGTEP-----GG---GARATPYSLOYTLVLCIAGLIMLTIVFGNV 52
DB 1 MDVLSPPGGN---NTTSPAPFETGNTGTSVTVSYQVTSL--LLGTLIFCAVAGNA 55
QY 53 LVIIAFTSRALKAPQNIIFLVLSADILVATLVIPEFLANEVWGMYFGKAMCEIYAL 112
DB 56 CVAVALAERLQNVANANLIGSLAVTDLVSVLVLPMAALYQVANKMTLGGVTDLFIAL 115
QY 113 DVLCTSSIVHLCALSDRYSTIQALIEYNLKRPRKAKIITVWVIAVISFPLISI 172
DB 116 DVLCTSSIVHLCALSDRYSTIQALIEYNLKRPRKAKIITVWVIAVISFPLISI 173
QY 173 EKKGGGGGPOP-AEP-RCEINDOKWYVISCIGSFAPCLIMLVYRIQIAK---RRT 227
DB 174 ---GWRTPEDRSDDACTISKDHGYITTYTFGAFYITLLMLVLVIGLIFRAAFRIKRT 229
QY 228 RVPSPRRGPD--VAAPPGTERRENG-----LGPERSAGFGAGAEPLPTQOLGA- 276
DB 230 VKKVEKTAGDRHGSAPAPQPKKSVNGSGSRNMLGVESKA--GALC-----ANGAV 281
QY 277 -PGEAPAGPRDTALDLE---SSSDHAERPPRPPRRGPRGRGKAKARASQVKKPDS 331
DB 282 RQGD-----DGALEVEYVHRVGNSEKHLPL-----SAGP----- 313
QY 332 LPRRPGATGIGTPAAGGEEVGAAKASRWGRQ--NREKFTFEVLAVIVGVVWCPPE 390
DB 314 -----TPCAPPSFEKKNRNNAEAKKMALEFETVKTGLIGIMGTFLICWLPF 361
QY 391 FFTYTLTAV---GCSVPRTLKFFPFMWGCVSSSLNPVITTYTFNHDFRAFKIL---CR 443
DB 362 FIVALLVPECESSCHMPTLLGAIINWLGYSNSLNPVIYAYENKDFONAFKKIKCNCA 421
QY 444 GDRKR 448
DB 422 AARGR 426

RESULT 9
US-10-005-010-2
; Sequence 2, Application US/10005010
; Patent No. US20020115149A1
; GENERAL INFORMATION:
; APPLICANT: Weinschank et al, Richard L.
; TITLE OF INVENTION: Method of Obtaining A Composition Comprising A 5-HT1D
; TITLE OF INVENTION: Selective Compound
; FILE REFERENCE: 36536-Ba
; CURRENT APPLICATION NUMBER: US/10/005,010
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/371,705
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-005-010-2

Query Match 24.6%; Score 585.5; DB 12; Length 377;
Best Local Similarity 31.2%; Pred. No. 5e-30;
Matches 138; Conservative 68; Mismatches 151; Indels 85; Gaps 9;

QY 4 LQPDAGNSWNGTEAPGGGARATPYSLOYTLVLCIAGLIMLTIVFGNVIIAFTSRA 63
DB 11 LQPDAGNSWNGTEAPGGGARATPYSLOYTLVLCIAGLIMLTIVFGNVIIAFTSRA 68
QY 64 LKAPQNIIFLVLSADILVATLVIPEFLANEVWGMYFGKAMCEIYALDVLFTSSIVH 123
DB 69 LKAPQNIIFLVLSADILVATLVIPEFLANEVWGMYFGKAMCEIYALDVLFTSSIVH 128
QY 124 LCAISIDRYSTIQALIEYNLKRPRKAKIITVWVIAVISFPLISIEKKGGGGPOP 183
DB 129 LCAISIDRYSTIQALIEYNLKRPRKAKIITVWVIAVISFPLISIEKKGGGGPOP 183
QY 184 AEPRECEIN-DOKWYVISCIGSFAPCLIMLVYRIQIAKRRTRVPPSRGPDVAAP 242
DB 184 EMDSDLVNLSQISITLYISGAFYIPSVLLIILYGRYRAARNRILNPSTLGGKFTTA- 242
QY 243 PGSTERRPNGLGERSAGGAGAEPLPTQOLGAPPEPAPAPRDTALDLESSSDA 302
DB 243 -----HLITGSAG-----SSLSLSSSLHEGHS 265
QY 303 ERPPGPRRPERGPRGKAKARASQVKKPDSLPRRPGATGIGTPAAGGEEVGAAKASRW 362
DB 266 HSAQSP-----FFNHVAKIKLADALER-----KRISA----- 294
QY 363 RGRNREKRETFEVLAVIVGVVWCPPEFTYTLTAV---GCSVPRTLKFFFWGYCNS 419
DB 295 -----REKATKILGIIIGAFIICWLPFVVSILVLPICRDSWIMHPLDFFTWLGILNS 349
QY 420 SLNPVITTYTFNHDFRAFKIL 441
DB 350 LNPVIYAYENKDFONAFKKIKL 371

RESULT 10
US-10-166-101-5
; Sequence 5, Application US/10166101
; Publication No. US20030008823A1
; GENERAL INFORMATION:
; APPLICANT: Weinschank, Richard L.
; APPLICANT: Branchek, Theresa
; TITLE OF INVENTION: DNA Encoding A 5-HT1F Receptor And Uses Thereof
; FILE REFERENCE: 39318-C
; CURRENT APPLICATION NUMBER: US/10/166,101
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 09/246,075
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 08/483,222

Query Match 47.2%; Score 1124; DB 10; Length 447;
Best Local Similarity 53.2%; Pred. No. 1.1e-63;
Matches 243; Conservative 49; Mismatches 103; Indels 62; Gaps 14.

RESULT 5

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1  APPLICANT: Khodadoust, Mehran M.
2  APPLICANT: Macbeth, Kyle J.
3  APPLICANT: Busfield, Samantha J.
4  APPLICANT: McCarthy, Sean A.
5  APPLICANT: Holtzman, Douglas A.
6  APPLICANT: Gu, Wei
7  APPLICANT: White, David
8  APPLICANT: Pan, Yang
9  TITLE OF INVENTION: NOVEL ITALY, LOR-2, STRIPE, TRASH, BDSF, LRSG, AND
10 TITLE OF INVENTION: STRET PROTEIN AND NUCLEIC ACID MOLECULES AND USES
11 TITLE OF INVENTION: THEREFOR
12 FILE REFERENCE: NMI-121CP
13 CURRENT APPLICATION NUMBER: US/09/782,980
14 CURRENT FILING DATE: 2001-02-13
15 PRIOR APPLICATION NUMBER: PCT/US00/02125
16 PRIOR FILING DATE: 2000-01-27
17 PRIOR APPLICATION NUMBER: 09/448,076
18 PRIOR FILING DATE: 1999-11-23
19 PRIOR APPLICATION NUMBER: 09/276,400
20 PRIOR FILING DATE: 1999-03-25
21 PRIOR APPLICATION NUMBER: 60/117,580
22 PRIOR FILING DATE: 1999-01-27
23 PRIOR APPLICATION NUMBER: 09/014,195
24 PRIOR FILING DATE: 1998-01-27
25 PRIOR APPLICATION NUMBER: 09/014,348
26 PRIOR FILING DATE: 1998-01-27
27 PRIOR APPLICATION NUMBER: 09/086,892
28 PRIOR FILING DATE: 1998-05-29
29 PRIOR APPLICATION NUMBER: 09/296,208
30 PRIOR FILING DATE: 1999-04-21
31 PRIOR APPLICATION NUMBER: 09/063,950
32 PRIOR FILING DATE: 1998-04-21
33 PRIOR APPLICATION NUMBER: 09/561,381
34 PRIOR FILING DATE: 2000-04-28
35 PRIOR APPLICATION NUMBER: 09/561,810
36 PRIOR FILING DATE: 2000-04-28
37 PRIOR APPLICATION NUMBER: 09/087,121
38 PRIOR FILING DATE: 1998-05-29
39 PRIOR APPLICATION NUMBER: 09/672,721
40 PRIOR FILING DATE: 2000-09-28
41 PRIOR APPLICATION NUMBER: 09/049,799
42 PRIOR FILING DATE: 1998-03-27
43 NUMBER OF SEQ ID NOS: 176
44 SOFTWARE: PatentIn Ver. 2.0
45 SEQ ID NO 84
46 LENGTH: 601
47 TYPE: PRT
48 ORGANISM: Drosophila melanogaster
49 US-09-782-980-84

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[illegible]

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QY 299 SDHAERPPGRPRRPGRGKARASOVKPGD--SLPRRPG-----ATGIGTPAAGPGE 351
Db 294 EDEAE-----EEEEEEBCECEPOAVPSPASACSPPLDQPGSRVLAATLRGOVLLGRG- 348
QY 352 ERGAANKASRWGRQ--NREKRTFVLAVVIGVFWCWPFFFTYTLTAV---GCSVPRT 406
Db 349 --VGAIGGOWMRRRAQLTREKRTFVLAVVIGVFWCWPFFFTYSLGAIKPKHCKVPHG 406
QY 407 LKFFFWFGYCNSSLNPNVITYTTFNODFRRAFKIICR 443
Db 407 LFOFFFWIGYCNSSLNPNVITYTTFNODFRRAFKIICR 443

RESULT 2
US-09-825-923-4
; Sequence 4, Application US/09825923
; Patent No. US20010016338A1
; GENERAL INFORMATION:
; APPLICANT: Snapir, Amir
; APPLICANT: Helinonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Matti
; APPLICANT: Koulu, Markku
; APPLICANT: Pesonen, Ollamari
; APPLICANT: Scheinin, Mika
; APPLICANT: Salonen, Jukka T
; APPLICANT: Tuomala, Tomi-Pekka
; APPLICANT: Lakka, Timo A
; APPLICANT: Nyysanen, Kristina
; APPLICANT: Salonen, Riitta
; APPLICANT: Kaunonen, Jussi
; APPLICANT: Valkonen, Veli-Pekka
; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
; FILE REFERENCE: Protein, and uses thereof
; CURRENT APPLICATION NUMBER: US/09/825,923
; PRIORITY FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/422,985
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-923-4

Query Match 47.2%; Score 1124.5; DB 10; Length 450;
Best Local Similarity 53.2%; Pred. No. 1e-63;
Matches 243; Conservative 49; Mismatches 106; Indels 59; Gaps 14;

QY 27 PYSLOVTLVYGLMLTLTFVGNVLIIVFTSRALKAPONLEFLVSLASADIVATLV 86
Db 6 PYSVQATAIAAATFTLFTIFGNALVILAVLSRLRAPONLEFLVSLAADIIVATLV 65
QY 87 IPFSLANEVGYWFGKACETIYALDVLCTSSIVHCAISLDYWSITQATEYNLKRT 146
Db 66 IPFSLANEVGYWFGKACETIYALDVLCTSSIVHCAISLDYWSITQATEYNLKRT 125
QY 147 PRRIKAITTYWVSAVSPPLISIEKGGGGGP--ABPCEINDQKVVYSSCIGSF 205
Db 126 PRRIKAITTYWVSAVSPPLISIEKGGGGGP--ABPCEINDQKVVYSSCIGSF 205
QY 206 FAPCLIMLVVRIYQIAKRTVPSPRRGPDVAAPPGTERRPNGLGERSAGGAGAE 265
Db 182 FAPCLIMLVVRIYQIAKRTVPSPRRGPDVAAPPGTERRPNGLGERSAGGAGAE 265
QY 266 AEPLPT-----OLNG--APGEPA--GPRDJDALDEES-----SS 298
Db 234 LPALASVASAREVNGHSGKSTGEKEEGEDTETGTRALPPSMALPNSGGQKEGVCGASP 293

QY 299 SDHAERPPGRPRRPGRGKARASOVKPGD--SLPRRPG-----ATGIGTPAAGPGE 351
Db 294 EDEAE-----EEEEEEBCECEPOAVPSPASACSPPLDQPGSRVLAATLRGOVLLGRG- 348
QY 352 ERGAANKASRWGRQ--NREKRTFVLAVVIGVFWCWPFFFTYTLTAV---GCSVPRT 406
Db 349 --VGAIGGOWMRRRAQLTREKRTFVLAVVIGVFWCWPFFFTYSLGAIKPKHCKVPHG 406
QY 407 LKFFFWFGYCNSSLNPNVITYTTFNODFRRAFKIICR 443
Db 407 LFOFFFWIGYCNSSLNPNVITYTTFNODFRRAFKIICR 443

RESULT 3
US-10-077-870-2
; Sequence 2, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077,870
; PRIORITY FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 3.1
; SEQ ID NO 2
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-077-870-2

Query Match 47.2%; Score 1124; DB 9; Length 447;
Best Local Similarity 53.2%; Pred. No. 1.e-63;
Matches 243; Conservative 49; Mismatches 103; Indels 62; Gaps 14;

QY 27 PYSLOVTLVYGLMLTLTFVGNVLIIVFTSRALKAPONLEFLVSLASADIVATLV 86
Db 6 PYSVQATAIAAATFTLFTIFGNALVILAVLSRLRAPONLEFLVSLAADIIVATLV 65
QY 87 IPFSLANEVGYWFGKACETIYALDVLCTSSIVHCAISLDYWSITQATEYNLKRT 146
Db 66 IPFSLANEVGYWFGKACETIYALDVLCTSSIVHCAISLDYWSITQATEYNLKRT 125
QY 147 PRRIKAITTYWVSAVSPPLISIEKGGGGGP--ABPCEINDQKVVYSSCIGSF 205
Db 126 PRRIKAITTYWVSAVSPPLISIEKGGGGGP--ABPCEINDQKVVYSSCIGSF 205
QY 206 FAPCLIMLVVRIYQIAKRTVPSPRRGPDVAAPPGTERRPNGLGERSAGGAGAE 265
Db 182 FAPCLIMLVVRIYQIAKRTVPSPRRGPDVAAPPGTERRPNGLGERSAGGAGAE 265
QY 266 AEPLPT-----OLNG--APGEPA--GPRDJDALDEES-----SS 298
Db 234 LPALASVASAREVNGHSGKSTGEKEEGEDTETGTRALPPSMALPNSGGQKEGVCGASP 293
QY 299 SDHAERPPGRPRRPGRGKARASOVKPGD--SLPRRPG-----ATGIGTPAAGPGE 351
Db 294 EDEAE-----EEEEEEBCECEPOAVPSPASACSPPLDQPGSRVLAATLRGOVLLGRG- 345
QY 352 ERGAANKASRWGRQ--NREKRTFVLAVVIGVFWCWPFFFTYTLTAV---GCSVPRT 406
Db 346 --VGAIGGOWMRRRAQLTREKRTFVLAVVIGVFWCWPFFFTYSLGAIKPKHCKVPHG 403
QY 407 LKFFFWFGYCNSSLNPNVITYTTFNODFRRAFKIICR 443
Db 404 LFOFFFWIGYCNSSLNPNVITYTTFNODFRRAFKIICR 440

RESULT 4
US-09-825-923-2
; Sequence 2, Application US/09825923

GenCore version 5.1.3
(c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2003, 12:02:50 ; Search time 12.5 Seconds
(without alignments)
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Title: US-09-636-259B-3

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reverse score: 2501
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Total number of hits satisfying chosen parameters:	140259
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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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5:  /cgn2.6/prodata/2/pubppaa/US06_PUBCOMB pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1124.5	47.2	450	9	US-10-077-870-4	Sequence 4, Appl1
2	1124.5	47.2	450	10	US-09-825-923-4	Sequence 4, Appl1
3	1124	47.2	447	9	US-10-077-870-2	Sequence 2, Appl1
4	1124	47.2	447	10	US-09-825-923-2	Sequence 2, Appl1
5	648	27.2	601	10	US-09-783-980-84	Sequence 84, Appl1
6	648	27.2	601	9	US-09-884-430-8	Sequence 8, Appl1
7	594	24.9	422	9	US-10-166-101-3	Sequence 3, Appl1
8	589	24.6	451	10	US-09-993-844-6	Sequence 6, Appl1
9	585.5	24.6	377	12	US-10-005-010-2	Sequence 2, Appl1
10	580	24.4	376	9	US-10-166-101-5	Sequence 5, Appl1
11	577.5	24.3	390	12	US-10-005-010-4	Sequence 4, Appl1
12	573.5	24.1	517	10	US-09-951-622-10	Sequence 10, Appl1
13	566.5	23.8	520	9	US-10-185-991-4	Sequence 4, Appl1
14	560	23.5	497	12	US-10-052-589-2	Sequence 2, Appl1
15	555	23.3	390	9	US-10-166-101-6	Sequence 6, Appl1
16	553.5	23.2	572	9	US-10-185-991-2	Sequence 2, Appl1
17	547	23.0	466	9	US-10-185-991-6	Sequence 6, Appl1
18	545.5	22.9	466	10	US-09-951-622-11	Sequence 11, Appl1
19	542.5	22.8	501	10	US-09-951-622-9	Sequence 9, Appl1

ALIGNMENTS

20	510.5	21.4	370	9	US-10-109-532A-1	Sequence 2, Appl1
21	505	21.2	400	10	US-09-895-211-4	Sequence 4, Appl1
22	505	21.2	400	10	US-09-895-211-6	Sequence 6, Appl1
23	498	20.9	366	9	US-10-166-101-2	Sequence 2, Appl1
24	498	20.9	366	9	US-10-166-101-7	Sequence 7, Appl1
25	496.5	20.9	445	9	US-09-349-755-5	Sequence 5, Appl1
26	496.5	20.9	445	9	US-09-166-334-5	Sequence 5, Appl1
27	496.5	20.9	445	10	US-09-350-206-5	Sequence 5, Appl1
28	489.5	20.6	408	10	US-09-895-211-5	Sequence 5, Appl1
29	489.5	20.6	445	9	US-09-349-755-2	Sequence 2, Appl1
30	489.5	20.6	445	9	US-09-166-334-2	Sequence 2, Appl1
31	489.5	20.6	445	10	US-09-350-206-2	Sequence 2, Appl1
32	486.5	20.4	394	10	US-09-993-844-7	Sequence 7, Appl1
33	482.5	20.3	408	10	US-09-895-211-2	Sequence 2, Appl1
34	479	20.1	382	10	US-09-993-844-5	Sequence 5, Appl1
35	464	19.5	498	9	US-10-020-009-10	Sequence 10, Appl1
36	464	19.5	498	9	US-10-020-009-22	Sequence 22, Appl1
37	463	19.4	460	10	US-09-782-980-82	Sequence 82, Appl1
38	463	19.4	460	10	US-09-884-330-6	Sequence 6, Appl1
39	461.5	19.4	279	10	US-09-864-761-3.6992	Sequence 36992, Appl1
40	460	19.3	359	10	US-09-951-622-1.3	Sequence 13, Appl1
41	452.5	19.0	445	10	US-09-989-861-16	Sequence 16, Appl1
42	444	18.6	388	10	US-09-989-861-8	Sequence 8, Appl1
43	441.5	18.5	359	10	US-09-989-861-19	Sequence 19, Appl1
44	441	18.5	460	9	US-10-166-101-4	Sequence 4, Appl1
45	435	18.3	387	10	US-09-989-861-2	Sequence 2, Appl1

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RESULT 1
US-10-077-870-4
; Sequence 4, Application US/10077870
; Publication No. US2003003470A1
; GENERAL INFORMATION:
; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077,870
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-077-870-4

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Query Match	47.28;	Score 1124.5;	DB 9;	Length 450;
Best Local Similarity	53.28;	Pred. No. 1e-63;		
Matches 243; Conservative	49;	Mismatches 106;	Indels 59;	Gaps 14;

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QY      27  PSLDVLTYLTVCAGLMLMLLVFEGVLYITIAVFPSSRLKAPQNFELVSLASADITVATLV  86
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QY      87  IFFSLANEVGYWYFGRKAMCEIYALDVLFTCSITVHLCAISIDRWYSTOAIIEYNLKRT  146
Db      66  IFFSLANELLGWYFRRTRMCEVYIALDVLFTCSITVHLCASIDRWYAVASRLTEYNKRT  125
QY      147  PRRIKAIITTVVIAVAVISFPPLSIIEKKGGGGQOP--AERCEINQKRWIVISGSGF  205
Db      126  PARICIIITVWLIAAVISLPLI---YKDQGGQOPGRGPOCKLNDQWAIITLSSIGSF  181
QY      206  FAPCIIIMIVYRIQIAIKKRTVPVPSRRGPDADVAAPGCTERRRNGICLPERASGPGAE  265
Db      182  FAPCIIIMIVYRIITLIKKR-----SNRRGPRAKGPGGSGSKOP--PDHGALASAK  233
QY      266  AEPLEPT---QLNG---APGEPAVA--GPROTDALDLEES-----SS  299

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1      APPLICATION NUMBER:  US 07/943,236
2
3      FILING DATE:  10-SEP-1992
4
5      ATTORNEY/AGENT INFORMATION:
6
7      NAME:  Townsend, Kevin G.
8
9      REGISTRATION NUMBER:  34,033
10
11     REFERENCE/DOCKET NUMBER:  MORPHY-2 PCT
12
13     TELECOMMUNICATION INFORMATION:
14
15     TELEPHONE:  202-628-5197
16
17     TELEFAX:  202-737-3528
18
19     TELE:  248633
20
21     INFORMATION FOR SEQ ID NO:  20:
22
23     SEQUENCE CHARACTERISTICS:
24
25     LENGTH:  330 amino acids
26
27     TYPE:  amino acid
28
29     STRANDEDNESS:  single
30
31     TOPOLOGY:  linear
32
33     MOLECULE TYPE:  peptide
34
35     PCT-US93-08528-20

```

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1  APPLICATION NUMBER:  US/07/676,174A
2  FILING DATE:  19910328
3  CLASSIFICATION:  435
4  ATTORNEY/AGENT INFORMATION:
5  NAME:  SCOTT, Watson T.
6  REGISTRATION NUMBER:  26,581
7  REFERENCE/DOCKET NUMBER:  WVS/5683/79117/KIK
8  TELECOMMUNICATION INFORMATION:
9  TELEPHONE:  (202)861-3000
10 TELEFAX:  (202)822-8944
11 TELE:  6714627 CUSH
12 INFORMATION FOR SEQ ID NO:  2:
13     SEQUENCE CHARACTERISTICS:
14         LENCTH:  601 amino acids
15         TYPE:  AMINO ACID
16         TOPOLOGY:  linear
17     MOLECULE TYPE:  protein
18     US-07-676-174A-2

```


LENGTH: 330 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 PCT-US93-08528-19

Query Match 44.0%; Score 1046.5; DB 5; Length 330;
 Best Local Similarity 50.7%; Pred. No. 4e-53;
 Matches 216; Conservative 38; Mismatches 55; Indels 117; Gaps 9;

36 LVCLAGLMLLTVEGNVLIYIAVTSRAKAPQNLFLVSLASADILVATLIPESLANEV 95
 4 LAAVGFLVETVGNVLVIAVLSRALAPQNLFLVSLASADILVATLIPESLANEI 63
 96 MGWYFGKAMCEIYLALDVLFCSTSIYHLCASIDRWYSITQAIETNLRPRRIKATII 155
 64 M-WYFGQWCVGLYALDVLFCSTSIYHLCASIDRWYSITQAVETNLRPRRIKATIV 122
 156 TWVIVSAVISFPPLISIEKKGGGQPAEPCEINDOKWYVYSSICISGFAPCLIMILV 215
 123 AWWLSAVISFPPLVSLYRQPDGA---AYPOCGINDETWTYSSICISGFAPCLILYLV 178
 216 YVRIYQIAKRTVRPPSRGPDVAAPGCTERRPNGLGPESAGPGAEAPLPQLNG 275
 179 YVRIYVAKRTTILSEKAP-----VGPDGAS---PTTENG 212
 276 APEPAPAGPRDTALDLESSSSDHAERPPGRPRERNGPRGKARASQVAPGDLPRR 335
 213 L----- 213
 336 GGGATGIGTPAGPGEERYGAK--ASRRGR-----QNRKRTFLVAVVIGVAV 384
 214 -----GAAGBARGTATRLSRKRRARSSVCRKRVADARERKTFVLAL---VFV 260
 385 VCMPEFFETTLTAV---GCSVPRTLFFEFWFGYCNLSNPVYITINHPERRAFKIL 441
 261 LCMPEFFETTLTAV---GCSVPRTLFFEFWFGYCNLSNPVYITINHPERRAFKIL 441
 442 CGGDKR 447
 321 FRRRRR 326

RESULT 13
 US-08-118-270-20
 Sequence 20, Application US/08118270
 Patent No. 5508384

GENERAL INFORMATION:
 APPLICANT: Murphy, Randall B.
 APPLICANT: Schuster, David I.
 TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
 TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
 NUMBER OF SEQUENCES: 348
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/118,270
 FILING DATE: 09-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/943,236
 FILING DATE: 10-SEP-1992
 ATTORNEY/AGENT INFORMATION:

NAME: Townsend, Kevin G.
 REGISTRATION NUMBER: 34,033
 REFERENCE/DOCKET NUMBER: MURPHY-2A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 330 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-118-270-20

Query Match 43.2%; Score 1029; DB 1; Length 330;
 Best Local Similarity 53.0%; Pred. No. 4e-52;
 Matches 221; Conservative 41; Mismatches 55; Indels 100; Gaps 14;

33 TLIVCLAGLMLLTVEGNVLIYIAVTSRAKAPQNLFLVSLASADILVATLIPESLA 92
 1 TAAIAATFLTLTIGNALVLIYIAVLSRALAPQNLFLVSLASADILVATLIPESLA 60
 93 NEVWYFGKAMCEIYLALDVLFCSTSIYHLCASIDRWYSITQAIETNLRPRRIKA 152
 61 NELGWYFRRTWCEVYALDVLFCSTSIYHLCASIDRWYASRALEYSKTRPRIKC 120
 153 IITVWISAVISFPPLISIEKKGGGQPOP-AEPCEINDOKWYVYSSICISGFAPCLT 211
 121 IITVWISAVISFPPLISIEKKGGGQPOP-AEPCEINDOKWYVYSSICISGFAPCLT 211
 212 MILVYVRIYQIAKRTVRPPSRGPDVAAPGCTERRPNGLGPESAGPGAEAPLPQL 271
 176 LLYVLIYIYIAKRTVRPPSRGPDVAAPGCTERRPNGLGPESAGPGAEAPLPQL 271
 272 QLNCAPEPAPAGPRDTALDLESSSSDHAERPPGRPRERNGPRGKARASQVAPGDS 331
 207 -----QPRP-----DH-----GGAIAAKLP--- 222
 332 LPRRGATGIGTPAGPGEERYGAKASRRGRON--REKRTFLVAVVIGVAVV 389
 223 -----AASRG---VGAIGGQWRRRAHYTRKRTFLVAVVIGVAVV 267
 390 FFFETTLTAV---GCSVPRTLFFEFWFGYCNLSNPVYITINHPERRAFKIL 443
 268 FFFETTLTAV---GCSVPRTLFFEFWFGYCNLSNPVYITINHPERRAFKIL 443

RESULT 14
 PCT-US93-08528-20
 Sequence 20, Application PC/TUS9308528
 GENERAL INFORMATION:
 APPLICANT: New York University
 TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
 TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
 NUMBER OF SEQUENCES: 348
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/08528
 FILING DATE: 09-SEP-1993
 PRIOR APPLICATION DATA:

```

|||||
Db 139 IVALCAISIDRWSTVGAVEYNLKRPRKATIVAVWIIISAVISPPPLVSLRQPDGA- 197
QY 181 POFAERCEIENDQKWTYVSSICISFFAPCLIMLVYVRIYQAKRTRVPPRRGPDAA 240
Db 198 ---AYPOCGINDETWYIISCIQSFAPCLINGLYARIRAKRTRTLSEKRAP---V 251
QY 241 APPGTERPNSGIPERSAGPGAE---AEPLETOINGAPGEPAPGPDOTALDLEESS 297
Db 252 GPGGASPTTENGIG-----AAGGARFTGTAAPR-----PTWARTR----- 287
QY 298 SSHAERP---PGRPRPERPGKAKARASQVKPQDSLPRRPGATGTCTAPAGGEER 353
Db 288 ---AAGPRGAGAPLR---RGGRRAGAG-----GAGGADGGAGGGAQ 328
QY 354 VGAKASRMWG-----RQNRERKFTFVLAVVIG 381
Db 329 SGALITRSRSPGGRSLRASRSVEFFLSRRARRSSVCRKVAQAAREKRTFVLAVWG 388
QY 382 VFVYCWPEFFTYTLAV---GCSVPRTLFKFFWFYGCNSLNPVITYITFNHDFRAK 438
Db 389 VFVLCWPEFFIYSLVIGICREACQVGPFLKFFFWIGYCNSINPLVYTFVNDFRASER 448
QY 439 KILCRGDRK 447
Db 449 HILFRRRR 457

RESULT 11
US-08-118-270-19
Sequence 19, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-19

```

```

Query Match 44.08; Score 1046.5; DB 1; Length 330;
Best Local Similarity 50.78; Pred. No. 4e-53; Indels 117; Gaps 9;
Matches 216; Conservative 38; Mismatches 55;
QY 36 LVCLAGILMLTFGNVNIIVAFVTSRALKAPQNLFTVSLASADILVATVIPSILANEV 95
Db 4 LAAVGFLLIVTYGNVLVAVLTSRLAPQNLFTVSIASADILVATVIMPSILANEI 63
QY 96 MGYWFGAMCEIYALDVFCTSSIVHLCASIDRWSTVQAAYEYNLKRPRKATII 155
Db 64 M-YWYFGWGVYLAIDVFCTSSIVHLCASIDRWSTVQAAYEYNLKRPRKATIV 122
QY 156 TWVTSAVISPPPLISIEKKGQGPAPERCEINDQKWTYVSSICISFFAPCLIMLV 215
Db 123 AVLILSAVISPPPLVSLRQPDGA---AYPOCGINDETWYIISCIQSFAPCLIVLY 178
QY 216 YVRIYQAKRTRVPPSRGPDAAVAPPGGTERPNSGIPERSAGPGAEAPLEPTQNG 275
Db 179 YVRIYAKRTRTLSEKRAP-----VGPDGAS---PTTENG 212
QY 276 APGEAPAPRQDOTALDLEESSSDHAERPPGPRRPERGPGKAKARASQVKPQDSLPRR 335
Db 213 L----- 213
QY 336 GPGATGIGTPAGPGEERYGAK--ASRWGR-----QNRERKFTFVLAVVIGVF 384
Db 214 -----GAAGGARFTGTAAPR-----VFW 260
QY 385 VCFWPEFFTYTLAV---GCSVPRTLFKFFWFYGCNSLNPVITYITFNHDFRAK 441
Db 261 LCFWPEFFIYSLVIGICREACQVGPFLKFFFWIGYCNSLNPVITYTFVNDFRSEFK 320
QY 442 CRGDRK 447
Db 321 FRRRRR 326

RESULT 12
PCT-US93-08528-19
Sequence 19, Application PC/US9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:

```

Db 361 XXXXXXXXREKRTFVLAVIGVFWCWFPEFTYTLTAAGCSVPRTLKFEFFWFGYCNSS 420
QY 421 LNPVIYITFNHDFRRAFKILC 442
Db 421 LNPVIYITFNHDFRRAFKILC 442

RESULT 9

US-08-760-936-11
; Sequence 11, Application US/08760936
; Patent No. 5856443
; GENERAL INFORMATION:
; APPLICANT: MacLennan, A. John
; TITLE OF INVENTION: Molecular Cloning and Expression of
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,936
; FILING DATE: December 6, 1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Doran R.
; REGISTRATION NUMBER: 38,261
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 450 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; US-08-760-936-11

Query Match 61.5%; Score 1465; DB 2; Length 450;
Best Local Similarity 68.6%; Pred. No. 6.9e-77;

Matches 303; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY 1 MSLDPDAGNANMNGTEAPGGARATPYSLOYTLTVCLAGLMLTVFGNVLTIAVFT 60
Db 1 MSLDPDAGNANMNGTEAPGGARATPYSLOYTLTVCLAGLMLTVFGNVLTIAVFT 60
QY 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEVNGWYFGKACETIYLDVLEFSS 120
Db 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEVNGWYFGKACETIYLDVLEFSS 120
QY 121 IYHLCAISLDKRWYSITQATEYLNKRTPRRIKAIITVWVISAVISFPLISIEKKGGGG 180
Db 121 IYHLCAISLDKRWYSITQATEYLNKRTPRRIKAIITVWVISAVISFPLISIEKKGGGG 180
QY 181 PQAPRCEINDQKMYVSSCIGSFAPCLIMLVYVRIYQIARRRTPVPSRKGPDAVA 240
Db 181 PQAPRCEINDQKMYVSSCIGSFAPCLIMLVYVRIYQIARRRTPVPSRKGPDAVA 240
QY 241 APGCTERRPNGLPERSAGPGGAEPPLPTQLNGAPGEPAPAGPRDTDALDLSESSSD 300
Db 241 APGCTERRPNGLPERSAGPGGAEPPLPTQLNGAPGEPAPAGPRDTDALDLSESSSD 300
QY 301 HAERPGRPRERGRGKARASQVVKRGDSLPRRGATGATGTPAAGGGEERVGAAKAS 360

Db 301 XXX 360
QY 361 RWRGRONREKRTFVLAVIGVFWCWFPEFTYTLTAAGCSVPRTLKFEFFWFGYCNSS 420
Db 361 RWRGRONREKRTFVLAVIGVFWCWFPEFTYTLTAAGCSVPRTLKFEFFWFGYCNSS 420
QY 421 LNPVIYITFNHDFRRAFKILC 442
Db 421 LNPVIYITFNHDFRRAFKILC 442

RESULT 10

US-08-194-338-4
; Sequence 4, Application US/08194338
; Patent No. 5474898
; GENERAL INFORMATION:
; APPLICANT: Venter, John C.
; APPLICANT: Fraser, Claire M.
; APPLICANT: McCombie, William R.
; TITLE OF INVENTION: OCTOPAMINE RECEPTOR
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,338
; FILING DATE: 08-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,174
; FILING DATE: 28-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 461 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-194-338-4

Query Match 48.2%; Score 1146.5; DB 1; Length 461;
Best Local Similarity 50.9%; Pred. No. 1e-58;

Matches 249; Conservative 41; Mismatches 98; Indels 101; Gaps 12;

QY 10 NASWNGTEAPGGARAT-----PYSLOYTLTVCLAGLMLTVFGNVLTIAVFT 60
Db 19 NAAGAGRGSGGVAANMNSGASWGPGRGYSAGAAAGLAAYGFLIVTVGNLVYIAVLT 78
QY 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEVNGWYFGKACETIYLDVLEFSS 120
Db 79 SRALKAPQNLFLVSLASADILVATLVIPFSLANELMAYVFGQVWCGVLTALDVLEFSS 138
QY 121 IYHLCAISLDKRWYSITQATEYLNKRTPRRIKAIITVWVISAVISFPLISIEKKGGGG 180

PCT-US93-08528-22
; Sequence 22, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08528
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US93-08528-22

Query Match 64.2%; Score 1529; DB 5; Length 334;
Best Local Similarity 71.8%; Pred. No. 1.2e-80;
Matches 301; Conservative 10; Mismatches 22; Indels 86; Gaps 3;

DB 33 TTTTCLAGLMLTLTFGNVLTITAVTSRALKAPQNLFLVSLASADILVATLVIPLPSLA 92
1 TTTTCLAGLMLTLTFGNVLTITAVTSRALKAPQNLFLVSLASADILVATLVIPLPSLA 60
QY 93 NEVGIWTFGKAMCEIYIALDVLFTCTSSIVHLCALISLDRWSTIQALIEYNLKRTPRIKA 152
DB 61 NEVM-YWYFGKWCETIYIALDVLFTCTSSIVHLCALISLDRWSTIQALIEYNLKRTPRIKA 119
QY 120 IIVTAVWISAVISFPPLISTEKKAGGCGQPAERSCKINQKMWISSISGSFAPCLI 179
DB 120 IIVTAVWISAVISFPPLISTEKKAGGCGQPAERSCKINQKMWISSISGSFAPCLI 179
QY 212 MLVYVRIYQIAKRRTRVPPSRGPDAAVAPPGTERRPGLGPERSGPGGAEBPLPT 271
DB 180 NMLVYVRIYQIAKRRTRVPPSRGPDAAVAPPGTERRPGLGPERSGPGGAEBPLPT 231
QY 272 QUNGAPGEPAAPGPRDTDLALDESSSSDHAERPPRPERGPGKKGKARASQVKKPDS 331
DB 232 ----- 231
QY 332 LPRRGATIGTTPAAGPEEERVGAAKASRMGRONREKRTFVLAVYIGVFVVCWPFEE 391
DB 232 -----GQSEERAGGAKASRMGRONREKRTFVLAVYIGVFVVCWPFEE 275
QY 392 FTYTTLAVGCSVPRLTFKFFWFGYCNSSLNVIYTIINHDRAKFKILCGDGKRRIV 450
DB 276 FTYTTLAVGCSVPYOLFNFEEFGYCNSSLNVIYTIINHDRAKFKILCGDGKRRIV 334

RESULT 8
US-08-196-989B-11
; Sequence 11, Application US/08196989B
; Patent No. 5585476
; GENERAL INFORMATION:
; APPLICANT: MacLennan, A. John
; TITLE OF INVENTION: Molecular Cloning and Expression of
; TITLE OF INVENTION: G-Protein Coupled Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanichik & Saliwanichik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/196,989B
; FILING DATE: 15-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lloyd, Jeff
; REGISTRATION NUMBER: 35,589
; REFERENCE/DOCKET NUMBER: MAC-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 450 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; US-08-196-989B-11

Query Match 61.5%; Score 1465; DB 1; Length 450;
Best Local Similarity 68.6%; Pred. No. 6.9e-77;
Matches 303; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY 1 MGSIQPAGNANWNGTAPGGAATPYSLQVTLTVCLAGLMLTLTFGNVLTITAVPT 60
DB 1 MGSIQPAGNANWNGTAPGGAATPYSLQVTLTVCLAGLMLTLTFGNVLTITAVPT 60
QY 61 SRALKAPQNLFLVSLASADILVATLVIPLPSLANEVGMYWFGKAMCEIYIALDVLFTCTSS 120
DB 61 SRALKAPQNLFLVSLASADILVATLVIPLPSLANEVGMYWFGKAMCEIYIALDVLFTCTSS 120
QY 121 IVHLCALISLDRWSTIQALIEYNLKRTPRIKAITIYVWISAVISFPPLISTEKKGGGG 180
DB 121 IVHLCALISLDRWSTIQALIEYNLKRTPRIKAITIYVWISAVISFPPLISTEKKGGGG 180
QY 181 POPAEPCEINDQKMWYISSISGSFAPCLIMILYVRIYQIAKRRTRVPPSRGPDAAVA 240
DB 181 POPAEPCEINDQKMWYISSISGSFAPCLIMILYVRIYQIAKRRTRVPPSRGPDAAVA 240
QY 241 APPGTERPRLGLPERSAGPGGAEBPLPTQUNGAPGEPAAPGPRDTDLALDESSSSD 300
DB 241 XXX 300
QY 301 HAEPGPGRPERPGRGKARASQVPGDSLPRGGAIGTTPAAGPEEERVGAAKAS 360
DB 301 XXX 360
QY 361 RWRGRONREKRTFVLAVYIGVFVVCWPFEEFTYTLAVGCSVPRLTFKFFWFGYCNSS 420
DB 361 RWRGRONREKRTFVLAVYIGVFVVCWPFEEFTYTLAVGCSVPRLTFKFFWFGYCNSS 420

```

: ADDRESSEE: BROWDY AND NEIMARK
: STREET: 419 Seventh Street, N.W., Suite 300
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/08528
: FILING DATE: 09-SEP-1993
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 07/943,236
: FILING DATE: 10-SEP-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Townsend, Kevin G.
: REGISTRATION NUMBER: 34,033
: REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-737-3528
: TELEX: 248633
: INFORMATION FOR SEQ ID NO: 21:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 330 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: PCT-US93-08528-21

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Query Match          64.8%; Score 1543; DB 5; Length 330;
Best Local Similarity 74.4%; Pred. No. 1.9e-81;
Matches 311; Conservative 7; Mismatches 12; Indels 88; Gaps 6;

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QY 33 TLTLVCLAGLMLTLVFGNVLVIAVFTSRALKAPQNLFLVSLASADILVATLVIPESLA 92
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1 TLTLVCLAGLMLTLVFGNVLVIAVFTSRALKAPQNLFLVSLASADILVATLVIPESLA 58
QY 93 NEVMGTYWEGKAMCEIYALDVLFCTSSIVHLCALISLDRYWSITQALEYNLKRTPRRIKA 152
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 59 NEVMGTYWEGKAMCEIYALDVLFCTSSIVHLCALISLDRYWSITQALEYNLKRTPRRIKA 117
QY 153 IITVWVIAVISPPLISIEKGGGQPPAPRCEIINDOKWYVSSCISFFAPCLIM 212
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 118 IITVWVIAVISPPLISIEKGGGQPPAPRCEIINDOKWYVSSCISFFAPCLIM 177
QY 213 ILVYVRIYQIAKRRTRVPSRRGPDVAAPPGTERRNGLGERSAGPGGAEAEPPLPTQ 272
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 178 ILVYVRIYQIAKRRTRVPSRRGPDVAAPPGTERRNGLGERSAGPGGAEAEPPLPTQ 227
QY 273 LNGAGEPAPAGPRDTALDLESSSSDHARPPGPRRPERGPGKAKARASQVKPGDSL 332
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 228 L-----GGRS-----ASGL 236
QY 333 PRRGATGIGTPAAGGEEERVGAAKASRMGRGKRNREKRTFVLAVYIGVFVWCWMPFF 392
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 237 PRRRAGA-----GGGNREKRTFVLAVYIGVFVWCWMPFF 272
QY 393 TYTLTAVGCSVPRTLKFFKFFWFGYCNSSLNPNVITTFNHDPRAAFKKILCRGDKRRI 450
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 273 TYTLTAVGCSVPRTLKFFKFFWFGYCNSSLNPNVITTFNHDPRAAFKKILCRGDKRRI 330

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RESULT 6
US-08-118-270-22
: Sequence 22, Application US/08118270
: Patent No. 5508384
: GENERAL INFORMATION:
: APPLICANT: Murphy, Randall B.

```

```

: APPLICANT: Schuster, David I.
: TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
: TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
: NUMBER OF SEQUENCES: 348
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROWDY AND NEIMARK
: STREET: 419 Seventh Street, N.W., Suite 300
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/118,270
: FILING DATE: 09-SEP-1993
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 07/943,236
: FILING DATE: 10-SEP-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Townsend, Kevin G.
: REGISTRATION NUMBER: 34,033
: REFERENCE/DOCKET NUMBER: MURPHY-2A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-737-3528
: TELEX: 248633
: INFORMATION FOR SEQ ID NO: 22:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 334 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-118-270-22

```

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Query Match          64.2%; Score 1529; DB 1; Length 334;
Best Local Similarity 71.8%; Pred. No. 1.2e-80;
Matches 301; Conservative 10; Mismatches 22; Indels 86; Gaps 3;

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QY 33 TLTLVCLAGLMLTLVFGNVLVIAVFTSRALKAPQNLFLVSLASADILVATLVIPESLA 92
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Db 1 TLTLVCLAGLMLTLVFGNVLVIAVFTSRALKAPQNLFLVSLASADILVATLVIPESLA 60
QY 93 NEVMGTYWEGKAMCEIYALDVLFCTSSIVHLCALISLDRYWSITQALEYNLKRTPRRIKA 152
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 61 NEVMGTYWEGKAMCEIYALDVLFCTSSIVHLCALISLDRYWSITQALEYNLKRTPRRIKA 119
QY 153 IITVWVIAVISPPLISIEKGGGQPPAPRCEIINDOKWYVSSCISFFAPCLIM 211
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 120 IITVWVIAVISPPLISIEKGGGQPPAPRCEIINDOKWYVSSCISFFAPCLIM 179
QY 212 ILVYVRIYQIAKRRTRVPSRRGPDVAAPPGTERRNGLGERSAGPGGAEAEPPLPT 271
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 180 ILVYVRIYQIAKRRTRVPSRRGPDVAAPPGTERRNGLGERSAGPGGAEAEPPLPT 231
QY 272 QLNGAGEPAPAGPRDTALDLESSSSDHARPPGPRRPERGPGKAKARASQVKPGDSL 331
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 232 L-----GGRS-----ASGL 231
QY 332 LPRRGATGIGTPAAGGEEERVGAAKASRMGRGKRNREKRTFVLAVYIGVFVWCWMPFF 391
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 232 L-----GGRS-----ASGL 275
QY 392 TYTLTAVGCSVPRTLKFFKFFWFGYCNSSLNPNVITTFNHDPRAAFKKILCRGDKRRI 450
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 276 TYTLTAVGCSVPRTLKFFKFFWFGYCNSSLNPNVITTFNHDPRAAFKKILCRGDKRRI 334

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RESULT 7

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,971B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33073
; REFERENCE/DOCKET NUMBER: 325800-453 (PFI187)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; US-08-465-971B-4

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Query Match          69.9%; Score 1665; DB 2; Length 358;
Best Local Similarity 74.0%; Pred. No. 2,2e-88;
Matches 339; Conservative 4; Mismatches 7; Indels 108; Gaps 7;

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QY 1 MGSLQPDAGNANMNGTEAPGAGATPYSLQVTLTLVCLAGLMLLTFGNVLVIAVPT 60
D 1 MGSLQPDAGNANMNGTEAPGAGATPYSLQVTLTLVCLAGLMLLTFGNVLVIAVPT 60
QY 61 SRAIKAPQNTFLV-SLASADILVA--TLVPEISLANEYKGYWFGKAMCEIYALDVLFC 117
D 61 SRAIKAPQNTFLV-SLASADILVA--TLVPEISLANEYKGYWFGKAMCEIYALDVLFC 120
QY 118 TTSIVHCAISLDKRYMSITQAIENLNKRTPRRIKAIITVWVISAVISFPLISIEKKG- 176
D 121 TTSIVHCAISLDKRYMSITQAIENLNKRTPRRIKAIITVWVISAVISFPLISIEKKG 180
QY 177 -GGGGPQPAERCEINDQKMYVSSCTGSEFPACLMILVYVRIYQAKRTVPSPSRG 235
D 181 XGGGGPQPAERCEINDQKMYVSSCTGSEFPACLMILVYVRIYQAKRTVPSPSRG 240
QY 236 PDVAAPPGGTERPENGIGPERSAGPGAEAPLPTQLNGAPGEPAPGPRDIALDLEE 295
D 241 PDVAAPPGGLQ----- 252
QY 296 SSSSDHAERPPRRPBERGPRGKAKARASQVKKPEDSLPRRGPGATGIGTPAAGBERVG 355
D 253 -----GGRGS-----ASGLPRRRAGA----- 268
QY 356 AAKASRMGRGRRERKREFVLAVYGVVQWPEFFTYTLTAAVGSVPRTLKFEFFWFG 415
D 269 -----GGONRKRREFVLAVYGVVQWPEFFTYTLTAAVGSVPRTLKFEFFWFG 320
QY 416 YCNSSLNPIVYITIFNHFRRAFKKI--LCGDRKKRIY 450
D 321 YCNSSLNPIVYITIFNHFRRAFKKIXXLXLCGRDKRIY 358

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RESULT 4
US-08-118-270-21
; Sequence 21, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington

```

```

; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 330 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-118-270-21

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Query Match          64.8%; Score 1543; DB 1; Length 330;
Best Local Similarity 74.4%; Pred. No. 1.9e-81;
Matches 311; Conservative 7; Mismatches 12; Indels 88; Gaps 6;

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QY 33 TLTIVCLAGLMLLVFGNVLTIVFTSRAIKAPQNTFLVISASADILVATVIPSLSA 92
D 1 TLTIVCLAGLMLLVFGNVLTIVFTSRAIKAPQNTFLVISASADILVATVIPSLSA 58
QY 93 NEVMGYWYKAMCEIYALDVLFCSTSVHLCALISLDKRYMSITQAIENLNKRTPRRIKA 152
D 59 NEVMGYWYKAMCEIYALDVLFCSTSVHLCALISLDKRYMSITQAIENLNKRTPRRIKA 117
QY 153 IITVWVISAVISFPLISIEKKGQGGGQPAERCEINDQKMYVSSCTGSEFPACLM 212
D 118 IITVWVISAVISFPLISIEKKGQGGGQPAERCEINDQKMYVSSCTGSEFPACLM 177
QY 213 IIVYVRIYQAKRTVPSPSRGPDVAAPPGGTERPENGIGPERSAGPGAEAPLPTQ 272
D 178 -LVYVRIYQAKRTVPSPSRGPDVAAPPGGTERPENGIGPERSAGPG----- 227
QY 273 LMGAPGEPAPGPRDIALDLESSSDHAERPPRRPBERGPRGKAKARASQVKKPEDSL 332
D 228 -----GGRGS-----ASGL 236
QY 333 PRRGPGATGIGTPAAGBERVGAAKASRMGRGRRERKREFVLAVYGVVQWPEFF 392
D 237 PRRRAGA-----GGONRKRREFVLAVYGVVQWPEFF 272
QY 393 TYTLTAAVGSVPRTLKFEFFWFGYCNSSLNPIVYITIFNHFRRAFKKILCRDRIY 450
D 273 TYTLTAAVGSVPRTLKFEFFWFGYCNSSLNPIVYITIFNHFRRAFKKILCRDRIY 330

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RESULT 5
PCT-US93-08528-21
; Sequence 21, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:

```

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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Internal
US-08-444-734A-8

Query Match          92.9%; Score 2211; DB 1; Length 450;
Best Local Similarity 93.8%; Pred. No. 1.9e-119;
Matches 422; Conservative 2; Mismatches 26; Indels 0; Gaps 0;

OY 1 MSLOPDAGASWNGTEAPGGARATPYSLOVTLTVCLAGLMLTVFGNVLVIAVFTS 60
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DB 1 MSLOPDAGASWNGTEAPGGARATPYSLOVTLTVCLAGLMLTVFGNVLVIAVFTS 60
OY 61 SRALKAPONLFLVSLASADILVATLVIPFSLANVWGYYFGKACEIYALDVLFC 120
   |||||||
DB 61 SRALKAPONLFLVSLASADILVATLVIPFSLANVWGYYFGKACEIYALDVLFC 120
OY 121 IYHLCASISDRWYSTQAIENLKRTPRIKAIITVWISAVISPPPLISIEKKG 180
   |||||||
DB 121 IYHLCASISDRWYSTQAIENLKRTPRIKAIITVWISAVISPPPLISIEKKG 180
OY 181 POPAEPRCEINDOKWYVISCISGFFAPCLIMILVYVRITYOLAKRTRVPSR 240
   |||||||
DB 181 POPAEPRCEINDOKWYVISCISGFFAPCLIMILVYVRITYOLAKRTRVPSR 240
OY 241 APPGCTERRPNCGLPERSAGPGAEAPLPTQNGAPGEPAPAGPRDLDLESS 300
   |||||||
DB 241 APPGCTERRPNCGLPERSAGPGAEAPLPTQNGAPGEPAPAGPRDLDLESS 300
OY 301 HAERPPGRRPGRPGKAKARASOVKPEDSLPRRGPATGIGTAAAGGEERVA 360
   |||||||
DB 301 HAERPPGRRPGRPGKAKARASOVKPEDSLPRRGPATGIGTAAAGGEERVA 360
OY 361 RHRGONRKRRTFYLAIVIGVVCWPEFFETTLTAAGSVPRTLKFFWEGY 420
   |||||||
DB 361 RHRGONRKRRTFYLAIVIGVVCWPEFFETTLTAAGSVPRTLKFFWEGY 420
OY 421 LNPVITTFNHDFRRAFKKILCRGDRKRIV 450
   |||||||
DB 421 LNPVITTFNHDFRRAFKKILCRGDRKRIV 450

RESULT 2
US-08-194-338-5
; Sequence 5, Application US/08194338
; Patent No. 5474898
; GENERAL INFORMATION:
; APPLICANT: Venter, John C.
; APPLICANT: Fraser, Claire M.
; APPLICANT: McComb, William R.
; TITLE OF INVENTION: OCTOPAMINE RECEPTOR
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,338
; FILING DATE: 08-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,174
; FILING DATE: 28-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned A.
```

```
;
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH101.001DV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 450 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Internal
US-08-194-338-5

Query Match          91.1%; Score 2170; DB 1; Length 450;
Best Local Similarity 92.9%; Pred. No. 4.1e-117;
Matches 416; Conservative 3; Mismatches 29; Indels 0; Gaps 0;

OY 3 SLOPDAGASWNGTEAPGGARATPYSLOVTLTVCLAGLMLTVFGNVLVIAVFTS 62
   |||||||
DB 3 SLOPDAGASWNGTEAPGGARATPYSLOVTLTVCLAGLMLTVFGNVLVIAVFTS 62
OY 63 ALKAPONLFLVSLASADILVATLVIPFSLANVWGYYFGKACEIYALDVLFC 122
   |||||||
DB 63 ALKAPONLFLVSLASADILVATLVIPFSLANVWGYYFGKACEIYALDVLFC 122
OY 123 HLCAISDRWYSTQAIENLKRTPRIKAIITVWISAVISPPPLISIEKKG 182
   |||||||
DB 123 HLCAISDRWYSTQAIENLKRTPRIKAIITVWISAVISPPPLISIEKKG 182
OY 183 PAERCEINDOKWYVISCISGFFAPCLIMILVYVRITYOLAKRTRVPSR 242
   |||||||
DB 183 PAERCEINDOKWYVISCISGFFAPCLIMILVYVRITYOLAKRTRVPSR 242
OY 243 PGCTERRPNCGLPERSAGPGAEAPLPTQNGAPGEPAPAGPRDLDLESS 302
   |||||||
DB 243 PGCTERRPNCGLPERSAGPGAEAPLPTQNGAPGEPAPAGPRDLDLESS 302
OY 303 ERPPGRRPGRPGKAKARASOVKPEDSLPRRGPATGIGTAAAGGEERVA 362
   |||||||
DB 303 ERPPGRRPGRPGKAKARASOVKPEDSLPRRGPATGIGTAAAGGEERVA 362
OY 363 RHRGONRKRRTFYLAIVIGVVCWPEFFETTLTAAGSVPRTLKFFWEGY 422
   |||||||
DB 363 RHRGONRKRRTFYLAIVIGVVCWPEFFETTLTAAGSVPRTLKFFWEGY 422
OY 423 PVITTFNHDFRRAFKKILCRGDRKRIV 450
   |||||||
DB 423 PVITTFNHDFRRAFKKILCRGDRKRIV 450

RESULT 3
US-08-465-971B-4
; Sequence 4, Application US/08465971B
; Patent No. 5942414
; GENERAL INFORMATION:
; APPLICANT: Yi Li and Mark D. Adams
; TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cecchi, Byrne, Bain, Gillfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: US
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 12:02:49 ; Search time 15.5 Seconds
(without alignments)
854,214 Million cell updates/sec

Title: US-09-636-259b-3

Perfect score: 2381

Sequence: 1 MGSLQPDAGNAGNMGTEAPG.....HFRRAFKKILCRGDRKRV 450

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCRV.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2211	92.9	450	1	US-08-444-734A-8
2	2170	91.1	450	1	US-08-194-338-5
3	1665	69.9	358	2	US-08-465-971B-4
4	1543	64.8	330	1	US-08-118-270-21
5	1543	64.8	330	5	PCT-US93-08528-21
6	1529	64.2	334	1	US-08-118-270-22
7	1529	64.2	334	5	PCT-US93-08528-22
8	1465	61.5	450	1	US-08-196-989B-11
9	1465	61.5	450	2	US-08-760-936-11
10	1146.5	48.2	450	1	US-08-194-338-4
11	1046.5	44.0	330	1	US-08-118-270-19
12	1046.5	44.0	330	5	PCT-US93-08528-19
13	1029	43.2	330	1	US-08-118-270-20
14	1029	43.2	330	5	PCT-US93-08528-20
15	648	27.2	601	1	US-07-676-174A-2
16	624.5	26.2	443	1	US-07-626-618A-18
17	624.5	26.2	443	1	US-08-333-977-18
18	619.5	26.0	415	1	US-08-194-338-10
19	618	26.0	444	1	US-07-626-618A-19
20	618	26.0	444	1	US-08-333-977-19
21	616	25.9	444	1	US-07-817-920A-1
22	594	24.9	422	1	US-07-817-920-3
23	594	24.9	422	1	US-08-370-542-3
24	594	24.9	422	1	US-08-117-006-3
25	594	24.9	422	1	US-08-216-594-3
26	594	24.9	422	1	US-08-542-358-3
27	594	24.9	422	2	US-08-157-185-13

28	594	24.9	422	3	US-08-281-526B-13	Sequence 13, Appl
29	594	24.9	422	3	US-09-018-351-3	Sequence 3, Appl1
30	594	24.9	422	4	US-09-332-837-13	Sequence 13, Appl
31	594	24.9	422	5	PCT-US93-00149-3	Sequence 3, Appl1
32	591.5	24.8	443	1	US-08-444-734A-3	Sequence 2, Appl1
33	585.5	24.6	377	2	US-08-461-812-2	Sequence 14, Appl
34	585.5	24.6	377	2	US-08-157-185-14	Sequence 14, Appl
35	585.5	24.6	377	2	US-08-281-526B-14	Sequence 14, Appl
36	585.5	24.6	377	4	US-09-450-790A-14	Sequence 14, Appl
37	585.5	24.6	377	4	US-09-332-837-14	Sequence 14, Appl
38	585	24.6	375	1	US-08-370-542-5	Sequence 5, Appl1
39	585	24.6	375	1	US-08-542-358-5	Sequence 5, Appl1
40	585	24.6	375	3	US-09-018-351-5	Sequence 5, Appl1
41	585	24.6	376	1	US-07-817-920-5	Sequence 5, Appl1
42	585	24.6	376	1	US-08-117-006-5	Sequence 5, Appl1
43	585	24.6	376	1	US-08-216-594-5	Sequence 5, Appl1
44	585	24.6	376	5	PCT-US93-00149-5	Sequence 5, Appl1
45	582	24.4	467	1	US-08-056-051-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-08-444-734A-8
; Sequence 8, Application US/08444734A
; Patent No. 5610282
; GENERAL INFORMATION:
; APPLICANT: Sibley, David R.
; APPLICANT: Monsma, Frederick J.
; APPLICANT: Mahan, Lawrence C.
; APPLICANT: McVittie, Loris D.
; TITLE OF INVENTION: CDNA encoding the rat D1 dopamine
; TITLE OF INVENTION: receptor linked to adenylyl cyclase activation and
; TITLE OF INVENTION: expression of the receptor protein in plasmid-transfected
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,734A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/029,917
; FILING DATE: 03-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/548,714
; FILING DATE: 06-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: NIH065.001FW1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 760-0404
; TELEFAX: (714) 760-9502
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 450 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

CC vascular contraction of coronary arteries which is clinically expressed
CC as coronary heart disease (CHD). unstable chronic angina pectoris which is
CC clinically expressed as Prinzmetal's variant form or acute myocardial
CC infarction (AMI). Alpha2B-AR gene is used in gene therapy.

XX
SQ Sequence 447 AA;

Query Match 47.2%; Score 1124; DB 22; Length 447;
Best local similarity 53.2%; Pred. No. 1.1e-77;
Matches 243; Conservative 49; Mismatches 103; Indels 62; Gaps 14;

QY 27 PYSLOVTLVLCVGLMLLVGVNVLIAVTSRAKAPONLFLVSLASADILVATLV 86
DB 6 PYSVQATAIAIAITFLIFTFIGNALVTLAVTSRLRAPONLFLVSLAADIIVATLI 65
QY 87 IPFSLANEVWGYYFGKAMCEIYLDVLFCTSSIVHLCALSLDRYWSITQAIENLKRT 146
DB 66 IPFSLANEILGTYFRFRWCEVYLDVLFCTSSIVHLCALSLDRYWAVSRALRYNSKRT 125
QY 147 PRRIAIITVWISAVISFPPLISIEKKGGGQGP-AEPRCIENDQKWYVSSCIGSF 205
DB 126 PRRIKIIITVWLIASVLSPLI-YKDGQGPQPRGPOCKLQEAWYILASSIGSF 181
QY 206 FAPCLIMILVYRITQIAKRTRVPPSRGPDVAAPPGTERPGLGPERSAQPGGAE 265
DB 182 FAPCLIMILVYRILYLIAR---SNRRGPRAKGPGQGESKQPR--PDHGALASAK 233
QY 266 AEPLPT-----QLNG--APGEPAPA-GPRDLDLDEES-----SS 298
DB 234 LPALASVASAREVNGHSKSTGEKEGETPEDTGRALPPSWMALPNSGQGEVCGASP 293
QY 299 SDHAERPPGPRRPERGPRGKARASQVKGPD--SLPRRPG---ATGIGTPAAGPE 351
DB 294 EDEAE-----EEEEEECEPQAVPVPASACSPLOQPGSRVLA TLRGVILGRG- 345
QY 352 ERVGA KASRMGRQ--NREKRTFVLAVYGVVYVCFEPFFETTLAV--GCSVPRT 406
DB 346 --VGAIGGOMRRRRQQLTRERKRTFVLAVYGVVLCWFEPFFESYSLGALCPKHCKVPHG 403
QY 407 LKFFFWFGYCNSSLNPVYITIFNHFERRAKKILCR 443
DB 404 LFOFFFWIGYCNSSLNPVYITIFNODFRRAFRIILCR 440

Search completed: February 15, 2003, 18:04:23
Job time : 50 secs

PM WO200179561-A2.
XX
PD 25-OCT-2001.
XX
PF 17-APR-2001; 2001WO-US12575.
XX
PR 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
XX
PA (LIGGETT S B.
PA (SMALL) SMALL K M.
XX
XX
PI Liggett SB, Small KM;
XX
DR WPI; 2001-611728/70.
DR N-PSDB; AA199906.
XX
XX
PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
PS Claim 20; Page 147-149; 163pp; English.

The invention relates to genotyping an alpha-2b, 2a, or 2c adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising:
 (a) obtaining a sample having a polynucleotide encoding an alpha-2b, alpha2 or alpha2c or fragment or complement of; and
 (b) detecting a polymorphic site comprising nucleotide positions 901-909 of (I), a site comprising cytosine or guanine at position 753 of (II) or a site comprising (a) (999gcggggccgc) or (b) (999gcggctgac) at positions 961-972 of (III). The method may be used for genotyping an alpha2b, alpha2a or alpha2c receptor gene and further used to determine whether an individual is at increased risk of developing a disease associated with alpha2b, alpha2a or alpha2, comprising detecting a polymorphic site which correlate to disease selected from cardiovascular disease, central nervous system disease and combinations of these. In addition, the technique may be used to predict an individual's response to an alpha2b, alpha2a, or alpha2c agonist (e.g. epinephrine, norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, rauwolfosine, idazoxan, tolazoline, phenolamine and combinations of these) by detecting the polymorphic site and correlating the site to a predetermined response (where the response is correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol phosphate levels). The present sequence is that of the third intracellular loop of the human alpha-2BAR variant protein, the sequence is deleted for the 3 amino acid polymorphic site at residues 301-303 (EEE) of the wildtype protein (AAW52117).

Query Match	47.28;	Score 1124;	DB 22;	Length 447;
Best Local Similarity	53.28;	Pred. No. 1.1e-77;		
Matches 243; Conservative	49;	Mismatches 103;	Indels 62;	Gaps 14;

[illegible]

```

QY 266 AEPLEPT-----QLNG--APCEPAPA-GPRTDALLDEE-----SS 298
      :      :      :      :      :      :      :      :
Db 234 LPALVASAREVINGHSKSTKEGETPBDTGTALRPPSMAALPNISGOGKEVCASP 293
      :      :      :      :      :      :      :      :
QY 239 SPHARRPPGPRPRENGSPRGKKARSOVKPPD--SLPRGSG-----ATGTPMAAPGE 351
      :      :      :      :      :      :      :      :
Db 294 EEEAEE-----EEEEEECEPQAVPVSAPSACSPLQCPQGSRLVLTIRGOLLRG- 345
      :      :      :      :      :      :      :      :
QY 352 EKVGAAKASRWGRG--NRKREFTVLAVVIGVFWCMPEPFYTYTLAV---GCSVPRT 406
      :      :      :      :      :      :      :      :
Db 346 --VGAIGGQWMMRRRQQLRREKFTVLAVVIGVFWLWCFPEFYSIGALCPKHCKVPHG 403
      :      :      :      :      :      :      :      :
QY 407 LKFFFFWGYCNSLNPVITYITFNHDFRARRKTLICR 443
      :      :      :      :      :      :      :      :
Db 404 LFQFFFWGYCNSLNPVITYITFNDFRARRRILICR 440
      :      :      :      :      :      :      :      :

```

RESULT 15	
AAE00989	
ID	AAE00989 standard; Protein; 447 AA
XX	
AC	
XX	AAE00989;
XX	
DT	04-JUL-2001 (first entry)

Human alpha2B-adrenoceptor (alpha2B-AR) variant protein.

Human; cardiac; gene therapy; alpha2B-adrenoceptor; alpha2B-AR; glutamic acid repeat; intracellular loop; chromosome 2; catecholamine; norepinephrine; epinephrine; therapy; vascular contraction; variant; coronary artery; coronary heart disease; CHD; chronic angina pectoris; acute myocardial infarction; AMI; Prinmetal's variant.

Homo sapiens.

Key Region	Location/Qualifiers 298...306
	/note= "Glutamic acid repeat"

WO200129082-A1.

26-APR-2001.

20-OCT-2000; 2000WO-FI00913.

22-OCT-1999; 99US-0422985.

(JUVA-) JUVANTIA PHARMA LTD OY.

Snäpär A, Heinoöen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U;

Salonen R, Kauphanen J, Valkonen V;
Scheinin M, Salonen O, Tuomimäki J;
Salonen R, Kauphanen J, Valkonen V;

WPI: 2001-300318/31.

N-PSDB; AAD04761.

New DNA molecule encoding variant specific adrenoceptor protein with

loop of the polypeptide, for treating vascular contraction of coronary

at 1237 p

Claim 8; Page 26-27; 37pp; English.

XX The present sequence is human alpha2B-adrenoceptor (alpha2B-AR) variant CC protein. Alpha2B-AR has a glutamic acid repeat element (amino acids CC 298-309) of 12 glutamates, in an acidic stretch of 18 amino acids (amino CC acids 294-311), located in the third intracellular loop of the receptor CC polypeptide. The variant is obtained by deletion of three glutamates from CC the Glu repeat (amino acids 307-309). Alpha2B-AR gene is located on CC chromosome 2. Alpha2-AR mediates many of the physiological effects of the CC catecholamines, norepinephrine and epinephrine. An antagonist of CC alpha2B-adrenoceptor is useful for treating a mammal suffering from CC vascular contraction of coronary arterioles and a disease involving

```

OY 206 FAPCLIMILVYRIYQIAKRRTPPSRRGPDVAAPPGTERRRNGLSPERSAGPGAE 265
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 182 FAPCLIMILVYRIYLIAR-----SNRGPRAKGPGQGESKQPR---PDHGALASAK 233
OY 266 AEPDPT-----QANG---APGEAPR-GRDPTDALDEES-----SS 298
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 234 LPAALASASARVNGSHSKSTGEKEGETPEDGTALPPSMAALPNSGGQKEGVCASP 293
OY 299 SDHAERPPGRRPRERPGKGRASOVKPGD--SLPRGPG-----ATGIGTPAAGGE 351
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 294 EDEAEE-----EEEEEEECERQAVPSPASACSPILQPGSRVLAFLRQVLLGRG- 348
OY 352 ERGAAKASRMGRQ--NREKRTFVLAVVIGFVVCWPFPPFTYTLTAV---GCSVPRT 406
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 349 --VGAIGGQWRRRAQLTRERKRTFVLAVVIGFVLCWPFPPFSYSLGAIQPKCKVPHG 406
OY 407 LKFFPFMGYCNSSLNPVITYTFNHDFRAFKILCR 443
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 407 LKFFPFMGYCNSSLNPVITYTFNHDFRAFKILCR 443

RESULT 13
AAE00990
ID AAE00990 standard; protein; 450 AA.
XX
AC AAE00990;
XX
DT 04-JUL-2001 (first entry)
DE Human alpha2B-adrenoceptor (alpha2B-AR) protein.
XX
KW Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
KW glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
KW norphenephrine; epinephrine; therapy; vascular contraction;
KW coronary artery; coronary heart disease; CHD; chronic angina pectoris;
KW acute myocardial infarction; AMI; Prinzmetal's variant.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 298..309
FT /note="Glutamic acid repeat"
XX
PN WO200129082-A1.
XX
PD 26-APR-2001.
XX
PF 20-OCT-2000; 2000WO-FI00913.
XX
PR 22-OCT-1999; 99US-0422985.
XX
PA (JUVV-) JUVANTIA PHARMA LTD OY.
XX
PI Snajir A, Heinoonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U;
PI Scheinin M, Salonen JT, Tuomala T, Lakka TA, Nyssönen K;
PI Salonen R, Kautanen J, Valkonen V;
XX
DR MPI: 2001-300318/31.
DR N-PSDB: AAD04762.
XX
PT New DNA molecule encoding variant specific adrenoceptor protein with
PT deletion of specific amino acids located in the third intracellular
PT loop of the polypeptide, for treating vascular contraction of coronary
PT arteries -
XX
PS Disclosure: Page 29-31; 37pp; English.
XX
CC The present sequence is human alpha2B-adrenoceptor (alpha2B-AR) protein.
CC Alpha2B-AR has a glutamic acid repeat element (amino acids 298-309) of
CC 12 glutamates, in an acidic stretch of 18 amino acids (amino acids
CC 294-311), located in the third intracellular loop of the receptor
CC polypeptide. Alpha2B-AR gene is located on chromosome 2. Alpha2-AR

```

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CC mediate many of the physiological effects of the catecholamines,
CC norepinephrine and epinephrine. An antagonist of alpha2b-adrenoceptor is
CC useful for treating a mammal suffering from vascular contraction of
CC coronary arteries and a disease involving vascular contraction of
CC coronary arteries which is clinically expressed as coronary heart disease
CC (CHD), unstable chronic angina pectoris which is clinically expressed as
CC Prinzmetal's variant form or acute myocardial infarction (AMI).
CC Alpha2B-AR gene is used in gene therapy.
XX
SQ Sequence 450 AA;
Query Match 47.2%; Score 1124.5; DB 22; Length 450;
Best local similarity 53.2%; Pred. No. 1e-77;
Matches 243; Conservative 49; Mismatches 106; Indels 59; Gaps 14;
OY 27 PYSQVTLTVLCIAGLMLLVFNGVLIIVAFVSRAKAPQNTFLVSLASADILVATLV 86
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 PYSQVQTAIAIAAIFELLFTIFGNALVLAFLTRSLRAPQNLFLVSLAADILVATLI 65
OY 87 IPFSLANEVNGYWGKAMCEIYLAADVLCFSSIVHLCASLDRTYSTQATIEYNLKR 146
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 IPFSLANEVNGYWGKAMCEIYLAADVLCFSSIVHLCASLDRTYSTQATIEYNLKR 125
OY 147 PRRIKAIITVWVISAIVSFPLISIEKKGGGQGPQ-APRCETINDQKMYVISGSGSF 205
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 126 PRRIKAIITVWVISAIVSFPLISIEKKGGGQGPQ-APRCETINDQKMYVISGSGSF 181
OY 206 FAPCLIMILVYRIYQIAKRRTPPSRRGPDVAAPPGTERRRNGLSPERSAGPGAE 265
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 182 FAPCLIMILVYRIYLIAR-----SNRGPRAKGPGQGESKQPR---PDHGALASAK 233
OY 266 AEPDPT-----QANG---APGEAPR-GRDPTDALDEES-----SS 298
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 234 LPAALASASARVNGSHSKSTGEKEGETPEDGTALPPSMAALPNSGGQKEGVCASP 293
OY 299 SDHAERPPGRRPRERPGKGRASOVKPGD--SLPRGPG-----ATGIGTPAAGGE 351
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 294 EDEAEE-----EEEEEEECERQAVPSPASACSPILQPGSRVLAFLRQVLLGRG- 348
OY 352 ERGAAKASRMGRQ--NREKRTFVLAVVIGFVVCWPFPPFTYTLTAV---GCSVPRT 406
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 349 --VGAIGGQWRRRAQLTRERKRTFVLAVVIGFVLCWPFPPFSYSLGAIQPKCKVPHG 406
OY 407 LKFFPFMGYCNSSLNPVITYTFNHDFRAFKILCR 443
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 407 LKFFPFMGYCNSSLNPVITYTFNHDFRAFKILCR 443

RESULT 14
AAM52118
ID AAM52118 standard; protein; 447 AA.
XX
AC AAM52118;
XX
DT 18-FEB-2002 (first entry)
DE Human alpha-2BAR third intracellular loop variant.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2BAR.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 170..193
FT /label= transmembrane_domain
FT Region 307..309
FT /label= polymorphic_site
FT Domain 370..393
FT /label= transmembrane_domain
XX

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CC levels). The present sequence is that of the human alpha-2C_{AR} variant
CC protein, deleted for a 4 amino acid polymorphic site at residues 321-324
CC of the wildtype protein (AAM52124).

SQ Sequence 457 AA;

Query Match	48.48;	Score 1152.5;	DB 22;	Length 457;
Best Local Similarity	51.28;	Pred. No. 7.6e-80;		
Matches 247;	Conservative 39;	Mismatches 105;	Indels 91;	Gaps 8

QY	10	NASNGTEAPPGGARRAT-----PYSLQVLTFTLVCGLMLTLVFGNVLIAVET	60
Db	19	NASGAGEGSGGVANNASASWGPGRQYSAQAVAGLAAYGCLIVETVGVNLVIAVLT	78
QY	61	SRALKAPONLFLVLSIASDILIVATLVLPFSLANVWGVTYFGKMCETIYALDLVLTCTSS	120
Db	79	SRALFAPONLFLVLSIASDILIVATLVMPFSLANELMAVYFGQVCGVYALDLVLTCTSS	138
QY	121	IVHCAISLDKRWYSITQAIENYLNKRTPRRIATIIYVWISAVISFPPLISIEKKGGGG	180
Db	139	IVHCAISLDKRWYSITQAVEYNLKRTPRKRVATIIYVWNLISAVISFPPLISVLRQPDGA	197
QY	181	POPAPRCEINDQKWTYVISCISGFAPCLIMLVYVRIQIYAKRRTVRPPSRGPDVA	240
Db	198	--AYPGGINDETWYIISLCISGFAPCLIMGLVYAIYVAKRRTLTSEKRAP--V	251
QY	241	APPGTEERRPNLIGSERAGGGAAPLPLQUNGAPGEPAPAGPRPTDLDLESSSSD	300
Db	252	GDGASPTTENLG-----AAAG-----EARTGT	275
QY	301	HAERPPGPRRPERGPRGKAKARASQVKPDLSLPRRGATGITGPAPGGEERYGAAKAS	360
Db	276	AAERPPGPRRPRGAPRPGAGPLRRGG---RRRAAEAGAGAGADQGAESGALTAS	331
QY	361	RRRG-----RNRERKFTVLAIVIGVYVCMF	388
Db	332	RRPGGRLSRASSSVSEFLLSRRRASSVCCRKYAQRERKRTFLVAVMGVFLCMF	391
QY	389	PEFFFTLTNAV--GCSVPRTLKFEFFWEGYCNSSLNPVIYTIENHDFRAAFKILLCGD	445
Db	392	PEFFFTSLVIGCREACQVGPPLKFEFFWIGYCNSSLNPVIYTVENDFRPSFKILLFRRR	451
QY	446	RR 447	
Db	452	RR 453	
RESULT 12			
AAM52117			
ID	AAM52117 standard; Protein; 450 AA.		
XX	AAM52117;		
AC			
XX			
DT	18-FEB-2002 (first entry)		
XX			
DE	Human alpha-2BAR third intracellular loop.		
XX			
XX	Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;		
KW	polymorphic site; allelic variant; cardiovascular disease;		
KW	central nervous system disease; adenylyl cyclase; MAP kinase activity;		
KW	phosphorylation; inositol phosphate; alpha-2BAR.		
XX			
OS	Homo sapiens.		
XX			
PH	Key		
FT	Region		
FT	Location/Qualifiers		
FT	167..399		
FT	/note="featured in figure 2"		
FT	170..193		
FT	/label= transmembrane_domain		
FT	301..303		
FT	Region		
FT	/label= polymorphic_site		
FT	/note="Polymorphic site absent in the variant protein		
FT	(AAM52118)."		

[illegible]

XX	N-PSDB; AAI99931.
PX	
PT	Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT	determining whether an individual is at increased risk of developing a
PT	disease associated with the corresponding receptor comprises detecting
PT	a polymorphic site -
PS	Claim 78; Page 158-160; 163pp; English.
XX	
CC	The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC	receptor gene (I)-(III) by detecting a polymorphic site, comprising;
CC	(a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC	alpha2 or alpha2C OR fragment or complement of; and
CC	(b) detecting a polymorphic site comprising nucleotide positions 901-909
CC	of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
CC	or a site comprising (A) (g99gcg99gcc) or (B) (g99gcgtctgg) at
CC	positions 961-972 of (IIIV). The method may be used for genotyping an
CC	alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC	whether an individual is at increased risk of developing a disease
CC	associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC	polymorphic site which correlate to disease selected from cardiovascular
CC	disease, central nervous system disease and combinations of these. In
CC	addition, the technique may be used to predict an individual's response
CC	to an alpha2B, alpha2A, or alpha2C agonist (e.g., epinephrine,
CC	norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC	combinations of these) or antagonist (e.g., yohimbine, prazosin, ARC 239,
CC	rauwolfscine, idoxozan, tolazolin, phenolamine and combinations of
CC	these) by detecting the polymorphic site and correlating the site to a
CC	determined response (where the response is correlated to adenyl
CC	cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC	levels). The present sequence is that of the human alpha-2CAR protein,
CC	the sequence includes a 4 amino acid polymorphic site at residues 321-324
CC	(GAGP), absent in the alpha-2CAR variant protein (AA052126).
SQ	
XX	Sequence 461 AA:
Query Match	48.9%; Score 1164.5; DB 22; Length 461;
Best Local Similarity	51.9%; Pred. No. 9.3e-81;
Matches 252; Conservative	38; Mismatches 101; Indels 95; Gaps 11.
OY	10 NASNNNGTEAPGGGARAT-----PYSLQYTTLTVLVLACGLMLTYFGNVYITANFT 60
DB	19 NASGSGRGSGCGVANNASGASMKPEPKQVSAGAVNACLAVAVFLLFFVWGVAVIAVLVT 78
OY	61 SPALKAPQNLEFLVASADILVATLVTPESLANENMGWYGKAMCEITYALTDLVCTOTS 120
DB	79 SRALRAPQNFELVLSASADILVATLVMPESLANELMAWVGWVCGYIALDLVEICTSS 138
OY	121 IVHCAISLDRYNSITQALEFNLRKPRIKAIIITWWVISAVISPPILSIEKKGGGG 180
DB	139 IVHCAISLDRYNSVTOAVEYNLKRPVRKATVAWVLISAVISFPFLSVLRPDGA- 197
OY	181 POPAPEPCETENDKWVVISCSIGSFAPCLMIITVVYIOIARFRPRRPPSRGDANA 240
DB	198 ---AYPCGLDEMTWTILTSCIGSFAPCLMGLVIARIYIWAARRKRITLSEKRA--V 251
OY	241 APPGGTTRRRNGICGPERSAGPGCAEABPLPQLNGARPGEPAAPGRDIDALESSSD 300
DB	252 GPDCASPTTENGIG---AAAGEART-----GTARPRP-----TWSTRIR 287
OY	301 HAERP-----GPRPRBRGRCGRKARAQVPRGSJLRPRGATGICTPAAGGERERRVA 356
DB	288 AAGRPRGAGAPRLR-RGGRRAAGEG-----GAGGADGGGAGPGAESA 331
OY	357 AKASRMWG-----RONREKRTFFVLAVYIVGV 384
DB	332 LTFASRSRPGRCGLRASASSRVFEFLSRRRRARSSVCRRKYAQRERKRTFFVLAVWGFV 391
OY	385 VCFAPPEFFYYTTLAV---GCSYPTRLKEFFWFBCSYCNSSLINPVYITFNHDFERRAFKITL 441
DB	392 LCWPFEPFYTSLYGICREACQVPGLKFFFWTCYCNSSLINPVYITVFNDPRSPFKITL 451
OY	442 CRGDRK 447

Db	452	FRRRRR	457
			11
			RESULT 11
			AAM52126
			ID AAM52126 standard; Protein; 457 AA.
			XX
			AC AAM52126;
			XX
			DT 18-FEB-2002 (first entry)
			XX
			Human alpha-2CAR variant protein.
			DE
			XX
			Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
			KM polymorphic site; allelic variant; cardiovascular disease;
			KM central nervous system disease; adenyl cyclase; MAP kinase activity;
			KW phosphorylation; inositol phosphate; alpha-2CAR.
			XX
			OS Homo sapiens.
			XX
			Key Location/Qualifiers
			XX
			FT Domain 208..231
			FT /label= transmembrane_domain
			FT 379..402
			FT /label= transmembrane_domain
			XX
			PN WO200179561-A2.
			XX
			PD 25-OCT-2001.
			XX
			PF 17-APR-2001; 2001MO-US12575.
			XX
			PR 17-APR-2000; 2000US-0551744.
			PR 10-AUG-2000; 2000US-0636259.
			PR 19-OCT-2000; 2000US-0692077.
			XX
			PA (LIGG/) LIGGETT S. B.
			PA (SMAL/) SMAL K M.
			XX
			LIGgett SB, Small KM;
			PI
			DR WPI: 2001-611728/70.
			DR NP-PSDB; AAI99933.
			XX
			Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
			PT determining whether an individual is at increased risk of developing a
			PT disease associated with the corresponding receptor comprises detecting
			PT a polymorphic site -
			XX
			PS
			Claim 78; Page 160-162; 163pp: English.
			XX
			The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
			CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
			CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
			CC alpha2A or alpha2C or fragment or complement of; and
			CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
			CC of (I), a site comprising cytosine or guanine at position 753 of (II) or
			CC a site comprising (A) (999gc9ggcgcg) or (B) (999gc9gtgcg) at
			CC positions 961-972 of (III). The method may be used for genotyping an
			CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
			CC whether an individual is at increased risk of developing a disease
			CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
			CC polymorphic site which correlate to disease selected from cardiovascular
			CC disease, central nervous system disease and combinations of these. In
			CC addition, the technique may be used to predict an individual's response
			CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
			CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHR933 and
			CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
			CC rauwolfiasins, idazoxan, tolazoline, phenolamine and combinations of
			CC these) by detecting the polymorphic site and correlating the site to a
			CC predetermined response (where the response is correlated to adenylyl
			CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
			CC cyclease, MAP kinase activity, phosphorylation or inositol phosphate

Qy	361	RWRGRNREKRFVILAVIGVFVCMPEFFTYTLTAVGCSVPRLTKFEEFGICNSS	420
Dd	231	-----REKFEFTVIIVIGMFVCMPEFFETITLAVGCSVPRLTKFEPMPGYCNS	283
Qy	421	LNPVIYTFENHDFRRAFKILCR	443
Dd	284	LNPVIYTLFNHDFRRAFKILCR	306
 RESULT 9 AAR54834 ID AAR54834 standard; Protein: 458 AA. XX AC AAR54834; XX DT 01-FEB-1995 (first entry) XX DE Human derived adrenaline alpha 2cII receptor. XX KW adrenaline receptor; alpha CII; screening; detection; pharmacology; XX OS drugs. XX OS Homo sapiens. FH Key location/qualifiers FH Misc-difference 1 /note= "may or may not be present, but is only FT present if amino acid residues 2-17 are FT present" FT Peptide 2..17 FT /label= N-terminal-peptide FT /note= "may or may not be present" PN JP06121686-A. XX PD 06-MAY-1994. XX PF 12-OCT-1992; 92JP-0272744. PR 12-OCT-1992; 92JP-0272744. XX PA (ASAH) ASAH1 KASEI KOITO KK. XX WPI; 1994-185923/23. DR N-PSDB; AAO64890. XX PT Adrenaline receptor gene encoding alpha 2cII receptor - for PT screening drugs reactive to the alpha 2cII receptor XX PS Claim 1; Page 9-11; 13pp; Japanese. XX CC AAO64890 encodes the amino acid sequence of a polypeptide CC (AAR54834) that constitutes human derived adrenaline alpha 2cII CC receptor. The DNA can be used for the study of the pharmacological CC importance of the gene expression in humans. CC SQ Sequence 458 AA;			
Qy	Query Match 49.4%; Score 1177; DB 15; Length 458; Best local Similarity 52.5%; Pred. No. 1e-81; Matches 253; Conservative 38; Mismatches 101; Indels 90; Gaps 9.		
Dd	19	NAGGAGRGSGGVANMSGASWPPRCQYSAGAVAGIAAAVGGFLVTVGNNLVYIAVL	78
Qy	61	SRAALKAPQNFIPLVSLASADILVATLYIPESIANEVNGWYFGKAWCEIYLADVICTSS	120
Dd	79	SRAALRAQNFELVLSIASADILVATLVMPFELANELMAWYVFGWGCVGLADLVICTSS	138
Qy	121	IYHLCAISLDRIYSTIOALEYNLKRPRIKAIITIYWVISANISPPLISTIEKKGGGGG	180

Db	139	IVHCAISLDRTWSVIAQVEYMLKTRPRKATIVAVWLISAVISFPPLVSLVRQPDGA-	197
Qy	181	POPAEPCEINDKRWYVISCIGSFAPCLIMILVYRIQIYIAKRTRVPPSRGDDAVA	240
Db	198	---AVPCGLNDETWTYLISSCIGSEFPACLLIMGLVYARIVAAKLRTLTSEKRAP--V	251
Qy	241	APPGCTRRRNGVGPERSAGPGCAEAEPILPTQINGAPEPEAPAPRDTDLIDESSSSD	300
Db	252	GPDASPTTENGGAAGAAGEHCHCA-----PPPA-----DVEPDESSA	290
Qy	301	HAERPPRPREPGPKGKARASQYKPGDSLPRRGATGIGTPAAGPEERYGAAKAS	360
Db	291	AAE-----RRRRGALRRG-----GRRRAGAEGGAGGAGGCAAESGALTAS	332
Qy	361	KWRG-----RQNRKRPFTYLAIVGIVGYWCF	388
Db	333	RSPFGRLSNASRSVEFPLSRRRARSSVCRKRYAQRKRTFYLAIVMGVFLCMF	392
Qy	369	PEFTPTYLITAV---GCSVPRTLKPEFMWGYNSSLINPYITIEIHNDFRAFKILCRGD	445
Db	393	PFESYSLYIGICRACQVPEPLPKFFFWIGYCNSSLINPYITIVFQDPRSRFKILRRR	452
Qy	446	RK 447	
Db	453	RR 454	
RESULT 10			
AAMS2124			
ID	AAMS2124	standard; Protein; 461 AA.	
AC	AAMS2124:		
XX			
DT	18-FEB-2002	(first entry)	
XX			
DE	Human alpha-2CAR protein.		
XX			
KW	Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;		
KW	polymorphic site; allelic variant; cardiovascular disease;		
KW	central nervous system disease; adenylyl cyclase; MAP kinase activity;		
KW	phosphorylation; inositol phosphate; alpha-2CAR.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Region	205..409	
FT		/note= "featured in figure 12"	
FT	Domain	208..231	
FT		/label= "transmembrane_domain	
FT	Region	321..324	
FT		/label= "polymorphic_site	
FT		/note= "Polymorphic site absent in the variant protein	
FT	Domain	(AAMS2126)"	
FT		383..406	
FT		/label= "transmembrane_domain	
XX			
PN	WO200179561-A2.		
XX			
PD	25-OCT-2001.		
XX			
PE	17-APR-2001; 2001WO-US12575.		
XX			
PR	17-APR-2000; 2000US-0551744.		
PR	10-AUG-2000; 2000US-0636259.		
PR	19-OCT-2000; 2000US-0692077.		
XX			
PA	(LIGG/) LIGETT S B.		
XX	(SMAL/) SMALL K M.		
PI	Liggett SB, Small KM;		
XX			
WPI	2001-611728/70.		

Query Match 64.2%; Score 1529; DB 17; Length 334;
Best Local Similarity 71.8%; Pred. No. 1e-108;
Matches 301; Conservative 10; Mismatches 22; Indels 86; Gaps 3;

QY	33	TLTIVCLAGLMLTLTVGNLVIIIVTSSRALKAPQNLFLVSLASADILVATLVIPFSLA	92
DB	1	TLTIVCLAGLMLTLTVGNLVIIIVTSSRALKAPQNLFLVSLASADILVATLVIPFSLA	60
QY	93	NEVGVYVFGKACEIYALDVLFCSTSYHLCALISDRWSTQALFVLTATPPRIRA	152
DB	61	NEVGVYVFGKACEIYALDVLFCSTSYHLCALISDRWSTQALFVLTATPPRIRA	119
QY	153	IITVWVIAVISFPP-LISIEKKGCGGPPAPRCEINDQKMYVSSCIGSFAPCLI	211
DB	120	IIVVWVIAVISFPP-LISIEKKGCGGPPAPRCEINDQKMYVSSCIGSFAPCLI	179
QY	212	MIIVVYIYQIAKRRTFVPSRRGPDAVNAPEGTERRNGLGPESAGPGAEAPLPT	271
DB	180	NHLYVYRIYQIAKRRTFVPSRRGPDAVNAPEGTERRNGLGPESAGPGAEAPLPT	231
QY	272	QLNGAPGEPAPAGRPDTALDLBESSSSDHAERPGRPRPERGPRGKARASQVKPGDS	331
DB	232	-----	231
QY	332	LPRRPGAGTGTTPAGPGEYVGAASAKSMRQRREKRTFFVLAVIVGVVWCFPPF	391
DB	232	-----GQGEERAGAKASMRQRREKRTFFVLAVIVGVVWCFPPF	275
QY	392	FTVTLTAVGCVPRTLFFKFFFMGCYSSLNPIYITFIHNDPRRAKKTILCGDRRTY	450
DB	276	FTVTLTAVGCVPRYQVLFNFEMVGCYSSLNPIYITFIHNDPRRAKKTILCGDRRTY	334
RESULT 8			
AAU08334	ID	AAU08334 standard; Protein; 307 AA.	
XX	AC	AAU08334;	
XX	DT	21-MAY-2002 (first entry)	
XX	DE	Human alpha 2 adrenergic receptor.	
XX	KM	Human; D2 dopamine receptor; RGB-2; antiparkinsonian; hormone secretion;	
KM	KM	G-protein coupled receptor; schizophrenia; drug addiction;	
KM	KM	Parkinson's disease; Tourette syndrome; tardive dyskinesia;	
XX	XX	receptor; neuroleptic.	
OS	XX	Homo sapiens.	
XX	XX		
XX	Key	Location/Qualifiers	
FT	FT	37..59	
FT	FT	/note="Transmembrane domain I"	
FT	FT	71..96	
FT	FT	/note="Transmembrane domain II"	
FT	FT	108..129	
FT	FT	/note="Transmembrane domain III"	
FT	FT	151..173	
FT	FT	/note="Transmembrane domain IV"	
FT	FT	190..213	
FT	FT	/note="Transmembrane domain V"	
FT	FT	238..261	
FT	FT	/note="Transmembrane domain VI"	
FT	FT	269..292	
FT	FT	/note="Transmembrane domain VII"	
XX	XX		
XX	XX	US6277591-B1.	
XX	XX	21-AUG-2001.	
XX	XX	07-JUN-1995; 95US-0480390.	
XX	XX		

PR	20-NOV-1989;	88US-0438544.	
PR	09-NOV-1992;	92US-0973588.	
PR	18-NOV-1988;	88US-0273373.	
XX			
PA	(UYOR-) UNIV OREGON HEALTH SCI.		
PI	Cleveland O, Bunzow JR, Grandy DK, Machida CA;		
XX			
DR	WPI: 2001-54045/60.		
XX			
PT	New isolated mammalian G-protein coupled D2 dopamine receptor		
PT	polynucleotide, useful in gene therapy and for treating schizophrenia,		
PT	drug addiction, Parkinson's disease, Tourette syndrome and Tardive		
PT	dyskinesia		
PS	Claim 1; Fig 2; 71pp; English.		
XX			
CC	This invention relates to the nucleotide and polypeptide sequences of an		
CC	isolated mammalian G-protein coupled D2 dopamine receptor. This protein		
CC	binds to G proteins to inhibit cyclic AMP generation and hormone		
CC	secretion. The nucleotide sequences of the invention are useful as		
CC	oligonucleotide probes and to screen nucleic acid libraries containing		
CC	dopamine receptor nucleic acid sequences. These probes are also useful		
CC	in hybridisation methods to locate the dopamine gene positions in		
CC	various mammalian chromosomal maps or to determine the levels of mRNA or		
CC	receptor concentrations in a sample. The nucleic acid sequences can also		
CC	be used to identify dopamine receptor gene disorders (defective or		
CC	aberrant genes) and for in vitro diagnostic procedures on DNA samples in		
CC	given patients. A composition comprising the nucleic acid may be used		
CC	for increasing the concentration of the receptor or its gene in a		
CC	sample, or for in vivo uses such as gene therapy to render a defective		
CC	gene or gene product inactive or to provide an increased concentration		
CC	of dopamine receptor in a given location. The nucleotide sequences are		
CC	useful for treating disease conditions associated with abnormalities in		
CC	its structure, expression or concentration of the dopamine receptor or		
CC	its gene, where the disease conditions are selected from neurological		
CC	and other disorders, including schizophrenia, drug addiction,		
CC	Parkinson's disease, Tourette syndrome, and Tardive dyskinesia. The		
CC	nucleotide sequence is also useful for preparing the corresponding		
CC	transgenic animals, in particular nonhuman mammals and to inject		
CC	oocytes from frogs, which can then be conventionally used in binding or		
CC	second messenger analyses. This sequence represents the human alpha 2		
CC	adrenergic receptor which has homology to the rat D2 dopamine		
CC	receptor of the invention receptor of the invention.		
XX			
SQ	Sequence 307 AA:		
Query Match 61.1%; Score 1454.5; DB 22; Length 307;			
Best Local Similarity 65.7%; Pred. No. 4.5e-103;			
Matches 291; Conservative 7; Mismatches 8; Indels 137; Gaps 1;			
QY	1	MGSLQDPAGNANWNGTEAPGGAATPYSLQVTLTVCLAGLMLTLVFGNVLTAVTF	60
DB	1	MGSLQDPAGNANWNGTEAPGGAATPYSLQVTLTVCLAGLMLTLVFGNVLTAVTF	60
QY	61	SRAIKAPQNLFLVSLASADILVATLVIPFSLANWGVYVFGKACEIYALDVLFCSTSS	120
DB	61	SRAIKAPQNLFLVSLASADILVATLVIPFSLANWGVYVFGKACEIYALDVLFCSTSS	120
QY	121	IYHCAISLRWYSTQALFVLTATPPRIRKATITVWVIAVISFPP-LISIEKKGCGG	180
DB	121	IYHCAISLRWYSTQALFVLTATPPRIRKATITVWVIAVISFPP-LISIEKKGCGG	180
QY	181	POPAEPCEINDQKMYVSSCIGSFAPCLIMILVYRIYQIAKRRTVPPSRGPDVA	240
DB	181	POPAEPCEINDQKMYVSSCIGSFAPCLIMILVYRIYQIAKRRTVPPSRGPDVA	240
QY	241	APPGTERRPNGLGPESAGPGAEAPLPTQLNGAPGEPAPAGRPDTALDLBESSSD	300
DB	231	-----	230
QY	301	HAERPPGRPRPERGPRGKARASQVKPGDSLPRRPGATGTGTTPAGPGEYVGAAS	360

DB	228	-----	-GGRS-----	-AGSL 236
QY	333	PRRPGATGTGTPAGPGGEERVGANAKASRWGRHONREKFTVLAVIGVYVWCPPEPF	392	
DB	237	PRRAGA-----	-GGRS-----	272
QY	393	TYTITAVGCSVPRTLKFEFFMFGCNSLNPVITYTFNDFERAFKKILCRGDKRIY	450	
DB	273	TYTITAVGCSVPRTLKFEFFMFGCNSLNPVITYTFNDFERAFKKILCRGDKRIY	330	
RESULT 6				
AA848701				
ID	AA848701	standard; Protein; 334 AA.		
XX	AA848701;			
XX	AC			
XX	DT			
XX	05-JUN-1996	(first entry)		
XX	G-protein coupled rat alpha-2 adrenergic receptor R20 protein.			
DE	G-protein coupled receptor; ligand binding assay; transmembrane domain;			
XX	G-protein coupled receptor; ligand binding assay; transmembrane domain;			
XX	psychotic disorder; schizophrenia; dopamine; GPCR; adenosine; thrombin;			
KW	muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;			
KM	rhodopsin; opsin; odorant; cytomagalovirus.			
XX	Rattus rattus.			
OS	Rattus rattus.			
XX	WO9405695-A1.			
XX	17-MAR-1994.			
PD	09-SEP-1993;	93WO-US08528.		
XX	10-SEP-1992;	92US-0943236.		
XX	(UYNV) UNIV NEW YORK STATE.			
PA	Murphy RB, Schuster DI;			
XX	WPI; 1994-101120/12.			
DR	Polypeptides of G-coupled receptor proteins (GPRs) - useful for			
XX	binding GPR ligands or modulating GPR binding			
PT	Disclosure; page 74-75; 160pp; English.			
XX	Proteins AAR4685-R48758 represent a range of G-protein coupled receptor			
CC	proteins selected from CAMP, adenosine, muscarinic acetylcholine,			
CC	adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,			
CC	odorant, cytomagalovirus and other G-protein coupled receptors. The			
CC	receptor proteins were used to design polypeptides, pref. based on the			
CC	transmembrane domains, for use in G-protein coupled receptor ligand			
CC	binding assays. The polypeptide fragments retain biological activity			
CC	such as binding a GPR ligand or modulating GPR ligand binding to a GPR			
CC	(see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples			
CC	of polypeptide fragments). The polypeptide fragments can be used in			
CC	compositions for treating subjects suffering from a pathology related to			
CC	a GPR abnormality e.g. a psychotic disorder such as schizophrenia.			
XX				
SO	Sequence 334 AA:			
QY	Query Match	64.2%	Score 1529;	DB 15; Length 334;
DB	Best Local Similarity	71.8%;	Pred. No. 1e-108;	
	Matches 301; Conservative 10; Mismatches 22; Indels 86; Gaps			
QY	33	TLTIVCAGLTLVFGVNLVLIIVFTSRALKAPQNLFIIVLSASADITLVATLIPESLA	92	
DB	1	TLTIVCAGLTLVFGVNLVLIIVFTSRALKAPQNLFIIVLSASADITLVATLIPESLA	60	
QY	93	NEWGATVYEGKACETIYLLDVLEFCTSSIVHCAISLDKRYSTQVATIEYNLKRTPRIKA	152	
DB	61	NEWGATVYEGKACETIYLLDVLEFCTSSIVHCAISLDKRYSTQVATIEYNLKRTPRIKA	119	

QY	153	ITITVWISAVISFP- LITIEKKGGGGGPQPAEPCEINDQKVVYSSCIGSFEAPCLI	211
Db	120	ITVTVWISAVISFPPLLIETIEKKGGGGQGPAPPEPCKLINDQKVVYSSISISFEAPCLI	179
QY	212	MLIVYVRIOYAKRRRTVPSPSRGCPDAVAAPPGCTGRRRNGIGPERSAGPGGAEPAPT	271
Db	180	NHLVYVRIOYAKRRRTVPSPSRGCPDCAAPPGGARRRRNNAVGPENGAETAQ-----	231
QY	272	QLNGAPGEPAPGRDITDALDLESSSSDHAERPPEPRRRPERGPRGKGAARASQVKGDS	331
Db	232	-----	231
QY	332	LPKRGPAITGICTAAGPGEERVGAAKASRWGRONREKFEFVLAVVIGVYVCMPEPF	391
Db	232	-----QGGERRAGGAARASRWGRONREKFEFVLAVVIGVYVCMPEPF	275
QY	392	FTYTLTAVGCVPRPTLEKFEFVFCYCNSSINPVIYTIFFNDFRAAKTILGSDRKRIV	450
Db	276	FTYTLTAVGCVPRPTLEKFEFVFCYCNSSINPVIYTIFFNDFRAAKTILGSDRKRIV	334
RESULT 7			
AAW02673			
ID	AAW02673	standard; peptide; 334 AA.	
AC	AAW02673:		
DT	12-NOV-1996	(first entry)	
DE	G-protein coupled rat alpha-2 adrenergic receptor.		
XX			
XX	G-protein coupled receptor; ligand binding assay; transmembrane domain;		
KW	schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin;		
KM	muscarinic acetylcholine; endothelin; Domestoin; endocrine; rhodopsin;		
XX	odorant; cytomegalovirus; serotonergic.		
OS	Rattus rattus.		
PN	US508384-A.		
PD	16-APR-1996.		
PF	10-SEP-1992; 92US-0943236.		
PR	09-SEP-1993; 93US-0118270.		
PR	10-SEP-1992; 92US-0943236.		
PA	(UYNV) UNIV NEW YORK STATE.		
PI	Murphy RB, Schuster DJ:		
XX	WPI; 1996-208785/21.		
DR	New dopamine receptor peptide - useful as antipsychotic agent, e.g.		
XX	for treating schizophrenia		
PS	Disclosure; Column 73-76; 184pp; English.		
XX	Proteins AAW02657-W02730 represent a range of G-protein coupled receptor		
CC	(GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine,		
CC	adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,		
CC	odorant, cytomegaloviral and other GPR proteins. The receptor proteins		
CC	were used to design polypeptides, pref. based on the transmembrane		
CC	domains, for use in G-protein coupled receptor ligand binding assays.		
CC	The polypeptide fragments retain biological activity such as binding a		
CC	GPR ligand or modulating GPR ligand binding to a GPR (see		
CC	AAW02747-W02999 for examples of polypeptide fragments).		
CC	fragments can be used in compositions for treating subjects suffering		
CC	from a pathology related to a GPR abnormality e.g. a psychotic disorder		
CC	such as schizophrenia.		
QY	Sequence 334 AA:		

KW muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;
 KW rhodopsin; opsin; odorant; cytomagalovirus.
 XX
 OS Homo sapiens.
 XX
 PN W09405695-A1.
 XX
 PD 17-MAR-1994.
 XX
 PF 09-SEP-1993; 93MO-US08528.
 XX
 PR 10-SEP-1992; 92US-0943236.
 XX
 PA (UYNY) UNIV NEW YORK STATE.
 XX
 PI Murphy RB, Schuster DI;
 XX
 DR WPI; 1994-101120/12.
 XX
 PT Polypeptides of G-coupled receptor proteins (GPRs) - useful for
 binding GPR ligands or modulating GPR binding
 XX
 PS Disclosure; Page 73-74; 160pp; English.
 XX
 CC Proteins AAR4685-R48758 represent a range of G-protein coupled receptor
 CC proteins selected from cAMP, adenosine, muscarinic acetylcholine,
 CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
 CC odorant, cytomagaloviral and other G-protein coupled receptors. The
 CC receptor proteins were used to design polypeptides, pref. based on the
 CC transmembrane domains, for use in G-protein coupled receptor ligand
 CC binding assays. The polypeptide fragments retain biological activity
 CC such as binding a GPR ligand or modulating GPR ligand binding to a GPR
 CC (see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples
 CC of polypeptide fragments). The polypeptide fragments can be used in
 CC compositions for treating subjects suffering from a pathology related to
 CC a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
 XX
 SQ Sequence 330 AA;
 XX
 Query Match 64.8%; Score 1543; DB 15; Length 330;
 Best Local Similarity 74.4%; Pred. No. 8.7e-110;
 Matches 311; Conservative 7; Mismatches 12; Indels 88; Gaps 6;
 OY 33 TLTVLCLAGLMLTIVFGNVLTIIAVFTSRALKAPONLFLVSIASADILVATLVPFSLA 92
 DB 1 TLTVLVCLIA--CLSLTVFGNVLTIIAVFTSRALKAPONLFLVSIASADILVATLVPFSLA 58
 OY 93 NEVNGWYFGKAWCETIYALADVLEFCTSSIVHLCALISLDRWSTQAIENLKRTPRRIKA 152
 DB 59 NEVNGWYFGK-WCEIYIALDVLEFCTSSIVHLCALISLDRWSTQAIENLKRTPRRIKA 117
 OY 153 IITVWVISAVISFPLISIEKKGGGQPAPEPRCEINDOKWYVSISSIGSFAPCLIM 212
 DB 118 IITVWVISAVISFPLISIEKKGGGQPAPEPRCEINDOKWYVSISSIGSFAPCLIM 177
 OY 213 ILVYVRIYQIAKRRTRVPSRRGPDVAAPPGGTERPNGLCPERSAGFGA-EAPLPQTQ 272
 DB 178 -LVYVRIYQIAKRRTRVPSRRGPDVAAPPGGTERPNGLCPERSAGFGG----- 227
 OY 273 LMGAGEPAPAGPRDTDALDLESSSSDHAERPPGRRRERPGRGKARASQVAPGDSL 332
 DB 228 -----GRGRS-----ASGL 236
 OY 333 PRKGATIGTAPAGPGEERVGAAKASRWGRONREKRFETFLAVYIGVYVWQWPFEPF 392
 DB 237 PRRRAGA-----GGONREKRFETFLAVYIGVYVWQWPFEPF 272
 OY 393 TYTLTAVGCSVPTLFEKFEFWGYCNSLNVITYTFNHFRRAFKKILCRGDKRRTIV 450
 DB 273 TYTLTAVGCSVPTLFEKFEFWGYCNSLNVITYTFNHFRRAFKKILCRGDKRRTIV 330

AAW02672
 ID AAW02672 standard; peptide; 330 AA.
 XX
 AC AAW02672;
 XX
 DT 12-NOV-1996 (first entry)
 XX
 DE G-protein coupled human alpha-2 C10 adrenergic receptor.
 XX
 KW G-protein coupled receptor; ligand binding assay; transmembrane domain;
 KW schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin;
 KW muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;
 KW odorant; cytomagalovirus; serotonergic.
 XX
 OS Homo sapiens.
 XX
 PN USS508384-A.
 XX
 PD 16-APR-1996.
 XX
 PF 10-SEP-1992; 92US-0943236.
 XX
 PR 09-SEP-1993; 93US-0118270.
 PR 10-SEP-1992; 92US-0943236.
 XX
 PA (UYNY) UNIV NEW YORK STATE.
 XX
 PI Murphy RB, Schuster DI;
 XX
 DR WPI; 1996-208785/21.
 XX
 PT New dopamine receptor peptide - useful as antipsychotic agent, e.g.
 for treating schizophrenia
 XX
 PS Disclosure; Column 71-74; 184pp; English.
 XX
 CC Proteins AAW02657-W02720 represent a range of G-protein coupled receptor
 CC (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine,
 CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
 CC odorant, cytomagaloviral and other GPR proteins. The receptor proteins
 CC were used to design polypeptides, pref. based on the transmembrane
 CC domains, for use in G-protein coupled receptor ligand binding assays.
 CC The polypeptide fragments retain biological activity such as binding a
 CC GPR ligand or modulating GPR ligand binding to a GPR (see
 CC AAW02747-W02999 for examples of polypeptide fragments). The polypeptide
 CC fragments can be used in compositions for treating subjects suffering
 CC from a pathology related to a GPR abnormality e.g. a psychotic disorder
 CC such as schizophrenia.
 XX
 SQ Sequence 330 AA;
 XX
 Query Match 64.8%; Score 1543; DB 17; Length 330;
 Best Local Similarity 74.4%; Pred. No. 8.7e-110;
 Matches 311; Conservative 7; Mismatches 12; Indels 88; Gaps 6;
 OY 33 TLTVLCLAGLMLTIVFGNVLTIIAVFTSRALKAPONLFLVSIASADILVATLVPFSLA 92
 DB 1 TLTVLVCLIA--CLSLTVFGNVLTIIAVFTSRALKAPONLFLVSIASADILVATLVPFSLA 58
 OY 93 NEVNGWYFGKAWCETIYALADVLEFCTSSIVHLCALISLDRWSTQAIENLKRTPRRIKA 152
 DB 59 NEVNGWYFGK-WCEIYIALDVLEFCTSSIVHLCALISLDRWSTQAIENLKRTPRRIKA 117
 OY 153 IITVWVISAVISFPLISIEKKGGGQPAPEPRCEINDOKWYVSISSIGSFAPCLIM 212
 DB 118 IITVWVISAVISFPLISIEKKGGGQPAPEPRCEINDOKWYVSISSIGSFAPCLIM 177
 OY 213 ILVYVRIYQIAKRRTRVPSRRGPDVAAPPGGTERPNGLCPERSAGFGA-EAPLPQTQ 272
 DB 178 -LVYVRIYQIAKRRTRVPSRRGPDVAAPPGGTERPNGLCPERSAGFGG----- 227
 OY 273 LMGAGEPAPAGPRDTDALDLESSSSDHAERPPGRRRERPGRGKARASQVAPGDSL 332

DR N-PSDB; AA199917.
 XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 PT determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting
 PS a polymorphic site -
 XX
 PS Claim 48: Page 152-154; 163pp; English.
 XX
 CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
 CC or a site comprising (A) (99ggcgggcg) or (B) (9ggcgctcga) at
 CC positions 961-972 of (III). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
 CC polymorphic site which correlate to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
 CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
 CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
 CC rauwolfine, idazoxan, tolazoline, phenolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC levels). The present sequence is that of the human alpha-2AAR protein.
 XX
 SQ Sequence 450 AA:
 Query Match 100.0%; Score 2381; DB 22; Length 450;
 Best Local Similarity 100.0%; Pred. No. 1, 5e-173;
 Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSLQPDGAGNSMNGTEAPGGARATPSLOVTLTVCLAGLMLTLTFGNVLIIVAVFT 60
 DB 1 MSLQPDGAGNSMNGTEAPGGARATPSLOVTLTVCLAGLMLTLTFGNVLIIVAVFT 60
 QY 61 SVALKAPONLFLVSLASADIVATVTPESLANEVMGYEFGAKMCEITVIALDYLCTSS 120
 DB 61 SVALKAPONLFLVSLASADIVATVTPESLANEVMGYEFGAKMCEITVIALDYLCTSS 120
 QY 121 IVHLCALISLDKRWYSITQAIEXNLKRTPRRIKAIITVWVISAVISFPPLISIEKKGSGG 180
 DB 121 IVHLCALISLDKRWYSITQAIEXNLKRTPRRIKAIITVWVISAVISFPPLISIEKKGSGG 180
 QY 181 POPAPREINDOKWYVSSICISGFAPCLIMLVYRITQIAKRRTPVPSRRGPDAAVA 240
 DB 181 POPAPREINDOKWYVSSICISGFAPCLIMLVYRITQIAKRRTPVPSRRGPDAAVA 240
 QY 241 APPGCTERRPGLPERSAGCGAEAPLPTQINGARGPAPAPRDTALDIESSSSD 300
 DB 241 APPGCTERRPGLPERSAGCGAEAPLPTQINGARGPAPAPRDTALDIESSSSD 300
 QY 301 HAEPGRRRRERPRKRGKARASQVPGSLPRRGATGIGTPAAGGEEERVAAKAS 360
 DB 301 HAEPGRRRRERPRKRGKARASQVPGSLPRRGATGIGTPAAGGEEERVAAKAS 360
 QY 361 RMGRORNERKRFTEVLAVVIGVFCVFPFFFTYTLAAGCSVPRLTFEFPMEGCSNS 420
 DB 361 RMGRORNERKRFTEVLAVVIGVFCVFPFFFTYTLAAGCSVPRLTFEFPMEGCSNS 420
 QY 421 LNPVITITFNHDPRAAKKILCGDKRRIV 450
 DB 421 LNPVITITFNHDPRAAKKILCGDKRRIV 450

ID AAM52123 standard; Protein; 450 AA.
 XX
 AC AAM52123;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Human alpha-2AAR variant protein.
 KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
 KW polymorphic site; allelic variant; cardiovascular disease;
 KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
 KW phosphorylation; inositol phosphate; alpha-2AAR.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 251
 FT /note= "Wild-type Asn substituted by Lys"
 XX
 PN WO200179561-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 17-APR-2001; 2001WO-US12575.
 XX
 PR 17-APR-2000; 2000US-0551744.
 PR 10-AUG-2000; 2000US-0636259.
 PR 19-OCT-2000; 2000US-0692077.
 XX
 PA (LIGG/) LIGGETT S B.
 PA (SMAL/) SMALL K M.
 XX
 PI Liggett SB, Small KM;
 XX
 DR WPI: 2001-611728/70.
 DR N-PSDB; AA199918.
 XX
 PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 PT determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting
 PT a polymorphic site -
 XX
 PS Claim 48: Page 154-155; 163pp; English.
 XX
 CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
 CC or a site comprising (A) (99ggcgggcg) or (B) (9ggcgctcga) at
 CC positions 961-972 of (III). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
 CC polymorphic site which correlate to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
 CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
 CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
 CC rauwolfine, idazoxan, tolazoline, phenolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC levels). The present sequence is that of the human alpha-2AAR variant
 CC protein.
 XX
 SQ Sequence 450 AA:
 Query Match 99.7%; Score 2375; DB 22; Length 450;
 Best Local Similarity 99.8%; Pred. No. 4, 3e-173;
 Matches 449; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 15, 2003, 13:41:57 : Search time 47 Seconds
[without alignments]
1275.804 Million cell updates/sec

Title: US-09-636-259b-3

Perfect score: 2381
Sequence: 1 MGSIQPDAGNSWNGTEAPG.....HDFRRAFKILICNGRRKRV 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
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9: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
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12: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
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16: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*
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19: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
20: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
21: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
22: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
23: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2381	100.0	450	22	AA052122 Human alpha-2AR p
2	2375	99.7	450	22	AA052123 Human alpha-2AR v
3	1554	65.3	324	10	AA090552 Hamster beta-2 -ad
4	1543	64.8	330	15	AA048700 G-protein coupled
5	1543	64.8	330	17	AA02672 G-protein coupled
6	1529	64.2	334	15	AA048701 G-protein coupled
7	1529	64.2	334	17	AA02673 G-protein coupled
8	1454.5	61.1	307	22	AA008334 Human alpha 2 adre
9	1177	49.4	458	15	AA054834 Human derived adre
10	1164.5	48.9	461	22	AA052124 Human alpha-2CAR p

11	1152.5	48.4	457	22	AA052126 Human alpha-2CAR v
12	1124.5	47.2	450	22	AA052117 Human alpha-2AR t
13	1124.5	47.2	450	22	AA050990 Human alpha-2AR t
14	1124	47.2	447	22	AA052118 Human alpha-2AR t
15	1124	47.2	447	22	AA050989 Human alpha-2AR t
16	1092.5	45.9	487	22	AA014149 Human alpha-2 beta
17	1092.5	45.9	487	18	AA011804 Human alpha-2b adr
18	1046.5	44.0	330	15	AA048698 G-protein coupled
19	1046.5	44.0	330	17	AA02670 G-protein coupled
20	1029	43.2	330	15	AA048699 G-protein coupled
21	1029	43.2	330	17	AA02671 G-protein coupled
22	901	37.8	437	22	AA059035 Sheep/barnacle G-pr
23	681.5	28.6	379	18	AA033185 Balanus amphitrite
24	651	27.3	476	18	AA024089 Drosophila melanog
25	648	27.2	601	13	AA021991 Drosophila melanog
26	648	27.2	601	23	AA080701 Human pituitary do
27	648	27.2	601	23	AA017036 Human pituitary do
28	648	27.2	601	23	AA011497 Human pituitary do
29	626.5	26.3	443	11	AA005541 Human dopamine rec
30	626.5	26.3	443	20	AA01600 Human D2 dopamine
31	626.5	26.3	443	20	AA01600 Human D2 dopamine
32	626.5	26.3	443	22	AA076292 Human D2 dopamine
33	626.5	26.3	443	22	AA069075 Human retinal dopa
34	626.5	26.3	443	13	AA051019 Non-endogenous hum
35	626.5	26.3	443	12	AA011800 Human dopamine re
36	619.5	26.0	443	11	AA056348 Human dopamine re
37	617.5	25.9	415	11	AA005539 Rat D2 dopamine re
38	617.5	25.9	415	20	AA01598 Mouse dopamine D2
39	616.5	25.9	415	17	AA009388 Mouse dopamine D2
40	616	25.9	444	12	AA010544 Rat D2 dopamine re
41	616	25.9	444	17	AA009387 Rat D2 dopamine re
42	615.5	25.9	415	22	AA008332 Rat D2 dopamine re
43	615.5	25.9	415	23	AA051017 HTR1A protein. Ho
44	594	24.9	422	22	AA070249 Invertebrate octop
45	590	24.8	637	20	AA013445

ALIGNMENTS

RESULT 1
ID AAM52122 standard; Protein: 450 AA.
AC AAM52122;
DT 18-FEB-2002 (first entry)
DE Human alpha-2AR protein.
KW Human; genotyping: alpha-2b; alpha-2a; alpha-2c; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2AR.
XX
XX Homo sapiens.
OS
PN WO200179561-A2.
PD 25-OCT-2001.
PF 17-APR-2001; 2001WO-US12575.
PR 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
PA (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
XX Liggett SB, Small KM.
PI
DR WPI; 2001-611728/70.